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Sequence:

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Porcine S
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Murine SC
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                              Antipsori
                                                                                                                                                                                                                                                                                Human
Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis; callosities; keratosis pilaris; ichthyoses; eczema.
Adj 68833
Adn39180
Adn05153
Adn05158
Adn05158
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                                     ADR72880
ADY67588
AEC00353
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ADI39727
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ABG23378
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AAY16777
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AAR67888
ID AAR67888 standard; protein; 253 AA.
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 (revised)
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N-PSDB; AAQ81203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SYMB-) SYMBICOM AB.
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WO9500651-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-1994;
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09-AUG-1995
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 Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/AbsS/ABSWEB spool/U80995083/runat_10032006_152452_29654/app_query.fasta_1
-Q=/ABSS/ABSSWEB spool/U80995083/runat_10032006_152452_29654/app_query.fasta_1
-DB=A Geneseq -QFWT=fastan -SUFFIX=n2p.xag -MINMÄTCH=0.I -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX-Eblosum62 -TRANS=human40.cdi -LifST=45
-DOCALIGN=200 -THR SCORE=pct -THR_MAX=100 -THR_MINEN=0 -MAXIGN=2000000000 -MODE=LOCAL
-UOTFWT=ppto -NORMMext - HEAPSIZE=500 -MININEN=0 -MAXIGN=2000000000 -MOST=abss02p
-UOTFWT=ppto -NORMMext - LI 348 @runat_10032006_152452_29654 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBIACK=100 -LOONGLOG -DEV TIMEOUT=120
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Abb84421 Humann SCC
Aab84406 Humann SCC
Aau82740 Aminno aci
Abu07440 Protein d
Abr58471 Human str
Adb80484 Ovarian c
                                                                // Search time 37.2 Seconds
(without alignments)
2289.022 Million cell updates/sec
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                                                                                                                         ggatttccgggctccatggc......aagaaacacaaaacctcag 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
         GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                           protein search using frame plus n2p model
                                                                                                                                                                                                                       hits satisfying chosen parameters:
                                                                                                                                                                                                     2443163 segs, 439378781 residues
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Maximum Match 100%
Listing first 45 summaries
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AAW05383
ABB84421
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Fgapop 6.0 , E
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Result

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                                                          The enzyme encoded by this sequence is used in pharmaceutical, cosmetic and skin care products, especially to treat and prevent acne, xeroderma, or other hyperkeratotic conditions (e.g. callosities or keratosis pilaris), ichthyoses, psoriasis, eczema, etc. It is produced recombinantly following mammal, insect, plant, or microorganism transformation with plasmid pS507. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                    ATGGCAAGATCCCTTCTCCTGCCCCTGCAGATCTTACTGCTATCCTTAGCCTTGGAAACT
                                                                                                                                                                                                                                                                                                                                                    GCAGGAGAAGAAGCCCAGGGTGACAAGATTATTGATGGCGCCCCCATGTGCAAGAGGCTCC
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  acne or psoriasis, and for identification of
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                     Disclosure; Page 97; 137pp; English
                                                                                                                                                                                                                                                                              US-09-905-083A-30 (1-969) x AAR67888
                                                                                                                                                                                             1.16e-134
1364.00
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76.6%
skin disorders, e.g.
specific inhibitors.
                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                           Sequence 253 AA;
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Pred. No.:
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Human amyloid precursor protein protease (AAW05383) is involved in the processing or clearance of amyloid precursor protein to form beta-amyloid peptide. Its amino acid sequence was deduced from a cDNA clone (AAR39783) obtd. from a human lung library. Recombinant protease can be produced in transformed or transfected prokaryoric (partic. E. coli) or eukaryotic and testing of cyds. useful for treating or develop products for the design associated with beta-amyloid peptide, esp. Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human amyloid precursor protein protease - used to develop prode. for the treatment or diagnosis of associated conditions, esp. Alzheimer's disease.
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N-PSDB; AAT39783.
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135

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TGGGGAACTTTCCCTTGCGGCCAACCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
                                           315
                                                             GlySerAspThrLeuGlyAspArgArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer
                                                                                   CACCCCGGCTACTCCACACAGACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC
                                                                                                                                                                                                                                                                        LysaspleuleuGluasnSerMetleuCysalaGly1leProaspSerLysLysAsnala
                                            GCCAGTGATACGCTGGGCGACAGAGAGCTCAGAGGATCAAGGCCTCGAAGGTCATTCCGC
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(HANS/) HANSSON L.
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This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneuw chymotryptic enzyme (SCCE) or its variant, or variant in skin. The product of the invention is useful as a model or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a common or a paramaceutical formulation, and for the development of a diagnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of the pridermal hyperkeratosis, epidermal inflammation, dermal inflammation, pruritus, atopic dermatitis, eczema, acne and inherited skin diseases with epidermal hyperkeratosis. The mammal of the invention is also useful as a model for further studies of itch mechanisms and the testing of potential compounds and compositions for relieve of various skin diseases where itch is a component. This sequence represents the N-terminal cynomymous with human stratum corneum chymotryptic enzyme, SCCE synonymous with human kallikrein 7 (KLKP), used in the development of the
Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
                                                                                                                                                  Example 6; Page 37; 74pp; English
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Sequence 253 AA;

253 0 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: (1-253)US-09-905-083A-30 (1-969) x ABB84421 1.16e-134 1364.00 100.0% 100.0% Percent Similarity: Best Local Similarity: Query Match: DB: ò

È	16 ATG	AIGGCAAGAICCCITCICCIGCCCCTGCAGAICITACTGCTAICCTIAGCCTIGGAAACT 75
qq	1 Met	
Š	76 GCAC	GCAGGAGAAGAAGCCCCAGGGGGACACAAGATTATTGATGGCGCCCCCATGTGCAAGAGGCTCC 135
qq	21 Alac	AlaGlyGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
ò	136 CACC	CACCCATGGCAGGTGGCCCTGCTCAGTGGCAATCAGCTCCACTGCGGAGGCGTCCTGGTC 195
qa	41 His	
à	196 AATC	AATGAGCGCTGGGTGCTCACTGCCCGCCCACTGCAAGATGAATGA
Op	61 AsnC	
È	256 GGCZ	GGCAGTGATACGCTGGGCGACAGGAGCTCAGAGGATCAAGGCCTCGAAGTCATTCCGC 315
qa	81 Gly8	
ò	316 CACC	CACCCGGGCTACTCCACACAGAGACCCATGTTAATGACCTCATGCTGGAAGCTCAATAGC 375
QQ	101 His	
ر م	376 CAG	CAGGCCAGGCTGTCATCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAACCCCCT 435
, 요	121 Gln	
λ̈	436 GGAZ	GGAACCACTGTACTGTCTCCGGGTGGGGCACTACCACGAGCCCAGATGTGACCTTTCCC 495

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This invention describes a novel non-human transgenic mammal or mammalian sembryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCB) or its variant, operably linked to a promoter that drives expression of heterologous scce or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a cosmetic or a pharmaceutical formulation, and for the development of a diagnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for screening or identifying a
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compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of inflammatory skin diseases selected from diseases consisting of epidermal hyperkeratosis, epidermal inflammation, dermal inflammation, prunitus, atopic dermatitis, eczema, acne and inherited skin diseases with epidermal hyperkeratosis. The mammal of the invention is also useful as a model for further studies of itch mechanisms and the testing of potential compounds and compositions for relieve of various skin diseases where itch is a component. This sequence represents the human stratum corneum chymotryptic enzyme, SCCB which is a serine protease synonymous with human kallikrein 7 (KLK7) and is used in the development of the
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                                                                                                                                                                                                        protease; cancer; immune-related disorder; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
                                                                                                                                                                                                                        neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder; hypertension; psychotic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; enzyme.
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TTCACCAAGTGGATAAATGACACCATGAAAAGCATCGC 774
                                                                                                                                                                               Amino acid sequence of novel human protease #39.
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                                                                                        AAU82740 standard; protein; 253
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Length:
Matches:
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Mismatches:
Indels:
Gaps:

1.16e-134 1364.00 100.0% 100.0%

Percent Similarity: Best Local Similarity: Query Match: DB:

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                                                                  21 AlaGlyGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer
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                                                                                                                                                                                                  Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.
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                                                                                                                                                                                                                                                              Claim 1; Page 293-294; 416pp; English
                                                                                                    (ORIG-) ORIGENE TECHNOLOGIES INC.
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                                                                                                     cancer, useful
                                                                                                                         for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.
                                                                                                   genes which are differentially regulated in prostate
                                                                                                                                                                                       Claim 1; Page 351; 416pp; English.
                                       WPI; 2003-058520/05
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Jay G;
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Length: Matches: Conservative: Mismatches: Indels: Gaps: 1.16e-134 1364.00 100.0% 100.0% 76.6% Similarity: Sequence 253 AA; Percent Similarity: Query Match: Best

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ć	16	GCAGGAGAAGAAGCCCAGGGTGACAAGATTATTGATGGCGCCCCATGTGCAAGAGGCTCC 135	
QQ	21	21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40	
ò	136	136 CACCCATGGCAGGTGGCCCTGCTCAGTGGCAATCAGCTCCACTGCGGAGGCGTCCTGGTC 195	
QQ	41		
ò	196	AATGAGCGCTGGGTGCTCACTGCCGCCCACTGCAAGATGAATGA	
qq	61	61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTyrThrValHisLeu 80	

200 220 615 675 735 375 120 435 140 495 160 555 180 New polynuclectide and polypeptide useful for diagnosing and/or treating cancer, particularly ovarian cancer, and as a vaccine. Human stratum corneum chymotryptic enzyme - ovarian cancer clone 01676P. The invention relates to a novel isolated polynucleotide. The polynucleotides of the invention have cytostatic activity, and may have 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 316 CACCCCGGCTACTCCACACACACACTTAATGACCTCATGCTCGTGAAGCTCAATAGC 376 CAGGCCAGGCTGTCATCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAACCCCCT 436 GGAACCACCTGTACTGTCTCCGGCTGGGGCACTACCACGAGCCCAGATGTGACCTTTCCC TCTGACCTCATGTGGGTGGATGTCAAGCTCATCTCCCCCCAGGACTGCACGAAGGTTTAC 556 AAGGACTTACTGGAAAATTCCATGCTGTGCGCTGGCATCCCCGACTCCAAGAAAACGCC 616 TGCAATGGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCCTGCAAGGTCTGGTGTCC 676 TGGGGAACTTTCCCTTGCGGCCAACCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG Human; cytostatic; gene therapy; vaccine; cancer; ovarian cancer 241 PheThrLysTrp1leAsnAspThrMetLysLysHisArg 253 TTCACCAAGTGGATAAATGACACCATGAAAAAGCATCGC 774 Claim 2; Page 157-158; 169pp; English. Ŕ ABR58471 standard; protein; 253 02-OCT-2002; 2002WO-US031467. 02-OCT-2001; 2001US-0327135P. (first entry) Algate PA, Mannion J; WPI; 2003-372001/35. (CORI-) CORIXA CORP. WO2003029468-A1. Homo sapiens. 10-APR-2003. 07-JUL-2003 496 736 ABR58471; RESULT 8 

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use in gene therapy, and in a vaccine. The composition and methods are useful in diagnosing and/or treating cancer, particularly ovarian cance. The composition may also be used as a vaccine to prevent cancer. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                     GCAGGAGAAGACCCAGGGTGACAAGATTATTGATGGCGCCCCATGTGCAAGAGGCTCC
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ADB80484 standard; protein; 253

RESULT 9
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The invention relates to a method of detecting an ovarian cancer-
associated transcript in a cell from a patient, by contacting a
biological sample from the patient with a polynucleotide that selectively
hybridizes to a sequence at least 80% identical to any of one of 80
nucleic acid sequences given in the specification. The method is useful
in diagnoshig ownrian cancer and in identifying and using agents and/or
targets that inhibit ovarian cancer. The nucleic acid molecule,
polypeptide and the antibody may also be used in detecting ovarian
cancers, monitoring and early detection of relapse following treatment,
monitoring response to therapy, selecting patients for post-operative
chemotherapy or radiation therapy, in selecting mode of therapy,
and as vaccines. This sequence corresponds to one of the proteins used
for the detection method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 ATGCCAAGATCCCTTCCTGCCCCCTGCAGATCTTACTGCTATCCTTAGCCTTGGAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient polynucleotide that hybridizes to an ovarian cancer gene.
                                                                                    cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection.
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Matches:
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Mismatches:
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                                                           Ovarian cancer-associated protein #24.
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                                                                                                                                                                                                                                                                                                                                                                          BIOTECHNOLOGY INC
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27-AUG-2001; 2001US-0315297P.
05-SEP-2001; 2001US-031544P.
13-NOV-2001; 2001US-0350666P.
                                                                                                                                                                                                                                               18-JUN-2002; 2002WO-US019297.
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                              (first entry)
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N-PSDB; ADB80483
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ADB80484;
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                                                                                                                                                                                                                                                                                                                                                                                         mitochondrial; human; screening assay; diabetes mellitus;
Huntington's disease; osteoarthritis;
Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalogathy lactic acidosis and stroke; MELAS;
myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
osteopathic; ophthalmological; cytostatic.
                                                           AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTyrThrValHisLeu
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                                                                             CACCCCGCTACTCCACACACACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC
                                                                                                                                                                                                                                                                                                                                                                              mitochondrial protein as a therapeutic target SeqID639
                                                                                                                                                                                                                                                                                      TTCACCAAGTGGATAAATGACACCATGAAAAGCATCGC 774
                                                                                                                                                                                                                                                                                                                                   ADJ68833 standard; protein; 253
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2002US-0412418P.
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20-SEP-2002;
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This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various disease associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's heredicary optic neuropathy (LHON), mitochondrial concephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRP) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypoptide sequence is a human heart mitochondrial protein of the invention.
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                                                                                                                              Identifying a mitochondrial target for drug screening assays and for. treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer
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Matches:
Conservative:
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Indels:
  Gibson BW,
                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 639; 180pp; English.
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Zhang B,
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  Fahy ED,
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Ghosh SS,
Warnock DE;
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whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and methods are useful for disapnosing, polypeptides and methods are useful for disapnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atterosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistaion syndromes; scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present
                                       Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACCCATGGCAGGTGGCCCTGCTCAGTGGCAATCAGCTCCACTGCGGAGGCGTCCTGGTC 195
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Matches:
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                                                                                                                             Claim 12; SEQ ID NO 498; 1385pp; English.
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                                                                seful for diagnosing, prognosing or to nucleic acid in a biological sample.
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Best Local Similarity:
N-PSDB; ADN39179
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  141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160
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fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
                                                                                                                                                                                                                                                                                                   TGGGGAACTTTCCCTTGCGGCCAACCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG
                                              1CTGACCTCATGTGCGTGGATGTCAAGCTCATCCCCCCCAGGACTGCACGAAGGTTTAC
                                                                      CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory disease; autoimmune disease;
retinal neovascularistaion syndrome; scarring; uterine fibroid;
detection; diagnosis; prognosis; drug screening; drug targeting;
wound healing; contraception; cytostatic; cardiant; immunomodulatory;
vulnerary; gene therapy; vaccine.
                                                                                                                                556 AAGGACTTACTGGAAAATTCCATGCTGTGCGCTGGCATCCCCGACTCCAAGAAAACGCC
                                                                                                                                                                                                                 TGCAATGGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCCTGCAAGGTCTGGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:498
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3, Zlotnik A;
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Wilson KE,
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Murray R, Watson SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-NOV-2001; 2001US-0350666P.
21-NOV-2001; 2001US-0332464P.
23-NOV-2001; 2001US-03333439P.
03-DEC-2001; 2001US-0335394P.
14-DEC-2001; 2001US-0335394P.
14-DEC-2001; 2001US-0343349P.
10-JAN-2002; 2002US-0347319P.
10-JAN-2002; 2002US-0347349P.
20-FEB-2002; 2002US-035555P.
20-FEB-2002; 2002US-0359077P.
20-MAR-2002; 2002US-035907P.
12-APR-2002; 2002US-035907P.
12-APR-2002; 2002US-035907P.
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ADN39180

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ADN39180

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21 AlaGlyGluGluAlaGlnGlyA8pLysIleIleAspGlyAlaProCysAlaArgGlySer
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                                                                                                                                                                               76 GCAGGAGAAGAAGCCCAGGGTGACAAGATTATTGATGGCGCCCCCATGTGCAAGAGGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCCCCAGGACTGCACGAAGGTTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    616 TGCAATGGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCCTGCAAGGTCTGGTGTCC
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                                                                                                                                                               ATGGCAAGATCCCTTCTCCTGCCCTGCAGATCTTACTGCTATCCTTAGCCTTGGAAACT
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                       (1-253)
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                                                                                                                       US-09-905-083A-30 (1-969) x ADL06515
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100.0%
76.6%
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                      Percent Similarity:
Best Local Similarity:
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                                                           Query Match:
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                        615
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                                                                                                                                                                                                    TGGGGAACTITCCCTTGCGGCCAACCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG
                                                                                                   TGCAATGGTGACTCAGGGGGGACCGTTGGTGTGCAGAGGTACCCTGCAAGGTCTGGTGTCC
                                                                                                                          CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer
                      AAGGACTTACTGGAAAATTCCATGCTGTGCGCTGGCATCCCCGACTCCAAGAAAACGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; tumour-associated antigenic target; TAT; cell death; tumour;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antibody that binds to a tumor-associated antigenic target (TR polypeptide, useful for preparing a composition for diagnosing or treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human tumour-associated antigenic target (TAT) polypeptide #14
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J Z;
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21-AUG-2002; 2002US-0405445P.
23-SEP-2002; 2002US-0413192P.
15-OV-2002; 2002US-0419008P.
15-OV-2003; 2002US-0426847P.
02-JUL-2003; 2003US-048959P.
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Spencer SD, Wu TD, Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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N-PSDB; ADL06435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; cytostatic
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AC ADIO6
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AC ADIOC
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Homo sapiens

253

1.16e-134

Alignment Scores: Pred. No.:

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Example 2; SEQ ID NO 10; 102pp; English
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                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                  The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.
                                                                                      Wood WI;
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                                                                                                                                     New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis in a
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The invention relates to a novel method for detecting a plurality of kallikrein markers associated with ovarian cancer. The method comprises obtaining a sample from a patient and detecting in the sample a plurality of kallikrein markers, and optionally carbohydrate antigen CA125, wherein the kallikrein markers are selected from the group consisting of kallikrein 5, kallikrein 6, kallikrein 7, kallikrein 8, kallikrein 10 and kallikrein 11. The detected amounts of the kallikrein markers are compared with standard amounts. The method of the invention may be useful for detecting kallikrein markers associated with ovarian cancer in a patient and thus for detecting ovarian cancer, particularly epithelial ovarian cancinoma. The current sequence is that of the human ovarian which is a secreted serine protease and is encoded by DNA located at
SerAspLeuMetCysValAspValLysLeuileSerProGlnAspCysThrLysValTyr 180
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                                                                                                                   AAGGACTTACTGGAAAATTCCATGCTGCGCTGGCATCCCCCGACTCCAAGAAAACGCC
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                                                                                                       21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer
                                                                                                                                                      196 AATGAGCGCTGGGTGCTCACTGCCGCCCACTGCAAGAAGAATGAGTACACCGTGCACCTG
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Human kallikrein 7 protein SEQ ID NO:1.

19-MAY-2005

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The invention describes a method for detecting kallikrein polypeptides or their encoding polymocleocides, associated with neurodegenerative disease in a patient, by taking a sample from a patient, detecting/identifying one or more kallikrein polypeptides or polymocleocides encoding kallikrein polypeptides or polymocleocides encoding with an amount detected for a standard, where kallikrein polypeptides are chosen from kallikrein 7 and kallikrein 10. Nootropic; Neuroprotective; Cerebroprotective; Antiparkinsonian. The method is useful for diagnosing, detecting and monitoring a neurodegenerative disease in a subject. The method is also useful for assessing whether a patient is afflicted with or has a pre-disposition for Alzheimer's disease or frontotemporal chementia. The present sequence represents human kallikrein 7. Human tissue kallikreins are secreted serine proteases encoded by genes that are tandemly localized on chromosome 19, more specifically to region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting kallikrein polypeptides or their polynucleotides, associated with neurodegenerative disease in patient, by identifying kallikrein polypeptides or polynucleotides, in patient's sample, comparing detected amount with standard.
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kallikrein; serine protease; neurodegenerative disease;
neurological disease; nootropic; neuroprotective; Alzheimer's disease;
dementia.
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N-PSDB; ADY67589, ADY67590.
GENBANK; L33404, AF166330.
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US-09-905-083A-30

1 ggatttccgggctccatggc......aagaaacacaaaacctcag 969 Title: Perfect score: Sequence:

**BLOSUM62** Scoring table:

0.5 7.0 7.0 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext 283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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2: pir2:\*
3: pir3:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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serine proteinase SCCE precursor - human

N;Alternate names: stratum corneum chymotryptic enzyme C;Species: Homo sapiens (man) C;Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 09-Jul-2004

Cipacesion: A53968
R; Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A; Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme A; Reference number: A53968; MUID: 94308225; PMID: 8034709
A, Accession: A53968
A, Accession: A53968
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A, Residues: preliminary
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A, Cross-references: UNIPROT: P49862; UNIPARC: UPI000001BC4; GB: L33404; NID: G521214; PIDN: J, Genetics: A, Genetics: GDB: 7730
A, Map position: 7435-7435
A, Cross-references: CBB: 77730
A, Map position: T4798in; trypsin homology <TRY>

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76 GCAGGAGAAGAAGCCCAGGGTGACAAGATTATTGATGGCGCCCCCATGTGCAAGAGGCTCC 135

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A,Accession: C29746
A,Molecule type: DN1
A,Residues: 1-261 - CDR1>
A,Residues: 1-261 - CDR1>
A,Residues: 1-261 - CDR1>
A,Cross-references: UNIPROT: P15949; UNIPARC: UPI00000019EA; GB:M17985; NID:G193476; PIDN: 1, Experimental source: strain BALB/c, salivary gland
A,Experimental source: strain BALB/c, salivary gland
R,Blabber, M.; Isackson, P. J.; Bradshaw, R.A.
Bjochemistry 26, 6742-6749, 1987
A,Title: A complete cDNA sequence for the major epidermal growth factor binding protein and the complete cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lissue kallikrein (EC 3.4.21.35) mGK-9 precursor, submandibular - mouse
N,Alternate names: glandular kallikrein mGK-9; major epidermal growth factor-binding p:
(S,Speciaes: Mus musculus (house mouse)
(S,Speciaes: Musculus (house mouse)
(S,Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text_change 09-Jul-2004
(S,Accession: C29746; A29745; \(\bar{A}27120\); I70015
(S,Accession: C29746; A29745; \(\bar{A}27120\); IRChards, R.I.

Biochemistry 26, 6750-6756, 1987
A;Pitle: Mouse glandular kallikrein genes: identification and characterization of the shreference number: A90522; MUID:88107594; PMID:3322387
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|SerLyslleLeuGluGlyArgGluCysIleProHisSerGlnProTrpGlnAlaAlaLeu
                                                 GCCGCCCACTGCAAGATGAATGACACCGTGCACCTGGGCAGTGATACGCTG----
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                                                                                                                                                                                                                                                                                                                                               382 AGGCTGTCATCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAACCCCCTGGAACC
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                                CCCCTGCAGATCTTACTGCTATCCTTAGCCTTGGAAACTGCAGGAGAAGAAGCCCAGGGT
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C;Species: Mus musculus (house mouse)
C;Accession: 156559
R;Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nishin
A;Title: Expression and activity-dependent changes of a novel limbic-serine protease gen
A;Reference number: 156559; MUID:95348817; PMID:7623137
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-260 <RES>
A;Cross-references: UNIPROT:Q61955; UNIPARC:UPI00000292C5; GB:D30785; NID:g1648847;
C;Superfamily: trypsin; trypsin homology
F;33-252/Domain: trypsin homology <TRY>
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 70-122 <RES>
A,Fesidues: 70-122 <RES>
A,Crose-references: UNIPARC:UPI000016CE69; GB:M18610; NID:g198529; PIDN:AAA39353.1; PID:g
C,Genetics:
A,Introns: 16/1; 69/2; 165/1; 210/3
C,Superfamily: trypsin; trypsin homology
C,Superfamily: trypsin; trypsin homology
C,Reywords: hydrolase; serine proteinase
F;1-17/Domain: signal sequence #status predicted <RIO>
F;18-24/Domain: propeptide #status predicted <RO>
F;25-261/Product: tissue Rallikrein #status predicted <MAT>
F;25-231/Domain: trypsin homology <TRX>
F;55-233/Domain: trypsin homology <TRX>
F;55-233/Domain: trypsin homology <TRX>
F;55-213/Active site: His, Asp, Ser #status predicted
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NyAlternate names: glandular kallikrein
C;Species: Mus musculus (house mouse)
C;Daccies: Mus musculus (house mouse)
C;Dacciesion: S01971; 170023
R;Drinkwater, C.C.; Richards, R.I.
Nucleic Acids Res. 16, 10918, 1988
A;Title: Sequence of mGK-11, a mouse glandular kallikrein gene.
A;Reference number: S01971;
MUD:89083511; PMID:3205728
                                                                                                                                                                                                                                                                                                                                                                                                       221 GlyValLeuGlnGlyIleThrSerTrpGlyPheThrProCysGlyGluProLysLysPro
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                                                                    ACGAGCCCAGATGTGACCTTTCCCTCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCC
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A;Reference number: A29745; WUID:88107593; PMID:3322386
A;Accession: A29746
A;Rocession: A29745
A;Rocession: A29745
A;Rocession: A29745
A;Rocession: A29745
A;Rocession: A29745
A;Rocession: A29745
A;Rocession: Diply
B;Jubernan, R. B.; Blaber, M.; Server, A.C.; Nichols, R.A.; Shocter, B.M.
B;Jubernan, R. B.; Blaber, M.; Server, A.C.; Nichols, R.A.; Shocter, B.M.
B;Jubernan, R. B.; Blaber, M.; Server, A.C.; Nichols, R.A.; Shocter, B.M.
A;Recession: A27120
A;Ritle: Epidermal growth factor binding procein: identification of a different protein. A;Reference number: A27120; MUID:87299636; PMID:3304419
A;Recession: A27120
A;Residues: 25-54;112-124, X., 126-130;165-184, X., 186-187, X., 189-192 <1SA>
A;Residues: 25-54;112-124, X., 126-130;165-184, X., 186-187, X., 189-192 <1SA>
A;Cros-references: UNIPARC;UPTO000175BEP; NIPARC;UPTO000175BFP;
B;BYans, B.A.; Drinkwater, C.C.; Richards, R.I.
J; Liller, Mouse glandular Kallikrein genes: Structure and partial sequence analysis of th A;Reference number: 155260; MUID:87250386; PMID:336794
A;Reference number: 155260; MUID:87250386; PMID:336794
A;Reference number: 155260; MUID:87250386; PMID:336794
A;Recension: 170015
A;Residues: 70-122 <RRS
A;Rccss-references: UNIPARC;UPT000016CE67; GB:M18608; NID:g198500; PIDN:AAA39351.1; PID:Comment: This sequence is one of approximately twenty-five members of a gene family of C;Comment: This sequence #status predicted <81G>
C;Comment: This sequence #status predicted <81G>
F;1-18/Domain: signal sequence #status predicted <81G>
F;1-24/Domain: signal sequence #status predicted <81G>
F;2-221/Domain: trypsin homology <RRY>
F;2-221/Pomain: trypsin homology <RRY>
F;2-221/Pomain: signal sequence #status predicted <81G>
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41 AlaValTyrArgTyrAsnGluTyrIleCysGlyGlyValLeuLeuAspAlaAsnTrpVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 GGCGACAGGAGA-----GCTCAGAGGATCAAGGCCTCGAAGTCATTCCGCCACCCGGC
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Best Local Similarity:
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Aintrons: 16/1; 69/2; 165/1; 210/3
Gisuperfamily: trypsin; trypsin homology
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Cisuperfamily: trypsin; trypsin factor; hydrolase; serine proteinase; submandibular glar
Ciscapordes: glycoprotein; growth factor; hydrolase; serine proteinase; submandibular glar
Ciscapordes: glycoprotein; growth factor; predicted csig>
Fils-25100main: segment B1 cdB1>
Fils-26100main: segment A cdAA>
Fils-26100main: segment A cdAA>
Fils-26100main: segment C cdCC>
Fils-2610main: segment C cdCC>
Fils-2610
                                                                                                                                                  mouse submaxillary gland 7 S
                               GB:X00472; NID:954260; PIDN:CAA25154.1;
                                                                                                                                                                                                               A,Accession: A92341
A,Molecule type: protein
A,Molecule type: protein
A,Residues: 25-107,112-261 <THO>
A,Residues: 25-107,112-261 <THO>
A,Cross-references: UNIPARC:UPI0000112CC7
A,Experimental source: outbred strain Swiss Webster
A,Experimental source: outbred strain Swiss Webster
C,Comment: 7S nerve growth factor is composed of two alpha chains, a beta dimer co
C,Comment: 7S nerve growth factor is composed of two alpha chains, a beta dimer co
C,Comment: The active form of the gamma chain occurs naturally as combinations of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::: ||||||| GluproSeralaGlnHisArgPheValSerLysAlaIleProHisProGlyPheAsnMet 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 AlaHisCysTyrAspAspAsnTyrLysValTrpLeuGlyLysAsnAsnLeuPheLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 AGTGGCAATCAGCTCCACTGCGGAGGCGTCCTGGTCAATGAGCGCTGGGTGCTCACTGCC
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112
42
87
16
                                                      A; Experimental source: inbred strain DBA/2J
R;Thomas, K.A.; Baglan, N.C.; Bradshaw, R.A.
D. Biol. Chem. 256, 9156-9166, 1981
A;Title: The amino acid sequence of the gamma-subunit of
A;Reference number: A92341; MUID:81264363; PMID:7263706
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Residues: 127-202,'E',204-261 <HOW>
Cross-references: UNIPARC:UPI00000E6698;
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A;Map position: 7
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C;Species: Mus musculus (house mouse)
C;Date: 18-Dec-1981 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C;Accession: A91005; A90949; A93810; A92341; A00942; A21093; A22705
R;Evans, B.A.; Richards, R.I.
BMBO J. 4, 133-138, 1985
A;Title: Genes for the alpha and gamma subunits of mouse nerve growth factor are contiguable and mouse number: A91005; MUID:85257431; PMID:3848399
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M.; Gross, K.W.
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A;Title: Use of a cDNA recombinant for the gamma-subunit of mouse nerve growth factor A;Reference number: A93510; MUID:84169573; PMID:6200835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         growth
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                                                                                                                                                         GCCCACTGCAAGATGAATGAGTACACCGTGCACCTGGGCCAGTGATACGCTGGGCGACAGG 279
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                                                                                                                                                                                            64 AlaHisCysHisValSerGlnTyrAsnValTrpLeuGlyLysThrLysLeuPheGlnArg
                                                                  224 HisGlyIleThrAlaTrpGlyProlleProCysGlyLysProAsnThrProGlyValTyr
                               .60 AGTGGCAATCAGCTCCACTGCGGAGGCGTCCTGGTCAATGAGCGCTGGGTGCTCACTGCC
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A;Molecule type: DNA
A;Cross-references: UNIPROT:P00756; UNIPARC:UPI0000020EF5
B;Ullrich, A.; Gray, A.; Wood, W.I.; Hayflick, J.; Seeburg, P.H.
DNA 3, 387-392, 1984
A;Title: Isolation of a cDNA clone coding for the gamma-subunit of mouse
A;Reference number: A90949; MUID:85076169; PMID:6548955
A;Accession: A90949
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A; Residues: 1-261 <ULL>
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A; Molecule type: mRNA
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219

273

83

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A;Accession: A20091; FULD: BDD9488U; FMID: 6094547
A;Mocleale type: DNA
A;Molecule type: DNA
A;Residues: 1-246 <CRA>
A;Cross-references: UNIPARC: UNIPARC: UPI00001376DD; GB: J00778; NID: g206507; PIDN: J4;Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue 17(
B;MacDonald, R.J.; Stary, S.J.; Swift, G.H.
J. Biol. Chem. 257, 9724-9732, 1982
A;Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of A;Reference number: A00948; MUID: 82265624; PMID: 6896710
A;Reference number: A00948; MUID: 82265624; PMID: 6896710
A;Residues: 1-246 <MAC>
A;Residues: 1-246 <MAC>
A;Cross-references: UNIPARC: UPI00001376DD; GB: J00778; NID: g206507; PIDN: AAA988518.1; PID: C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        trypsin (EC 3.4.21.4) I precursor - rat
NyAlternate names: trypsinogen I
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Dec-1982 Esequence_revision 17-Dec-1982 #text_change 09-Jul-2004
C;Accession: B22657; A00948
R;Craik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.
J. Biol. Chem. 259, 14255-14264, 1984
A;Itile: Structure of two related rat pancreatic trypsin genes.
A;Reference number: A22657; MUID:85054880; PMID:6094547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  654
                                                                                                                                                                                  202 MetAspGlyGlyLysAspIleCysLysGlyAspSerGlyGlyProLeuIleCysAspGly 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aintrons: 14/1; 67/2; 152/1; 197/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-23/Domain: activation peptide #status predicted <APT>
F;24-246/Product: trypsin I #status predicted <ENZ>
                                                                                                                                                      ---GGCGACAGGAGAGCTCAGAGGATCAAGGCCTCGAAGTCATTCCGCCACCCCGGCTAC 327
                                                                                                                                                                                                                                                        328 TCCACA-----CAGACCCATGTTAATGACCTC 354
                                                                                                                                                                                                                                                                                                    102 AsnLeuAspIleIleLysAsnHisThrArgLysProGlyAsnAspTyrSerAsnAspLeu 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       475 AGCCCAGATGTGACCTTTCCCTCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCCC 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          535 CAGGACTGCACGAAGGTTTACAAGGACTTACTGGAAAATTCCATGCTGTGCGCTGGCATC 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               655 ACCCTGCAAGGTCTGGTGTCCTGGGGAACTTTCCCTTGCGGCCAACCCAATGACCCAGGA 714
     42 ValTyrHisPheAsnGluProGlnCysGlyGlyValLeuIleHisProSerTrpValIle 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              715 GTCTACACTCAAGTGTGCAAGTTCACCAAGTGGATAAATGACACCATGAAAAAGCAT 771
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A;Experimental source: prostate
R;Elmoujahed, A.; Gutman, N.; Brillard, M.; Gauthier, F.
FEBS Lett. 265, 137:140, 1990
A;Title: Substrate specificity of two kallikrein family gene products isolated from the
A;Reference number: S10698; MUID:90306305; PMID:2194829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A34079
tissue kallikrein (EC 3.4.21.35) P1 precursor - rat
tissue kallikrein (EC 3.4.21.35) P1 precursor - rat
N;Alternate names: kallikrein-related proteinase k8
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004
C;Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004
C;Accession: A34079; B10700
R;Brady, J.M.; Wines, D.R.; MacDonald, R.J.
Biochemistry 28 5203-5210, 1989
Biochemistry 28 5203-5210, 1989
A;Title: Expression of two kallikrein gene family members in the rat prostate.
A;Reference number: A34079; MUID:89352606; PMID:2765531
A;Accession: A34079
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C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;25-253/Domain: trypsin homology <TRY-
F;25-111/Product: tissue kallikrein Pl light chain #status experimental <WAT1-
F;112-261/Product: tissue kallikrein Pl heavy chain #status experimental <WAT2-
F;65,120,213/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                9
204 GlyGlyLysAapThrCysLysGlyAspSerGlyGlyProLeuIleCysAapGlyValLeu 223
                                                                                                                                                                                                                                                                             720
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                                                                                                          ---SerArgileIleGlyGlyPheAsnCysGluLysAsnSerGlnProTrpGlnValAla
                                                                             TGCACGAAGGTTTACAAGGACTTACTGGAAAATTCCATGCTGTGCGCTGGCATCCCCGAC
                                                                                                                                                                          601 TCCAAGAAAACGCCTGCAATGGTGACTCAGGGGGACCGTTGGTGCAGAGGTACCCTG
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Mismatches:
Indels:
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A,Residues: 25-43;112-138 <ELM>
A;Cross-references: UNIPARC:UPI0000175BEB;
A;Experimental source: submaxillary gland
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43.2%
31.6%
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A,Status: preliminary
A,Molecule type: DNA; mRNA
A,Residues: 1-261 <BRA>
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|GluAlaAlaTyrProGlyGluIleThrSerSerMetIleCysValGlyPheLeuGluGly 191
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                                                                                                                                                                                                                                    16 ATGGCAAGATCCCTTCTCCTGCCCTGCAGATCTTACTGCTATCCTTAGCCTTGGAAACT
F;24-239/Domain: trypsin homology <TRX>
$130-160, 48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F;63,107,200/Active site: His, Asp, Ser #status predicted
F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
                                                                                                                                                                                                                                                                                           74 GlyGluHisAsnIleAsnValLeuGluGlyAspGlu-----GlnPheileAsnAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIGACCTTICCCTCTGACCTCATGIGCGIGGATGICAAGCTCATCTCCCCCCAGGACTGC
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Best Local Similarity:
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A/Gene: mGK-1
A/Gene: mGK-1
A/Gene: mGK-1
A/Gene: mGK-1
A/Jutrons: 16/1; 165/1; 210/3
A/Jutrons: 16/1; 17/95in; trypsin homology
C;Superfamily: trypsin; trypsin homology
C;Reywords: glycoprotein; hydrolase; saliva; serine proteinase; submandibular gland;
F;19-24/Domain: signal sequence #status predicted <APT>
F;19-24/Domain: activation peptide #status predicted <APT>
F;25-25/JDomain: trypsin homology <TRX>
F;25-25/JDomain: trypsin homology <TRX>
F;25-25/JDomain: trypsin homology <TRX>
F;21-173,50-66,152-219,184-198,209-234/Pisulfide bonds: #status predicted
F;11-173,50-66,152-219,184-198,209-234/Pisulfide bonds: #status predicted
F;102/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                              A;Accession: A00941
A;Molecule type: DNA
A;Residues: 1-261 ANANA
A;Residues: 1-261 ANANA
A;Cross-references: UNIPROT: P00755; UNIPARC: UPI0000001A0C; GB: V00829; NID: 952775;
A;Experimental source: Quakenbush inbred strain
C;Comment: mGK-1 belongs to a family of 25 to 30 homologous kallikrein genes.
C;Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to rel
C;Genetics:
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Rimason, A.J.; Evans, B.A.; Cox, D.R.; Shine, J.; Richards, R.I. Nature 303, 300-307, 1983
A;Title: Structure of mouse kallikrein gene family suggests a role A;Reference number: A00941; MUID:83219214; PMID:6602295
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Lissue kallikrein (EC 3.4.21.35) submandibular precursor - mouse
N,Alternate names: glandular kallikrein; kininogenin
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A25606, S0661
R;van Leeuwen, B. H.; Evans, B.A.; Tregear, G.W.; Richards, R.I.
R;van Leeuwen, B. H.; Evans, B.A.; Tregear, G.W.; Richards, R.I.
A;Title: Mouse glandular kallikrein genes. Identification, structure, and expression of A;Reference number: A25606, MUID:86168299; PMID:3007510
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   Conservative:
Mismatches:
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Best Local Similarity:
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A; Residues: 1-261 <VAN>
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A; Residues: 1-261 < CHS>
A; Crosex-references: UNIPROT: P36373; UNIPARC: UPI000012DEE6; GB:M19647; GB:J02837; NID:g20
B; Elmoujahed, A.; Gutman, N.; Brillard, M.; Gauthier, F.
FEBS Lett. 265, 137-140, 1990
A; Title: Substrate specificity of two kallikrein family gene products isolated from the A; Reference number: S10698; MUID:90306305; PMID:2194829
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Listane kallikrein (EC 3.4.21.35) 7 precursor, submandibular - rat
Listane kallikrein (EC 3.4.21.35) 7 precursor, submandibular - rat
NyAlternate names: glandular prokallikrein 7, submandibular; proteinase A
NyAlternate nareses: Rattus norvegicus (Norway rat)
C;Species: Al-Mar-1990 #sequence revision 31-Mar-1990 #text change 09-Jul-2004
C;Accession: A31136; S10699; D41429; B41429; S09315
C;Accession: A31136; Ando, L.
Biochemistry 27, 7189-7196, 1988
A;Title: Molecular cloning and characterization of two rat renal kallikrein genes.
A;Reference number: A31136; MUID:89088074; PMID:2849988
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Arch. Biochem. Biophys. 278, 342-349, 1990

A;Title: The expression of two kallikrein gene family members in the rat kidney.

A;Reference number: S09315; MUID:90225801; PMID:2183721

A;Accession: S09315

A;Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                           243
                                                                                                                                                                              223
                                                                                                                                                                                                                                                    CAAGGTCTGGTGTCCTGGGGAACTTTCCCTTGCGGCCAACCCAATGACCCAGGAGTCTAC 720
||| ||| ||| ||| CysAspLysAlaTyrValGlnLysValThrAspValMetLeuCysAlaGlyValLysGly
                                                                                                                                                        224 GlnGlyLeuThrSerTrpGlyTyrAsnProCysGlyGluProLysLysProGlyValTyr
                                                                                                       601 TCCAAGAAAACGCCTGCAATGGTGACTCAGGGGGACCGTTGGTGCAGAGGTACCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                   721 ACTCAAGTGTGCAAGTTCACCAAGTGGATAAATGACACCATGAAAAAGCAT 771
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F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-261/Product: tissue prokallikrein 7, submandibular #status
F;25-253/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261
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A,Molecule type: protein
A,Rosidues: 112-133 - KAT>
A,Cross-references: UNIPARC:UPI0000175BE5
A,Accession: B41429
A,Rolecule type: protein
A,Residues: 25-34, 'D', 36-45, 'S',47-67,'X',69-75 < KAZ>
A,Cross-references: UNIPARC:UPI0000175BE5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
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A;Cross-references: UNIPARC:UP10000175BE7
C;Superfamily: trypsin; trypsin homolomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.65e-39
552.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: S10698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores
Pred. No.:
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201 AspMetAspGlyGlyLysAspThrCysAlaGlyAspSerGlyGlyProLeuIleCysAsp
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547.50
56.7%
42.9%
30.8%
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                                  for residue 105
A;Cross-references: UNIPROT:P15947; UNIPARC:UP10000161DD6; GB:M13498
A;Experimental source: renal
A;Note: the authors translated the codon GTC for residue 57 as Ala, CTC for resi
R;Murakami, K.; Ikigai, H.; Nggumo, N.; Tomita, M.; Shimamura, T.
ESES Lett. 257, 400-402, 1389
A;Title: A cytocidal tissue kallikrein isolated from mouse submandibular glands.
A;Reference number: S06660; MUID:90060365; PMID:2581286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCCTGCTCAGTGGCAATCAGCTCCACTGCGGAGGCGTCCTGGTCAATGAGCGCTGGGTG 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::: |||||||
81 LeuGluAspGluProSerAlaGlnHisArgLeuValSerLysAlaIleProHisProAsp 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCATGCTCGTGAAGCTCAATAGCCAGGCCAGGCTGTCATCCATGGTGAAGAAGTCAGG 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGCCCTCCCGCTGCGAACCCCCTGGAACCACCTGTACTGTCCCGGCTGGGGCACTACC 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuProThrGluGluProLysLeuGlySerThrCysLeuAlaSerGlyTrpGlySerIle 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 ValGlnSerArgIleValGlyGlyPheAsnCysGluLysAsnSerGlnProTrpGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        532 CCCCAGGACTGCACGAAGGTTTACAAGGACTTACTGGAAAATTCCATGCTGTGCGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 CTGCAGATCTTACTGCTATCCTTAGCCTTGGAAACTGCAGGAGAAGAAGCCCAG--
                                                                                                                                                                                                      Aintrons: 16/1; 69/2; 165/1; 210/3
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin bomology
C; Keywords: hydrolase; serine proteinase
F; 1-24/Domain: signal sequence #status predicted <SIG>F; 25-261/Product: tissue kallikrein #status predicted <MAT>F; 25-253/Domain: trypsin homology <TRY>F; 55, 120, 213/Active site: His, Asp, Ser #status predicted
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105
47
92
16
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                             A;Accession: S06661
A;Molecule type: protein
A;Residues: 165-174 <MUR>
A;Cross-references: UNIPARC:UPIO000175BEE
C;Genetics:
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551.00
58.5%
40.4%
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                                                                                                                                                                                           A;Gene: mGK-6
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Lissue kallikrein (BC 3.4.21.35), prostatic, precursor - dog
NyAlternate names: kallikrein homolog
C;Species: Canis lupus familiaris (dog)
C;Date: 21.Feb-1992 #sequence revision 21-Feb-1992 #text_change 09-Jul-2004
C;Accession: A37938; S00613; A61555
R;Chapdelaine, P.; Gauthier, E.; Ho-Kim, M.A.; Bissonnette, L.; Tremblay, R.R.; Dube, J.)
By Cell Biol. 10, 49-59, 1991
A;Title: Characterization and expression of the prostatic arginine esterase gene, a canir
A;Reference number: A37938; MUID:91119675; PMID:1991049
                                                                                                                                                                                                                                                                                                                                                240
220
                               711
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                                                                                                                    TTACTGCTATCCTTAGCCTTGGAAACTGCAGGAGAAGAAGCCCAG---GGTGACAAGATT 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 AATCAGCTCCACTGCGGAGGCGTCCTGGTCAATGAGCGCTGGGTGCTCACTGCCGCCCAC 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45
                                 GGTACCCTGCAAGGTCTGGTGTCCTGGGGAACTTTCCCTTGCGGCCAACCCAATGACCCA
                                                   221 GlyValLeuGlnGly11eThrSerTrpGlyProSerProCysGlyLyBFroAsnValPro
                                                                                                  712 GGAGTCTACACTCAAGTGTGCAAGTTCACCAAGTGGATAAATGACACCATGAAAAAGCAT
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6 LeuCysLeuAlaMetSerLeuGlyTrpThrdJyAlaGluProHisPheGlnProArgIle
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GGCGACAGGAGAGCTCAGAGGATCAAGGCCTCGAAGTCATTCCGCCACCCCGGCTACTCC 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                     103 ATTATTGATGGCGCCCCATGTGCAAGAGGCTCCCACGCATGGCAGGTGGCCCTGCTCAGT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AlaArgvalAlaThrvalAlaLeuProSerSerCysAlaProAlaGlyThrGlnCysLeu 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 LeuAspAlaProLeuLeuProGlnAlaAspCysGluAlaSerTyrProGlyLysIleThr 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   631 GGGGGACCGTTGGTGCAGAGGTACCCTGCAAGGTCTGGTGTCCTGGGGAACTTTCCCT 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 IleValGlyGlyTyrThrCysGlnGluAsnSerValProTyrGlnValSerLeuAsnSer 43
  F;24-246/Product: trypsin II #status predicted <ENZ>
F;24-239/Domain: trypsin homology <TRY>
F;24-239/Domain: trypsin homology <TRY>
F;30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F;53.107,200/Active site: His, Asp, Ser #status predicted
F;57,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  691 TGCGGCCAACCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAGTTCACCAAGTGGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 CysAlaLeuProAspAsnProGlyValTyrThrLysValCysAsnTyrValAspTrplle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCATGGTGAAGAAGTCAGGCTGCCCTCCCGCTGCGAACCCCCTGGAACCACCTGTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  571 AATTCCATGCTGTGCGCTGGCATCCCCGACTCCAAGAAAAACGCCTGCAATGGTGACTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 GlyGlyProValValCy8A8nGlyGluLeuGlnGlyIleValSerTrpGly---TyrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCTCCGGCTGGGGCACTACCACGAGCCCAGATGTGACCTTTCCCTCTGACCTCATGTGC
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108
38
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                        US-09-905-083A-30 (1-969) x TRRT2
                                                                                                                                                1.32e-38
541.50
59.8%
44.3%
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                                                                                                                                                                                               Percent Similarity:
                                                                                                                                   Alignment Scores:
Pred. No.:
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A;CroBe-references: UNIPROT: P00763; UNIPARC: UP10000172AAB
A;CroBe-references: UNIPROT: P00763; UNIPARC: UP10000172AAB
R;MacDonald, R.J.; Stary, S.J.; Swift, G.H.
J. Biol. Chem. 257, 9724-9732, 1382
A;Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences A;Reference number: A00948; MUID: 82265624; PMID: 6896710
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C;Comment: The trypsin II mRNA is present in much lower quantities than the try
C;Genetics:
A;Introns: 14/1; 67/2
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; panctess; protesin digestion; serine proteinase; zymogen
F;1-15/Domain: squan sequence #status predicted <&IG>
F;16-23/Domain: activation peptide #status predicted <APT>
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NyAlternate names: trypsinogen II
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Apr-1983 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: A22657; A00949
C;Accession: A22657; A00949
J;Biol. Chem. 259, 14255-14264, 1984
A;Title: Structure of two related rat pancreatic trypsin genes.
A;Reference number: A22657; MUID:85054880; PMID:6094547
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|ValTyrThrGlnLysValThrLysPheMetLeuCysAlaGlyValLeuGluGlyLysLys
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                                                                                                                                                                                                                                                                                                                            370 AATAGCCAGGCCAGGCTGTCATCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GITTACAAGGACTTACTGGAAAATTCCATGCTGTGCGCTGGCATCCCCGACTCCAAGAAA
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                                                                                                        CysAlaAsnSerAsnCysGluValTrpLeuGlyArgHisAsnLeuSerGluSerGluAsp
                                                                                                                                                     280 AGAGCICAGAGGAICAAGGCCICGAAGICATICCGCCACCCCGGCTACICCACA----
                                                                                                                                                                                                                                       ------CAGACCCATGTTAATGACCTCATGTCGTGAAGCTC
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A; Residues: 9-246 < MA(
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270

82

450

160

630 200

222

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Pillos. Trans. K. Soc. Lond. B257, 77-87, 1970

A)Reference number: A30755

A;Contents: annotation; revisions

R;Titani, K.; Exicason, L.H.; Neurath, H.; Walsh, K.A.

B;Contents: annotation; revisions

R;Title: Amino acid sequence of dogfish trypsin.

A;Reference number: A00950; MUID:75146445; PMID:1092332

A;Contents: annotation; revisions

A;Contents: annotation; revisions

A;Contents: annotation; revisions

A;Note: the sequence agrees with that shown

R;Bode, W.; Schwager, P.

J, Mol. Biol. 98, 693-717, 1975

A;Title: The refined crystal structure of bovine beta-trypsin at 1.8 angstrom resolution.

A;Reference number: A92954; MUID:76072097; PMID:512

C;Comment: Trypsinogen is synthesized in the acinar cells of the pancreas

C;Comment: Trypsinogen is synthesized and second after Agriculation activation peptide #status experimental <APT>

F;1-222/Domain: trypsin homology <ARY:

F;7-222/Domain: trypsin homology <ARY:

F;7-222/Domain: trypsin homology <ARY:

F;7-111,132-229/Product: alpha-trypsin #status experimental

F;6-7/Cleavage site: Lys-116,122-189; L34-168; L34-168; L34-168; L34-147, L31-216; L32-189; L34-168; L34-168; L34-168; L34-147, L31-216; L32-189; L34-168; L34-1
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   146 TrpGiyAsnThrLeuSerSerGlySerLeuTyrProAspValLeuGlnCysLeuAsnAla 165
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                                                                                                                                                                                                                                                                                                                                                                                                                           166 ProValLeuSerSerGerGlnCysSerSerAlaTyrProGlyArgIleThrSerAsnMet 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       640 TIGGIGIGCAGAGGIACCCIGCAAGGICTGGIGICCIGGGGAACTITCCCTIGCGGCAA 699
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Cispecies: Bos primigenius taurus (cattle)
Rimikes, O.; Holeysovsky, V.; Tomasek, V.; Sorm, F.
Biochem. Biophys. Res. Commun. 24, 346-352, 1966
A;Title: Covalent structure of bovine trypsinogen. The position of the remai
A;Reference number: A90164; MUID:67168848; PMID:5967094
A;Accession: A90164; MUID:67168848; PMID:5967094
A;Molecule type: protein
A;Residues: 1-57, Q'. 59-67, Q'. 69-150, N', 152-176, N', 178-229 cMIK>
A;Cross-references: UNIPARC:UPI0000172AAD
B;Hatley, B.S.
                                                                                                                                                                                                                            TGGGGCACTACCACGAGCCCAGATGTGACCTTTCCCTCTGACCTCATGTGCGTGGATGTC
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A, Residues: 1-102, 74, 104-248 cWANS>
A, Residues: 1-102, 74, 104-248 cWANS>
A, Cross-references: UNIPARC: UPIO0001376E4; EMBL: U15156; NID:g603904; PIDN:AAA79913.1; PI
A, Experimental source: clone 1-P38
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin homology
C; Reywords: hydrolase; pancrass; protein digestion; serine proteinase; zymogen
F; 1-15/Domain: signal sequence #status predicted <SIG>
F; 1-5/Domain: activation peptide #status predicted <APT>
F; 56-244 Product: trypsin I #status predicted <WAT>
F; 56-241/Domain: trypsin homology <TRY>
F; 65, 109, 202/Active site: His, Asp, Ser #status predicted
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A; Residues: 1-248 <WANI>
A; Cross-references: UNIPROT:Q90627; UNIPROT:Q90628; UNIPARC:UPI0000047172; EMBL:U15156;
A; Experimental source: clone 1-P38
A; Accession: S72345
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A;Residues: 1-9,'V',11-12,'T',14-102,'A',104-214,'I',216-248 <WAN4>
A;Cross-references: UNIPARC:UPI0000047171; GB:U15155; NID:g603902; PIDN:AAA79912.1; PID
                                                                                                                                                                                                                                                                                                                                                            A;Accession: S72345
A;Molecule type: DNA
A;Estidues: 1-248 wANA2>
A;Exestidues: 1-248 wANA2>
A;Experimental source: clone 1-P38
A;Accession: S55065
A;Accession: S55065
A;Rolecule type: mRNA
A;Residues: 1-9, V', 11-12, T', 14-102, A', 104-214, I', 216-248 wAN3>
A;Cross-references: UNIPARC:UPI0000047171; EMBL:U15155; NID:g603902; PIDN:AAA79912.1;
C;Date: 28-Oct-1996 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004 C;Accession: S55067; S72345; S55065; S72346; S71155 R;Wang, K.; Gan, L.; Lee, I.; Hood, L. Biochem J. 307, 471-479; 1995 A;Title: Isolation and characterization of the chicken trypsinogen gene family. A;Reference number: S55065; MUID:95251611; PMID:7733885 A;Accession: S55067
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Matches:
Conservative:
Mismatches:
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A, Accession: S72346
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A;Accession: S71155
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Best Local Similarity:
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Lissue kallikrein (EC 3.4.21.35) precursor - rat
Lissue kallikrein (EC 3.4.21.35) precursor - rat
N;Alternate names: glandular kallikrein; kininogenin; true tissue kallikrein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 09-Jul-2004
C;Accession: A00944; A41429; A25137; JX0073; A23863; A33359
R;Swift, G.H.; Dagorn, J.C.; Ashley, P.L.; Cummings, S.W.; MacDonald, R.J.
Proc. Natl. Acad. Sci. U.S.A. 79, 7263-7267, 1982
A;Title: Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid sequence ch;Reference number: A00944; MUID:83117659; PMID:6961406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---GACAGGAGAGCTCAGAGGATCAAGGCCTCGAAGTCATTCCGCCACCCCGGCTACTCC 330
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F;58,60,63,68/Binding site: calcium (Glu, Asn, Val, Glu) #status
F;131-132/Cleavage site: Lys-Ser (autolytic) #status experimental
                                                                        Length:
Matches:
Conservative:
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Indels:
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                                                                    4.79e-38
535.00
60.7%
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A;Experimental source: pancreatic
Kykato, H.; Nakanishi, E.; Enjyoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
J. Biochem. 102, 1389-1404, 1387
A;Title: Characterization of serine proteinases isolated from rat submaxillary gland: wir
A;Reference number: A41429; MUID:88198057; PMID:3482210
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Biochim. Biophys. Acta 866, 1-14, 1986
A;Title: Immunological identification of rat tissue kallikrein cDNA and characterization
A;Reference number: A25137; MUID:86131678; PMID:3004582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inoue, H.; Fukui, K.; Miyake, Y.
- Blochem. 105, 834-840, 1989
- Title: Identification and Erructure of the rat true tissue kallikrein gene expressed in
Reference number: JX0073; MUID:89327211; PMID:2753879
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| Molecule type: DNA
| Residues: 1-265 < INO>
| Residues: 1-265 < INO
| Resid
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A;Molecule type: DNA
A;Residues: 5.265 «WIN>
A;Crossidues: 5.265 «WIN>
A;Crossidues: 5.265 «WIN>
C;Cromment: The kallikreins liberate lysyl-bradykinin, a vasoactive decapeptide, from kini C;Comment: The kallikreins liberate lysyl-bradykinin, a vasoactive decapeptide, from kini C;Comment: The protein presumably assumes the two-chain form by cleavage between residues C;Comment: The protein presumably assumes the two-chain form by cleavage between residues C;Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kiningen to release ly
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Title: Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences
Reference number: A23863; MUID:86051477; PMID:2998455
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C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin perine serine proteinase; zymogen
F; H-17/Domain: signal sequence #status predicted <SIG>
F; 18-28/Domain: activation peptide #status predicted <APT>
F; 29-25/Product: tissue Kallikrein, pancreatic #status predicted <MPT>
F; 29-257/Domain: trypsin homology <TRYF
F; 29-257/Domain: trypsin homology <TRYF
F; 29-257/Domain: trypsin homology <TRYF
F; 20-257/Domain: Trypsin homo
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Residues: 1-265 <SWI>
;Cross-references: UNIPROT:P00758; UNIPARC:UPI0000167958
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A;Residues: 29-53,'X',55-87 <KAT>
A;Cross_references: UNIPARC:UP10000172ABF
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;Molecule type: mRNA
;Residues: 115-265 <GRR>
;Cross-references: UNIPARC:UP10000172ACO
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;Molecule type: mRNA
;Residues: 1-265 <ASH>
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                                                                                                                                                                                                                                                                                                                                                                                                          208 GlyGlyLysAspThrCysLysGlyAspSerGlyGlyProLeulleCysAsnGlyValLeu 227
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                                                                                        28 ArgValValGlyGlyTyrAsnCysGluMetAsnSerGlnProTrpGlnValAlaValTyr 47
                                                                                                                               TTACTGCTATCCTTAGCCTTGGAAACTGCAGGAGAAGAAGCCCCAG------GGTGAC 99
         ACTCAAGTGTGCAAGTTCACCAAGTGGATAAATGACACCATGAAAAAGCAT 771
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Search completed: March 11, 2006, 01:55:32 Job time : 50 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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protein search, using frame\_plus\_n2p model OM nucleic

March 11, 2006, 01:39:02; Search time 52.9 Seconds (without alignments) 2584.714 Million cell updates/sec Run on:

US-09-905-083A-30 Title: Perfect score:

1 ggatttccgggctccatggc.....aagaaacacaaaacctcag 969 Sequence:

**BLOSUM62** Scoring table:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

2166443 segs, 705528306 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/Abss/ABSS/MEB spool/US09905083/runat\_10032006\_152453\_29666/app\_query.fasta\_1
-Q=/Abss/ABSS/MEB spool/US09905083/runat\_long.minMaTGH=0.1 -LOOPCL=0 -LOOPEXT=0
-UBITS-bits -CFMT=fastan -SUFFIX=n2p.rup\_-MINMATGH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -CTARR=1 -END=-1 -MATRIX-Blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL
-UOTFWT=ppto -NORM=ext -HEAPSIZE=500 -MINIMEN=0 -MAXIEN=20000000000 -HOST=bbss02p
-USER=US09905083 @CGM 1 1466 @cunat\_10032006\_152453\_29666 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLCCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	P49862 homo sapien	Q91ve3 mus musculu	QSr567 pongo pygma	Q61955 mus musculu	Q9y337 homo sapien	Q53zr3 homo sapien	O88780 rattus norv	Q8cgr6 mus musculu	Q53f68 homo sapien	Q6p3z0 mus musculu	Q8cgr5 mus musculu	Q9d140 mus musculu	Q80vs4 mus musculu	homo	Q6b089 homo sapien	O60259 homo sapien
		ai .	KLK7 HUMAN	KLK7 MOUSE	Q5R567 PONPY	NRPN MOUSE	KLK5 HUMAN	Q53ZR3 HUMAN	NRPN RAT	Q8CGR6_MOUSE	Q53F68 HUMAN	Q6P3Z0_MOUSE	Q8CGR5 MOUSE	Q9D140 MOUSE	Q80VS4 MOUSE	KLK14 HUMAN	Q6B089 HUMAN	NRPN_HŪMAN
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	,	Match Length DB	253	249	140	260	293	293	260	276	293	246	250	293	242	251	251	260
de	Query	Match	9.94	57.8	42.7	34.5	34.4	34.4	34.4	34.2	34.2	34.0	33.3	33.1	32.9	32.8	32.8	32.7
		Score	1364	1028.5	160	614	612.5	612.5	611.5	609.5	608.5	604.5	593.5	589	586.5	583	583	582.5
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NUCLEOTIDE SEQUENCE [GENOMIC DNA].
PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
Moss P., Paeper B., Wang K.;

P15949 mus musculu	Q8iw69 homo sapien	Q9ukr3 homo sapien	Q63275 rattus norv	-		mus n	рошо	homod	homo	P00756 mus musculu	P36374 rattus norv		Q9qyn3 m hippostas	н	Q9jm71 mus musculu	Q4vb17 homo sapien	рошо	Q8ixd7 homo sapien	homo	рошо	Q9cv76 mus musculu	Q9qyn4 mus musculu	P09582 canis famil	P00755 mus musculu	P15947 mus musculu	P36373 rattus norv	Q6ie66 rattus norv	Q8c232 mus musculu
KLK9 MOUSE	Q8IW69 HUMAN	KLK13 HUMAN	Q63275 RAT	KLK15 SAGOE	KLK11 HUMAN	KLK11 MOUSE	KLK4 HUMAN	Q4VB16 HUMAN	KLK15 HUMAN	KLK3 MOUSE	KLK8 RAT	Q6ISTO HUMAN	Q9QYN3 MOUSE	TRY1 RAT	KLK27 MOUSE	Q4VB17 HUMAN	Q96RQ0 HUMAN	Q81XD7 HUMAN	KLK12 HUMAN	Q53YL3 HUMAN	Q9CV76 MOUSE	Q9QYN4 MOUSE	ESTA CANFA	KLK1 MOUSE	KLK6 MOUSE	KLK7 RAT	Q6IE66 RAT	Q8C232_MOUSE
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32.7	32.6	32.5	32.4	32.2	32.1	31.9	31.9	31.9	31.6	31.6	31.6	31.5	31.5	31.5	31.5	31.4	31.4	31.2	31.2	31.2	31.2	31.1	31.0	31.0	31.0	31.0	31.0	31.0
582	580.5	578	576.5	573.5	571.5	568	567.5	567.5	563	563	563	561.5	561.5	561	260	559.5	559.5	556	555	555	554.5	553.5	552.5	552	552	552	551.5	551
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## ALIGNMENTS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53 MEDLINE-94308225; PubMed-8034709;
MEDLINE-94308225; PubMed-8034709;
Hansson L., Stroemgvist M., Baeckman A., Wallbrandt P., Carlstein A., Diamandis B.P.;
"The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic enzyme is a new member of the human kallikrein gene family - genomic characterization, mapping, tissue expression and hormonal NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION Egelrud T.; "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase."; J. Biol. Chem. 269:19420-19426 (1994). P49862; QRNSN9; QRNFV7; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 13-SFP-2005 (Rel. 48, Last annotation update) 13-SFP-2016 (Rel. 48, Last annotation update) chymotryptic enzyme) (hSCCB). TISSUE=Keratinocyte; PubMed=10974542; DOI=10.1016/S0378-1119(00)00280-8; Yousef G.M., Scorilas A., Magklara A., Soosaipillai A., Diamandis E.P.; 253 AA PRT; STANDARD; Gene 254:119-128(2000). Homo sapiens (Human) NCBI\_TaxID=9606; HUMAN 

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INDUCTION:
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Isod=P49862-1; Sequence=Displayed;
Name=2: Synonyms=Short;
Name=2: Synonyms=Short;
Isod=P49862-1; Sequence=VSP_013581;
Isod=P49862-1; Sequence=VSP_013581;
TISSUB SPECIFICITY: Abundantly expressed in the skin and is
TISSUB SPECIFICITY: Abundantly expressed in the brain, mammary gland, cerebellum, spinal cord and kidney. Lower levels in salivary gland, cerebellum, spinal cord and kidney. Lower levels in salivary glands, uterus, thyroid, placenta, trachea and testifs. Up-regulated in ovarian carcinoma, especially late-etage serous carcinoma, compared with normal ovaries and benign adenomas (at the protein level).
                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22223266; PubMed=12738725;
Dong Y., Kaushal A., Brattsand M., Micklin J., Clements J.A.;
"Differential splitching of Kirks and Kirk? in epithelial ovarian cancer
produces novel variants with potential as cancer biomarkers.";
Clin. Cancer Res. 9:1710-1720(2003).
                                                                                                                     Hansson L., Baeckman A., Ny A., Edlund M., Edholm E., Tornell J., Wallbrandt P., Egelrud T., Edlund m., Edholm E., Tornell J., "Epidermal overexpression of stratum corneum chymotryptic enzyme in mice; a model for chronic ithchy dermatitis."; Stomitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skytt A., Stroemgvist M., Egelrud T.; "Primary substrate specificity of recombinant human stratum corneum
     the serine protease gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Event-Alternative splicing; Named isoforms=2;
     expression analysis of the ser
in chromosome 19q13 region.";
                                                                                                          NUCLEOTIDE SEQUENCE [GENOMIC DNA]
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                                                                                                                                                                                                                                                                                                                                                 TISSUE=Ovarian carcinoma;
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"Sequencing and expres
cluster located in chr
Gene 257:119-130(2000)
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                             cell line.
SIMILARITY: Belongs to the peptidase SI family. Kallikrein
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2D68B6B15A76A668 CRC64;
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Kallikrein 7.
Peptidaes S1.
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N-linked (GLONG...) (PP 8:
By similarity.
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InterPro; IPR001254; Peptidase S1 S6.
InterPro; IPR001314; Peptidase S1 S6.
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    -!- SIMILARITY: Contains 1 peptidase S1 domain.

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Ensembl; ENSG00000169035; Homo sapiens
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HSSP; P00760; 1EZX.
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                                                                                                                          GlySerAspThrLeuGlyAspArgArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
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21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
                     CACCCATGGCAGGTGGCCCTGCTCAGTGGCAATCAGCTCCACTGCGGAGGCGTCCTGGTC
                                                                         CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer
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                                                                                                                                              CACCCCGGCTACTCCACACACACATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC
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                                41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal
                                                                                                                                                                                        CAGGCCAGGCTGTCATCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGGTGCGAACCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hansson L., Baeckman A., Ny A., Edlund M., Edholm E., Tornell J., Wallbrandt P., Egelrud T., "Epidermal overexpression of stratum corneum chymotryptic enzyme in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q91VE3; Q9R048;
10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kallikrein 7 precursor (EC 3.4.21.-) (Stratum corneum chymotryptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       novel cDNA cloning of mouse serine protease, thymopsin."; omitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                             736 TTCACCAAGTGGATAAATGACACCATGAAAAAGCATCGC 774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Klk7; Synonyms=Prss6, Scce;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (OCT-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Thymopsin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamaguchi N.;
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RA Nozazki Y., Furno M., Kabukawa T., Adachi J., Bono H., Kondo S., Radines. Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagil K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Ra aldarelli R., Tumaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Ra Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Baldarelli R., Hill D.P., Bult C., Hume D.A., Ouackenbush J., Baldarelli R., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Ra Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Ra Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., R. Graminod S., Gustinnich S., Hirckawa N., Jackson I.J., Jarvis B.D., Ranai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Ranai A., Wantara K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Ranachandran S., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., R. Sandelin A., Schneider C., Wang Y., Watanabe Y., Wells C., Wusner A., Hashizume N., Takone H., Nakamura M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Rakawa T., Pukuda S., Hirozane-Kishikawa T., Kawai J., Alzawa K., Arakawa T., Pukuda S., Katanishi A., Yoshino M., Waterston R., Lander B.S., Rogers J., Ranalysis of the mouse transcriptome based on functional annotation of Narray A., Narray C., Narray C., Cont. C., Carnic C., Narray C., Carnic 
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murine analog to human
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MEDLINE-93939282: PubMed=10465296;

DOI=10.1046/j.1523-1747.1999.00662.x;

DOI=10.1046/j.1523-1747.1999.00662.x;

DOI=10.1046/j.1523-1747.1999.00662.x;

Molecular cloning and tissue expression of the murine analog to huma stractum corneum chymotryptic enzyme.";

J. Invest. Dermatol. 113:152-155(1999).

J. Invest. Dermatol. 113:152-155(1999).

J. Invest. Dermatol. 113:152-155(1999).

J. Invest. Dermatol. 113:152-155(1999).

J. Invest of the skin in the continuous structures in the cornified layer of the skin in the continuous shedding of cells from the skin surface. Specific for amino acid residues with arcmatic side chains in the PI position. SCCE cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-
                                                                                                                                                                                                                 MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
mice, a model for chronic ithchy dermatitis.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE OF 1-234, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                            [LARGE SCALE MRNA].
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                                                                                                                            NUCLEOTIDE SEQUENCE (LARGE SO
STRAIN=C57BL/6J; TISSUE=Head
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162 SerAspValLysLeuIleSerSerArgGluCysLysLysValTyrLysAspLeuLeuGly 181
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
  TGCGGCCAACCCAATGACCCAGGGTCTACACTCAAGTGCGAAGTTCACCAAGTGGATA
                                             |||||||::
| GlyaspGlnSerAlaGlnLysIleLysAlaThrLysSerPheArgHisProGlyTyrSer
                                                                                                                             511 GTGGATGTCAAGCTCATCTCCCCCCAGGACTGCACGAAGGTTTACAAGGACTTACTGGAA
                                                                                                                                                                                                                                           571 AATTCCATGCTGTGCGCTGGCATCCCCGACTCCAAGAAAACGCCTGCAATGGTGACTCA
                                  GGCGACAGGAGAGCTCAGAGGATCAAGGCCTCGAAGTCATTCCGCCACCCCGGCTACTCC
                                                                          ACACAGACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGCCAGGCCAGGCTGTCA
                                                                                                                                                           GTCTCCGGCTGGGGCACTACCACGAGCCCAGATGTGACCTTTCCCTCTGACCTCATGTGC
                                                                                                                                                                                                                                                        GGGGGACCGTTGGTGCAGAGGTACCCTGCAAGGTCTGGTGTCCTGGGGAACTTTCCCT
                                                                                                                    TCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAACCCCCTGGAACCACCTGTACT
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Sponpy

PERSON PRELIMINARY;

OSRS677

O1-FBB-2005 (TrEMBLrel. 29, Created)

O1-FBB-2005 (TrEMBLrel. 29, Last sequence update)

O1-FBB-2005 (TrEMBLrel. 29, Last annotation update)

Hypothetical protein DKFZp459E0918;

Name=DKFZp459E0918;
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                                                                                                        This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                       Activation peptide (By similarity).
Kallikrein 7 (By similarity).
Serine protease (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
Phe-|-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the activation of precursors to inflammatory cytokines. SUBJECTIONER EACHION: Secreted (By similarity).
TISSUE SPECIFICITY: Expressed in skin and, at lower levels, lung, kidney, brain, heart and spleen. In skin, expressed in suprabasal keratinocytes and in the luminal parts of hair follicles. Not detected in liver and skeletal muscle.
SIMILARITY: Belongs to the peptidase SI family. Kallikrein subfamily.
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|LeuLeuSerLeuIleThrValLeuLeuSerLeuAlaLeuGluThrAlaGly
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0D4E380F12D14F87 CRC64;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                     EMBL, AB008371; BAB55604.1; -; EMBL; AR332940; ARK69552.1; -; EMBL; AK07406; BAC36467.1; -; EMBL; AK077406; BAC36787.1; -; EMBL; BC027823; AAH27823.1; -; EMBL; AF124299; AFF01139.1; -; HSSP; P00760; 1EZX.
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Best Local Similarity:
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81 ProAspSerLysLysAsnAlaCysAsnGlyAspSerGlyGlyProLeuValCysArgGly 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Neuropsin precurer (RC 3.4.21...) (NP) (Kallikrein 8).
Name=Klk8; Synonyms=Nrpn, Prss19;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammmalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95348817; PubMed=7623137; Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T., Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.; "Expression and activity-dependent changes of a novel limbic-serine protease gene in the hippocampus."; Juneurosci. 15:5088-5097(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
STRAIN=Czech II; TISSUB=Mammary gland;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Mismatches:
Indels:
                Length:
Matches:
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98.6%
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NUCLEOTIDE SEQUENCE.
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                                           Percent Similarity:
Best Local Similarity:
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Q61955;
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Statchenko L., Marusina K., Esmarant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Caraninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., N. Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Maring M., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.B., Generation and initial analysis of more than 15,000 full-length human mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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pyramidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Ly8-.
-!- ENZYME REGULATION: Strongly inhibited by diisopropyl
fluorophosphate, leupeptin and (4-amidinophenyl)methanesulfonyl 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BALBSC; TISSUE=Brain;
MEDLINE=98225202; PubMed=9556608; DOI=10.1074/jbc.273.18.11189;
Shimzu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K., Shiosaka T., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.;
"Characterization of recombinant and brain neuropsin, a plasticity-related serine protease.";
J. Biol. Chem. 273:11189-11196(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kindling epileptogenesis.";
J. Biol. Chem. 274:4220-4224(1999).
-!- FUNCTION: Suggested to be involved in kindling epileptogenesis and
hippocampal plasticity. Has a strong proteolytic activity against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- TISSUE SPECIFICITY: Expressed specifically in the limbic system mouse brain and is localized at highest concentration in pyramid neurons of the hippocampal CA1-3 subfields.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Hippocampus;
MEDLINE-9913451; PubMed=9933620; DOI=10.1074/jbc.274.7.4220;
Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,
Shiosaka S., Hakoshima T.;
"Crystal structure of neuropsin, a hippocampal protease involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE=Ref.4.
-!- MASS SPECTROMETRY: MW=26229; METHOD=MALDI; RANGE=33-260;
                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN SEQUENCE OF N-TERMINUS, CHARACTERIZATION, AND MASS
                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SIMILARITY: Contains 1 peptidase S1 domain.
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PDB; 1MPM; X-ray; A/B=33-257.
MEROPS; S01.244; ...
MGI; MGI:892018; K1k8.
InterPro; 1PR001254; Peptidase_S1_S6.
InterPro; 1PR001254; Peptidase_S1_S6.
Pfam; PP00089; Trypsin; 1.
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EMBL; AB032202; BAA92435.1; -; Genomic_DNA.
EMBL; BC055895; AAH55895.1; -; mRNA.
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382 AGGCTGTCATCCATGGTGAAGAAGTCAGGCTGCCCTCCCGGTGCGAACCCCCTGGAACC 441
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                                                                                                                  11 ProTrpIleLeuLeuLeuLeuPheMetGlyAlaTrpAlaGlyLeuThrArgAlaGlnGly 30
                                                                                                                                                                                                                                                           GGCGACAGGAGAGCTCAGAGGATCAAGGCCTCGAAGTCATTCCGCCACCCCGGCTACTCC
                                                                                                                                                                                                                                                                                                                                                   331 ACA------CAGACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGCCAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCATGTGCGTGGATGTCAAGCTCATCTCCCCCCAGGACTGCACGAAGGTTTACAAGGAC
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09Y337; 09HBGB;
16-0CT-2001 (Rel. 40, Created)
13-SEP-2005 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Kallikrein 5 precursor (EC 3.4.21..) (Stratum corneum tryptic enzyme)
(Kallikrein 5 precursor (EC 3.4.21..) (Stratum corneum tryptic enzyme)
Mama—KIKS; Synonyme=SCTE; ORFNames=UNQS70/PR01132;
Homo sapiens (Human)
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JOURN TRYPSIN DOM; 1.

JESOURAL SER, 1.

JESUULFID SER, 1.

JESUULFID STRANT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae. TISSUE=Stratum corneum;
MEDLINE=99445563; PubMed=10514489; DOI=10.1074/jbc.274.42.30033;
Brattesand M., Egelrud T.;
"Purification, molecular cloning, and expression of a human stratum corneum trypsin-like serine protease with possible function in desquamation."; NUCLEOTIDE SEQUENCE NCBI\_TaxID=9606; 

US-09-905-083A-30 (1-969) x NRPN\_MOUSE (1-260)

indels:

Percent Similarity: Best Local Similarity: Query Match: DB:

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ACCARAGO ANA AMARANA A
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Margner L., Shenmen C.M., Schuler G.D.,

A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Capleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

B Rownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

B And Mary B. M. Analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,

Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

Baton D., Roster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

Lewis L., Liso D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,

Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,

Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,

Wood W.I., Godowski P.J., Gray A.M.;

"The secreted protein discovery initiative (SPDI), a large-scale

effort to identify novel human secreted and transmembrane proteins: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse CDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: May be involved in desquamation.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed in skin, breast, brain and testis.
-!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
                                                                                MEDLINE=20118156; PubMed=10652563;
Yousef G.M., Luo L.-Y., Diamandis E.P.;
"Identification of novel human kallikrein-like genes on chromosome
                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                                        PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6; Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J Moss P., Paeper B., Mang K.; Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region."; Gene 257:119-130(2000).
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EMBL; AF135028; AAD26429.1; -; Genomic_DNA.
EMBL; AF243527; AAG33358.1; -; Genomic_DNA.
EMBL; AY359010; AAG89369.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [5]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
Biol. Chem. 274:30033-30040(1999)
                                                                                                                                                                            19q13.3-q13.4.";
Anticancer Res. 19:2843-2852(1999)
                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
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                                                       NUCLEOTIDE SEQUENCE.
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94 GlyAlaValLeuValHisProGlnTrpLeuLeuThrAlaAlaHisCysArgLysLysVal 113
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114 PheArgValArgLeuGlyHisTyrSerLeuSerProValTyrGluSerGlyGlnGlnMet 133
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                                                                                                                                                                                                                                                                                                                                                                                                          (By similarity).
(By similarity).
(By similarity).
(Cotential).
(Cotential).
(Cotential).
(Cotential).
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PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Glycoprotein; Hydrolase; Protease; Serine protease; Signal.
SIGNAL
                                                                                                            GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
GO; GO:000654; P:epidermis development; TAS.
GO; GO:0006508; P:proteolygis and peptidolysis; NAS.
InterPro; IPR001254; Peptidase 31 S6.
InterPro; IPR001314; Peptidase 51Ā.
PF00089; Trypsin; 1.
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Matches:
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Kallikrein 5.
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                                      MEROPS; S01.017; -.
Ensembl; ENSG0000167754; Homo sapiens
EMBL; BC008036; AAH08036.1; -; mRNA.
HSSP; P00760; 1EZX.
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612.50
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                                                                            HGNC; HGNC: 6366; KLK5
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                    472 ACGAGCCCAGATGTGACCTTTCCCTCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCC 531
                                                              532 CCCCAGGACTGCACGAAGGTTTACAAGGACTTACTGGAAAATTCCATGCTGTGCGCTGGC 591
                                                                                                         ATCCCCGACTCCAAGAAAAACGCCTGCAATGGTGACTCAGGGGGGACCGTTGGTGTGCAGA 651
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                 GGTACCCTGCAAGGTCTGGTGCTGGGGAACTTTCCCTTGCGGCCAACCCAATGACCCA
                                                                                                                                                                                                       GGAGTCTACACTCAAGTGTGCAAGTTCACCAAGTGGATAAATGACACCATGAAA 765
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Identification of splice variants for the human kallikrien gene
                                                                                                                                                                                                                                                                               13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Kallikrein 5 splice variant 2 (Kallikrein 5 splice variant 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vector.",
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; AY279381; AP442276.1; -; mRNA.
EMBL; BT006667; AAP32513.1; -; mRNA.
EMBL; AY279380; AAP42275.1; -; mRNA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0006295; F:crypmin activity; IEA.
GO; GO:0006509; P:trypmin activity; IEA.
InterPro; IPR001254; Peptidase_S1_S6.
InterPro; IPR001314; Peptidase_S1A.
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Matches:
Conservative:
Mismatches:
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SEQUENCE 293 AA; 32020 MW; D92C92F5609E5946
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PRINTS; PR00722; CHYMOTRYPSIN.
SMARY; SM00020; Tryp SPC; 1.

PROSITE; PS50240; TRYPSIN DOW; 1.

PROSITE; PS00134; TRYPSIN IS; UN
PROSITE; PS00135; TRYPSIN SER; 1.
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Q53ZR3;
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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Percent Similarity:
Best Local Similarity:
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124 GCAAGAGGCTCCCACCCATGGCAGGTGGCC---CTGCTCAGTGGCAATCAGCTCCACTGC 180
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114 PheArgValArgLeuGlyHisTyrSerLeuSerProValTyrGluSerGlyGlnGlnMet 133
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                                                                                        GCAGGAGAAGAAGCCCAGGGTGAC-----AAGATTATTGATGGCGCCCCATGT 123
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Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontcoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
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15-JUL-1999 (Rel. 38, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine protease 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAGTCTACACTCAAGTGTGCAAGTTCACCAAGTGGATAAATGACACCATGAAA 765
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MEDLINE=98389725; PubMed=9722524; DOI=10.1074/jbc.273.36.23004;
Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lathe R.;
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                                             US-09-905-083A-30 (1-969) x Q53ZR3_HUMAN (1-293)
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Gaps:
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447
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173 CyshlaGluValLysIleTyrSerGlnAsnLysCysGluArgAlaTyrProGlyLysIle 192
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                                                                                                                                                                                                                                           388 TCATCCATGGTGAAGAAGTCAGGCTGCCCTCCCGCTGCGAACCCCCTGGAACCACGTGT
                                     277 AGGAGAGCTCAGAGGATCAAGGCCTCGAAGTCATTCCGCCACCCCGGCTACTCCACA---
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MEDLINE=22325484; PubMed=12437987; DOI=10.1016/S0006-291X(02)02629-3; Olsson A.Y., Lundwall A.; "Orson A.Y., Lundwall A.; "Orson A.Y., Lundwall A.; "Organization and evolution of the glandular kallikrein locus in Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinee, Mus.
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AYIS-232, AAN78420.1; -; Genomic_DNA.
HSSP; P00760; 1EZX.
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Last annotation update)
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Ensembl; ENSMUSGO000054046; Mus musculus.
MG1; MG1:9292; KIN13.
GG7; GO:0005615; C:extracellular space; TAS.
InterPro; IPR001254; Peptidase_S1_S6.
InterPro; IPR001314; Peptidase_S1A.
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
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Q8CGR6;
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                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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|TheLeuGluGlyGlnGluCysLysProHisSerGlnProTrpGlnThrAlaLeuPheGln 52
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R HSSP; Q61955; 1NPM.

R RSP(801955; 1NPM.

R RSP(801955; 1NPM.

R RNSTORS; SO1. 244; -.

R Ensembl; ENSRNOG0000018580; Rattus norvegicus.

R InterPro; IPR001314; Peptidase_S1_K.

R PRINTS; PR000189; Trypsin, 1.

R PRINTS; PR000189; Trypsin, 1.

R PROSITE; PS00134; TRYPSIN DWN 1.

R PROSITE; PS00134; TRYPSIN HIS; 1.

R PROSITE; PS00135; TRYPSIN HIS; 1.

R PROSITE; PS00135; TRYPSIN HIS; 1.

R GIGNAL 1.

SIGNAL SYMORA SER; 1.

R PROSITE; PS00135; TRYPSIN HIS; 1.

R ROSITE; PS00135; TRYPSIN HIS; 1.

R ROSITE; PS00135; TRYPSIN HIS; 1.

R ROSITE; PS00135; TRYPSIN HIS; 1.
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27 LeuAsnGlyThrAsnGlyThrSerGlyPheLeuProGlyGlyTyrThrCysLeuProHis
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|LeuGlyLysHisAlaLeuGlyArgValGluAsnGlyGluGlnAlaMetGluValValArg
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SerAlaAspAspCysLeuProThrGlyThrCysCysArgValSerGlyTrpGlyThrThr
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120
43
76
119
                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                             US-09-905-083A-30 (1-969) x Q8CGR6_MOUSE (1-276)
   1.
UNKANOWN_1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOW
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 276 AA; 30360 MW; 33E189
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Q53F68 HUMAN PRELIMINARY;
Q53F68 TUMAN PRELIMINARY;
13-SEP-2005 (TrEMBLrel. 31, Created)
                                                                                                                  1.31e-43
609.50
63.2%
46.5%
34.2%
                                                                                                                                                                           Best Local Similarity:
                                                                                                                                                         Percent Similarity:
                                                                                                       Alignment Scores:
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Kallikrein 5 preproprotein variant (Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 ACCGTGCACCTGGGCAGTGATACGCTGGGC-----GACAGGAGAGCTCAGAGGATC
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95 AlaValLeuValHisProGlnTrpLeuLeuThrAlaAlaHisCysArgLysLysValPhe
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115 ArgValArgLeuGlyHisTyrSerLeuSerProValTyrGluSerGlyGlnMetPhe
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GlnGlyValLysSerIleProHisProGlyTyrSerHisProGlyHisSerAsnAspLeu
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Matches:
Conservative:
Mismatches:
Indels:
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Name=Klk14;
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RY MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA MILESTURE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA AILSTONE R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA AILSTONE R.F., Zebeberg B., Buetow K.H., Schemfer C.F., Bhat N.K.,

RA AILSTONE R.P., Jordan H., Moore T., Max S.I., Wang J., Haieh P. K.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Boaks S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunatane C.H.,

RA Boaks S.A., McGwan P.J., McKernan R.J., Malek J.A., Gunatane P.H.,

RA Rochards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Pahey J., Helton E. Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhaceley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rhackeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA "Generation and initial analysis of more than 15,000 full-length human
               234 AspLysAlaGlyArgAspSerCysGlnGlyAspSerGlyGlyProValValCysAsnGly 253
                                                            714
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                                                          655 ACCCIGCAAGGICIGGIGCCIGGGAACTITCCCITGGGGCCAACCCAATGACCCCAGGA
                                                                            CCCGACTCCAAGAAAACGCCTGCAATGGTGACTCAGGGGGACCGTTGGTGTGCAGAGGT
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                       GTCTACACTCAAGTGTGCAAGTTCACCAAGTGGATAAATGACACCATGAAA 765
                                                                                                                                       274 ValtyrThrAsnLeuCysLysPheThrLysTrpIleGlnGluThrIleGln 290
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SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Hypothetical protein; Protease; Serine protease.
SEQUENCE 246 AA; 27213 MW; OBC1454D6CC8CDEC CRC64;
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Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCG63763; AAH63763.1; -; mRNA.
HSSP; P00761; 1AKS.
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Last sequence update)
Last annotation update)
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MGI; MGI:95292; Klk13.

GO; GO:0005515; C:extracellular space; TAS.

InterPro; IPR001254; Peptidase_S1_S6.

InterPro; IPR001314; Peptidase_S1_A.

PF00089; Trypsin; 1.
                                                                                                                                                                                                                MOUSE PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                              286 CAGAGGATCAAGGCCTCGAAGTCATTCCGCCACCCCGGCTACTCC---ACACAGACCCAT 342
                                                                                                                                                                                                                                                                                                                                                                                                                                   691 TGCGGCCAACCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAGTTCACCAAGTGGATA 750
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NUCLEOTIDE SEQUENCE.
MEDLINE=22325484; PubMed=12437987; DOI=10.1016/S0006-291X(02)02629-3;
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Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
112
39
67
7
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Last annotation update)
                Conservative:
Mismatches:
Indels:
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                                                                          Gaps:
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604.50
67.1%
49.8%
34.0%
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AC QBCGR5,
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                  Percent Similarity:
Best Local Similarity:
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Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373 AGCCAGGCCAGGCTGTCATCCATGGTGAAGAAGTCAGGCTGCCCTCCCGCTGCGAACCC 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::: |||||| |||
LysLysValArgLeuGlyArgAlaValLysThrIleSerValAlaSerSerCysAlaSer 137
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|ProGlyThrProCybArgValSerGlyTrpGlyThrIleAlaSerProIleAlaArgTyr
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Olsson A.Y., Lundwall A.; "Organization and evolution of the glandular kallikrein locus in Mus
                                                                                                                    Adams M., Mural R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AYIS2433; AAN78421.1; -; Genomic_DNA.
HSSP; P00760; 1EZX.
                                                                                                                                                                       HSSP; P00760; 1EZX.

MBROPS; S01.029;

Ensembl; ENSWIGS00000044737; Mus musculus.

MGI; MGI:2447564; KIk14.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:rppptidase activity; IEA.

GO; GO:0004295; F:rppptidase activity; IEA.

GO; GO:0006239; F:rppptidase activity; IEA.

GO; GO:0006299; P:rproteolysis and peptidolysis; IEA.

InterPro; IPR001254; Peptidase_S1_S6.
                                                                                                                                                                                                                                                                                                                                                                   PERMI, PF00.089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
BMART; SM0020; Tryp SPC; 1.
PROSITE; PS0240; TRYPSIN DOM; 1.
PROSITE; PS0134; TRYPSIN LHS; UNKNOWN 1.
PROSITE; PS0135; TRYPSIN LHS; UNKNOWN 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 250 AA; 27016 MW; F62FEBF2290FEBE8 CRC64;
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1114
42
86
111
                                                           Biochem. Biophys. Res. Commun. 299:305-311(2002)
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Mismatches:
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Matches:
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593.50
61.7%
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TACAAGGACTTACTGGAAAATTCCATGCTGTGCGCTGGCATCCCCGACTCCAAGAAAAC 612
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annoctation update)
Mus musculus 18-day embryo whole body CDNA, RIKEN full-length enriched
11brary, clone:1110030019 product:weakly similar to KALLIKREIN 5
18C 3+21.-) (STRATUM CORNEUM TRYPTIC ENZYME) (KALLIKREIN-LIKE
PROTEIN 2) (KLK-L2).
Name=1110030019Rik;
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                                                                                                                                                                                                                                   GCCTGCAATGGTGACTCAGGGGGACCGTTGGTGTGCAGAGGTACCCTGCAAGGTCTGGTG
                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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156 MetLeulleLysMetAsnArgLyslleArgAspSerHisSerValLysProValGlulle 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::: ||| |||||||||||| 216 GluargCysLysAsnSerTyrProGlyGlnIleAspLysThrMetPheCysAlaGly--- 234
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A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausher R.D., Colling F.S., Magner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B tapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
B Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Retteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
                                                                                                              244 ACCGTGCACCTGGGCAGTGATACGCTGGGC-----GACAGGAGAGCTCAGAGGATC 294
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116 ArglleArgLeuGlyHisHisSerMetSerProValTyrGluSerGlyGlnGlnMetPhe
                                                                                                                                                                                                                                                                                                                                                                                                            355 ATGCTCGTGAAAGCTCAATAGCCAGGCCAGGCTGTCATCCATGGTGAAGAAAGTCAGGCTG
                                                                                                                                                                                                                                                           295 AAGGCCTCGAAGTCATTCCGCCACCCCGGCTACTCCACACAGACCCATGTTAATGACCTC :::
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Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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Last annotation update)
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Name=Klk14;
Mus musculus (Mouse).
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Q80VS4;
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Arakawa T., Bono H., Carninci P., Pukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
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Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Obno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogbe Y., Suzuki H., Tagawa A., Takahashi F., Tanaka T.,
A Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
R EMBL, AK003996, BAB23113.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 GCAGGAGAAGAAGCCCAGGGTGAC-----AAGATTATTGATGGCGCCCCATGTGCA 126
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56 SerGlyGluAspThrArgSerAspSerSerSerArgIleValAsnGlySerAspCysGln 75
                                                                STRAIN=CS7BL/6J; TISSUB=Whole body;
MBDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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prepare full-length cDNA libraries for rapid discovery of new genes.";
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                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/63; TISSUE=Whole body;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
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Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M.,
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RIKEN integrated sequence analysis (RISA) system-384-format
Sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ED1F45D8226FE911 CRC64;
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Mismatches:
Indels:
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PRINTS; PR00722; CHYMCHRYESIN.
SMART; SMO0202; Tryp_SPC; 1.
PROSITE; PS0020; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROCICE 293 AA; 31908 MM; ED1F45D8226FE
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Matches:
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InterPro; IPR001254; Peptidase_S1_S6.
InterPro; IPR001314; Peptidase_S1A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI; MGI:1915918; 1110030019Rik.
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63.6%
45.2%
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RP NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RA INCLEDITIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,

Aprimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,

RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,

RA Aerts A., Altherr M., Caolle C., Chan Y.M., Christensen M.,

RA Cleland C.A., Copeland A., Dains E., Dehal P., Denys M., Detter J.C.,

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RA Escobar J., Plowers D., Fotopulos D., Garcia C., Georgescu A.M.,

RA Escobar J., Plowers M., Gonzales E., Groza M., Hammon N., Hawkins T.,

RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,

RA Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,

RA Hajdatti S., Martinez D., McCready P.M., Medina C., Morgan J.,

RA Blatti S., Martinez D., Salamov A., Salazar A., Salex A.,

ROGERS A., ROGERS S., Salamov A., Salazar A., Salex M., Salex R.,

RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,

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RUEY T.S., DeJong P., Dickson M., Gordon D., Eichler B.E.,

RUEN T.S., Luck A., Rogers S.M.,

RA Rubin E.M., Lucas S.M.,

RY The DNA sequence and biology of human chromosome 19.";

Nature 4028 6.524 6.76 (2014)
                                                                                                                                                          649 AGAGGTACCCTGCAAGGTCTGGTGTCCTGGGGAACTTTCCCTTGCGGCCAACCCAATGAC 708
                                                                                                                                                                                        162 SerGluGlnAlaCysHisArgAlaTyrProGlyIleIleThrSerGlyMetValCysAla 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification and characterization of KLK14, a novel kallikrein serine protease gene located on human chromosome 19q13.4 and expressed in prostate and skeletal muscle.";
                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                       GGCATCCCCGACTCCAAGAAAACGCCTGCAATGGTGACTCAGGGGGACCGTTGGTGTGC
                                                                                                                                                                                                                                                                CCAGGAGTCTACACTCAAGTGCAAGTTCACCAAGTGGATAAATGACACCATGAAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yousef G.M., Diamandis E.P.;
"Molecular characterization, mapping, and tissue expression of KLKLG,
a hormonally regulated allikrein-like gene.";
submitted (UUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kallikrein 14 precursor (EC 3.4.21.-) (Kallikrein-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.
MEDLINES-125.0997; PubMed=11352573; DOI=10.1006/geno.2000.6490;
Hooper J.D., Buil L.T., Rae F.K., Harvey T.J., Myers S.A.,
Ashworth L.K., Clements J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=KLK14; Synonyms=KLKL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics 73:117-122(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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242 Asn 242
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  Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AlaLeuAlaValAlaIleAlaGlnSerGlnGlyAspHisLysIleIleGlyGlyTyrArg
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                                                                                                                                                  STRAIN-NNRI; TISSUE-Mammary tumor. WAP-Tag model. 5 months old;
Strausberg R.; ISSUE-Mammary tumor. WAP-Tag model. 5 months old;
Strausberg R.; ISSUE-Mammary tumor. WAP-Tag model. 5 months old;
Strausberg R.; ISSUE-Mammary tumor. WAP-Tag model. 5 months old;
Exbal; BC044756; AAH44756.1; -; mRNA.
REMBL; BC044756; AAH44756.1; -; mRNA.
REMBL; BC044756; AAH44756.1; -; mRNA.
RGO; GO:0004263; F:chymotrypsin activity; IEA.
RGO; GO:0004293; F:chymotrypsin activity; IEA.
RGO; GO:0004295; F:trypsin activity; IEA.
RGO; GO:0004295; F:trypsin activity; IEA.
RGO; GO:0006208; P:progative regulation of blood coagulation; IEA.
RGO; GO:0006508; P:progative regulation of blood coagulation; IEA.
RINTERPRO; IPR001314; Peptidase_S1A.
RINTERPRO; IPR001314; Peptidase_S1A.
R InterPro; IPR001314; Peptidase_S1A.
R Pfam. PR001089: Trynsin:
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                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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SMART; SM00020; Tryp SPC; 1.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.

PROSITE; PS00135; TRYPSIN SER; 1.
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586.50
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46.1%
                                                    mouse cDNA sequences.
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NUCLEOTIDE SEQUENCE
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                    202 GCTGGGTGCTCACTGCCGCCCACTGCAAGATGAATGAGTACACCGTGCACCTGGGCAGT
                                                                                                          262 GATACGCTG-----GGCGACAGGAGAGCTCAGAGGATCAAGGCCTCGAAGTCATTCCGC
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo K.P., Carainci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Rokbard S.S., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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      148 GIGGCCCIGCICAGIGGC-
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                                                                                                                                                                                 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MEDLINE=20545474; PubMed=10969073; DOI=10.1074/jbc.M004525200; Harvey T.J., Hooper J.D., Myers S.A., Stephenson S.A., Ashworth L.K., Clements J.A.; Hooper J.D., Myers S.A., Stephenson S.A., Ashworth L.K., Tissue-specific expression patterns and fine mapping of the human kallikrein (KLK) locus on proximal 19q13.4."; J. Biol. Chem. 275:37397-37406(2000).
--- SUBCELLUIAR LOCATION: Secreted (Probable).
--- TISSUE SPECIFICITY: High expression in brain, bone marrow and fetal liver. Also expressed in liver, pancreas, fetal spleen, prostate and skeletal muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
similarity).
similarity).
                                                                                                                                 SIMILARITY: Belongs to the peptidase S1 family. Kallikrein subfamily.
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Kallikrein 14.
Peptidase S1.
Charge relay system (By similarit Charge relay system (By similarit By similarity.
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson W.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schlan J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
R EMBL; BC074905, AM474905.1; -; mRNA.
EMBL; BC074904, AA474905.1; -; mRNA.
R EMBL; BC074904, AA474904.1; -; mRNA.
R GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
R GO; GO:0004295; F:trypsin activity; IEA.
R GO; GO:000508; P:proteolysis and peptidolysis; IEA.
NR InterPro; IPR001354; Peptidase S1 S6.
InterPro; IPR001314; Peptidase S1 S6.
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Director MGC Project;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp. SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
PROSITE; PS00135; TRYPSIN SER; 1.
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NUCLEOTIDE SEQUENCE
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Sequence 33,
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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/cgn2_6/ptodata/1/iaa/5_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RC_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                                           protein search, using frame_plus_n2p model
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US-08-557-146-2
US-08-824-874-3
US-09-154-344-2
US-09-210-084-3
US-09-210-084-3
US-09-027-337-4
US-09-027-337-4
US-09-644-600-4
US-09-644-600-4
US-09-644-600-4
US-09-644-600-4
US-09-644-600-4
US-09-644-600-3
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                                                                                                                                                                                                                     572060 seqs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
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                                                               March 11, 2006, 01:54:13
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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DB seq length: 200000000
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Match Length
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Maximum |
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Sequence 395, App
Sequence 395, App
Sequence 8166, Ap
Sequence 7, Appli
Sequence 1, Appli
Sequence 2, Appli
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Sequence 2, Appli
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4, Appli
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712, Ap
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7, Appli
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Sequence 2, A
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS:
TITLE OF INVENTION: POLYMORPH: WELLOW, DETERMINATION: WITH HUMAN DISEASE, METHODS OF:
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-0-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FBALSEQ for Windows Version 4.0
SEQ ID NO 7716
MANDER PAREST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-905-083A-30 (1-969) x US-09-949-016-7716 (1-265)
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-070-526-2
US-09-08-18-299-7
US-09-999-833A-395
US-10-020-445A-395
US-09-949-016-8166
US-09-968-415-7
US-09-068-21A-7
US-09-05-258-427
US-09-05-258-427
US-09-205-258-427
US-09-205-258-427
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US-10-006-041A-170
US-10-012-064A-170
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US-09-949-016-7712
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US-10-015-389A-170
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US-10-015-671A-170
US-10-015-393A-170
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US-09-997-333-309
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US-09-991-181-3(
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Patent No. 6812339
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100.0%
99.6%
77.0%
Percent Similarity:
Best Local Similarity:
Query Match:
TYPE: PRT
ORGANISM: Human
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Matches:
Conservative:
Mismatches:
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REFISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 3103326-181
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                          1.19e-130
1364.00
100.0%
100.0%
76.6%
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Best Local Similarity:
Query Match:
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 CACCTGGGCAGTGATACGCTGGGCGACAGGAGGACTCAGAGGATCAAGGCCTCGAAGTCA
                                                                                                                                                               Sequence 2, Application US/08557146
Patent No. 5834290
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bealand, Torbjorn
APPLICANT: Hanseon, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 CygLysPheThrLysTrplleAsnAspThrMetLysLysHisArg 265
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        730 TGCAAGTTCACCAAGTGGATAAATGACACCATGAAAAAGCATCGC
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STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
COUNTRY: U.S.A.
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US-08-557-146-2
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                                                      256 GGCAGTGATACGCTGGGCGACAGGAGAGCTCAGAGGATCAAGGCCTCGAAGTCATTCCGC 315
                                                                             61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTyrThrValHisLeu 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer
316 CACCCCGGCTACTCCACACACACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC
                                                                                                                                                                                                                                                                                                                                                 436 GGAACCACCTGTACTGTCTCCGGCTGGGGCACTACCACGAGGCCCAGATGTGACCTTTCCC
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COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER BLOADELS FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPC
TURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     736 TTCACCAAGTGGATAAATGACACCATGAAAAAGCATCGC 774
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GENERAL INFORMATION:
FORMERAL INFORMATION:
TAPELICANT: Egalrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneu.
TITLE OF INVENTION: Brayme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A
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; Patent No. 5981256
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: F8845EQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
                                                                                                                                                                                                                             APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STRRET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: Filed Herewith CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: ATTORNEY, LUCY J.
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMUNICATION INCORMATION:
TELECHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                              ; Sequence 3, Application US/08824874; Patent No. 5962300; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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MEDIUM TYPE: Diskett
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CLONE: 532504
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Query Match:
DB:
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Pred. No.:
                                                                                                                                          RESULT 3
US-08-824-874-3
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
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NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELEPANTICATION INFORMATION:
TELEPAN: (212) 819-8783
TELEPHONE: (212) 819-8783
TELEPHONE: (212) 819-8783
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TYPE: Jinear
MOLECULE TYPE: protein
                                                                                                                                                                                      Indels:
                                                                                                                                              1.19e-130
1364.00
100.0%
100.0%
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Best Local Similarity:
                                                                                                                                     Alignment Scores:
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US-08-930-188-2

INC-08-930-188-2

Sequence 2, Application US/08930188

Patent No. 6093397

GENERAL INFORMATION:

APPLICANT: Dixon, Eric P.

APPLICANT: Little, Sheila P.

TITLE OF INVENTION: RELATED NUCLEIC ACIDS

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSE: Eli Lilly and Company

STREE: Lilly Corporate Center

CITY: Indianapolis

STATE: Indiana

COUNTY: Indianapolis

STATE: Indiana

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATION SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/930,188

FILING DATE:

REGIGATION NUMBER: US 08/416,257

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/416,257

PRIORENT INFORMATION:

REGISTATION NUMBER: 38,082

PREPERANCE/COCKETP WIMBER: 38,082

PREPERANCE/COCKETP WIMBER: 38,082

PREPERANCE/COCKETP WIMBER: 38,082
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Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
TELEPRX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.19e-130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 253 amino acids TYPE: amino acid
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221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys
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Matches:
Conservative:
Mismatches:
Indels:
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1364.00
100.0%
100.0%
76.6%
TELEFAX: 415-845-4166
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
                                                                                                                                                                                                                            Similarity:
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                                           315
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                                                                                                                                                                                                                            TGGGGAACTTTCCCTTGCGGCCAACCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
                                                           201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer
AAGGACTTACTGGAAAATTCCATGCTGTGCGCTGGCATCCCCGACTCCAAGAAAACGCC
                                                                                                                                                                                                                                                                                                                                                                                  TGCAATGGTGACTCAGGGGGACCGTTGGTGTGCAGAGGTACCCTGCAAGGTCTGGTGTCC
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MEDIUM TYPE: Diskette
COMPUTER: DES ENSERTE
COMPUTER: DES COMPUTER: DES COMPUTER: DES COMPUTER: DES COMPUTER: DES COMPUTER: DESCRIPTION DATA:
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09210084
Patent No. 6197511
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TILLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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US-09-210-084-3
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201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
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                    161 SerAspLeuMetCysValAspValLysLeulleSerProGlnAspCysThrLysValTyr
GGCAGTGATACGCTGGGCGACAGGAGCTCAGAGGATCAAGGCCTCGAAGTCATTCCGC
                                                               CACCCCGGCTACTCCACACACACATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC
                                                                                 AAGGACTTACTGGAAAATTCCATGCTGTGCGCTGGCATCCCCGACTCCAAGAAAACGCC
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                                                                                                                               376 CAGGCCAGGCTGTCATCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAACCCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9604294

GENERAL INFORMATION:

APPLICANT: Dixon, Eric P.

APPLICANT: Little, Shella P.

ITILE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: RELATED NUCLEIC ACIDS

NUMBER OF SEQUENCES: 3

CORRESPONDENCE: Bli Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis STATE: Indiana

COUNTRY: United States of America
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COMPUTER READABLE FORM:
MEDUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNBER:
APPLICATION UNBER:
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalcok, Dorna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: 38,082
TELECHOME: 317-277-1090
TELECHOME: 317-277-1090
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIFICATION: <UNKnown>
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                                                                          APPLICANT: Hillman, Jennifer L.
Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/210,084
                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY DATE: «UNKNOWN:
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-02
TELECOMMULCATION INFORMATION:
TELEPHONE: 415-845-4166
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                               Sequence 3, Application US/09764762
Patent No. 6472195
GENERAL INFORMATION:
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TYPE: amino acid
STRANDEDNESS: single
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100.0%
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Best Local Similarity:
Query Match:
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Pred. No.:
                 US-09-764-762-3
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Percent Similarity:
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TYPE: PRT
ORGANISM: Unknown
FEATURE:
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Pred. No.:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                       1.19e-130
1364.00
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76.6%
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TYPE: amino acid
; TYPE: propology: linear
; MOLECULE TYPE: protein
PCT-US96-04294-2
                                                                                        Score:
Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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US-09-027-337-4
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Sequence 4, Application US/09027337B
Patent No. 5972616
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REFERENCE: D6064
CURRENT APPLICATION NUMBER: US/09/027,337B
CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 4
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US-09-027-337-4
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Matches:
Conservative:
Mismatches:
Indels:
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                                 21 SerGlyAsnGlnLeuHisCysGlyGlyValLeuValAsnGluArgTrpValLeuThrAla
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US-09-654-600A-4

Sequence 4, Application US/09654600A

Sequence 4, Application US/09654600A

Sequence 4, Application US/09654600A

Sequence 4, Application US/09654600A

GENERAL INFORMATION:

APPLICANT: Tanimoto, Hirotoshi

TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease

TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease

TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease

TITLE OF INVENTION: TADG-15: An Extracellular Serine

FILE REFERENCE: D6064CIP/D

CURRENT APPLICATION NUMBER: 09/621,213

09/027,337

PRIOR FILING DATE: 1999-10-20

1998-02-20

1998-02-20

NUMBER OF SEQ ID NOS: 98

SEQ ID NO 4

LENGTH: 225
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Matches:
Conservative:
Mismatches:
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                                                                                                                                    OTHER INFORMATION: SCCE
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ORGANISM: Homo sapiens
FEATURE:
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Pred. No.:
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Matches:
Conservative:
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Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                             1.69e-117
1235.00
100.0%
100.0%
                        FEATURE: OTHER INFORMATION: SCCE
                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                          LENGTH: 225
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US-09-644-600-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 CACTGCAAGATGAATGAGTACACCGTGCACCTGGGCAGTGATACGCTGGGCGACAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 ValCysArgGlyThrLeuGlnGlyLeuValSerTrpGlyThrPheProCysGlyGlnPro
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Lennart
Recombinant Stratum Corneum Chymotryptic
Enzyme (SCCE)
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                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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Patent No. 5834290
GENERAL INFORMATION:
APPLICANT: Egalrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Str
TITLE OF INVENTION: Recombinant Str
TITLE OF SEQUENCES: 17
NUMBER OF SEQUENCES: 17
                                                                                                                                      5.48e-117
1230.00
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                                                 No. 6232456e
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Best Local Similarity:
                       TOPOLOGY: lir
MOLECULE TYPE:
STRANDEDNESS:
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US-08-557-146-12
                                                   ; MOLECULE TYI
US-08-944-483-33
                                                                                                                         Alignment Scores
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                                                                                                                                                   Pred. No.:
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Sequence 33, Application US/08944483
Patent No. 6232456
GENERAL INFORMATION:
PAPLICANT: CCHEITS, TRACEY L.
APPLICANT: CCHEITS, TRACEY L.
APPLICANT: GRANDOS, EDWALD N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: STEWART, KENED N.
APPLICANT: STEWART, KENED N.
APPLICANT: STEWART, KENED N.
APPLICANT: STEWART, KENED N.
APPLICANT: STEWART, STEWART, THE CHEVEN D.
TITLE OF INVENTION: NOVEL SERINB PROTEASE REAGENTS
TITLE OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
                                                                      140
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                                                                                                                       AAGCTCATCTCCCCCCAGGACTGCACGAAGGTTTACAAGGACTTACTGGAAAATTCCATG
                                                                                                                                                                                                                       CTGTGCGCTGGCATCCCCGACTCCAAGAAAACGCCTGCAATGGTGACTCAGGGGGACCG
                                                                                                                                                                                                                                                                                                                         TTGGTGTGCAGAGGTACCCTGCAAGGTCTGGTGTCCTGGGGAACTTTCCCTTGCGGCCAA
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NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
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100 Abbott Park Road
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SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         760 ATGAAAAGCATCGC 774
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ADDRESSEE: Abbott Lal
STREET: 100 Abbott Pa
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US-08-944-483-33
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US-09-905-083A-30 (1-969) x US-09-154-344-12 (1-225)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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1215.50
99.6%
99.1%
68.3%
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MOLECULE TYPE: polypeptide
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TYPE: amino acida
STRANDEDNESS: single
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-277
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460 TGGGGCACTACCACGAGCCCCAGATGTGACCTTTCCCTCTGACCTCATGTGCGTTGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 GGCAATCAGCTC---CACTGCGGAGGCGTCCTGGTCAATGAGCGCTGGGTGCTCACTGCC
                                                   COUNTRY: U.S.A.

ZIP: 10036-2787

COUNTRY: U.S.A.
ZIP: 10036-2787

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATION WINDER: PATENTIN Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION NUMBER: 108/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: RECARACTION:
NAME: Sterner, Richard J.
REGISTRALION NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 12:
SEQUENCE CHARACTERISTICS:
LEUGTH: 225 amino acide
TYPE: amino acide
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Matches:
Conservative:
Mismatches:
Indels:
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              ADDRESSEE: White & Case, Patent Department STREET: 1155 Avenue of the Americas
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1215.50
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MOLECULE TYPE: polypeptide

US-08-557-146-12
CORRESPONDENCE ADDRESS
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Best Local Similarity:
Query Match:
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Pred. No.:
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CCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAGTTCACCAAGTGGATAAATGACACC 759
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COMPUTER: IBM PC Compatible
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
NAME: STEETEY NUMBER: 35,372
REGISTRATION NUMBER: 35,372
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 35,372
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APPLICANT: Bgelrud, Torbjorn
APPLICANT: Bgelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corne
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
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Patent No. 629163
GENERAL INFORMATION:
APPLICANT: 0. Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: TAGG-12: A No. 6291663el Transmembrane Serine Protease
FILE REFERENCE: D6192
CURRENT APPLICATION NUMBER: US/09/261,416A
CURRENT APPLICATION NUMBER: US/09/261,416A
SEQ ID NO 5: 14
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                                                                         GCCCACTGCAAGATGAATGAGTACACCGTGCACCTGGGCAGTGATACGCTGGGCGACAGG
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                                                                                                                                                                                        AAGAAAGTCAGGCTGCCCTCCCGCTGCGAACCCCTGGAACCACCTGTACTGTCTCCGGC
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                                     GGCAATCAGCTC - - CACTGCGGAGGCGTCCTGGTCAATGAGCGCTGGTGCTCACTGCC
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chymotryptic enzyme (Scce) homologous to similar
domain in TADG-12
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US-09-261-416-7
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ORGANISM: Unknown
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Pred. No.:
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                                                                                                                                              1 CysGlyGlyValLeuValAsnGluArgTrpValLeuThrAlaAlaHisCysLySMetAsn 20
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Search completed: March 11, 2006, 01:57:03 Job time : 48.5 secs



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US-10-461-787-4
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 TYPE: PRT
ORGANISM: Homo sapiens
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Percent Similarity:
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-MODEL=frame+ n2p.model. -DEV=xlp
-Q= dabsg/ABSSWEB = pool/US09905083/runat 10032006_152504_29930/app_query.fasta_1
-Q= dabsg/ABSSWEB = pool/US09905083/runat 10032006_152504_29930/app_query.fasta_1
-DB=Published Applications AA Main -QFWT=fastan -SUFFIX=n2p.rapbm
-MINWATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-THR MAX=100 -TRR MIN=0 -LOOPCL=0 -UNITS=bits -START=1 -END=-1
-THR MAX=100 -THR MIN=0 -ALIGN=15 -OODE=LOCALIGN=200 -THR SCORE=pct
-HEAPSIZE=500 -MINIEN=0 -MAXIEN=200000000 -HOST=abs802p
-USRS=US09905083 aCGN 1 1 307 extuat 10032006 152504 29930 -NCPU=6 -ICPU=3
-UND MMAP -NEG-SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0,5 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0,5 -DELOP=6 -DELEXT=7
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Sequence 2, Appli
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Sequence 48, Appl
Sequence 90, Appl
Sequence 48, Appl
Sequence 639, Appl
Sequence 95, Appl
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2: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
/ /cgn2_6/ptodata/1/pubpaa/USOA_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
                   GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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                                                                                         protein search, using frame_plus_n2p model
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US-09-764-762-3
US-10-071-214-2
US-10-071-214-48
US-10-264-283-90
US-10-295-027-498
US-10-408-765A-639
US-10-408-755A-639
US-10-643-795A-95
US-10-948-518-95
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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            APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIPICATION: CURNOWN>
PRIOR APPLICATION OFF:
APPLICATION NUMBER: 09/210,084
FILING DATE: CURNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEPHONE: 415-85-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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STRANDEDNESS: single
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CURRENT APPLICATION DATA
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                     1 MetAlaArgSerLeuLeuLeuProLeuGInIleLeuLeuSerLeuAlaLeuGluThr
                                                                                                      21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer
                                                                                                                                                                                     41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYETEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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TTCACCAAGTGGATAAATGACACL

TITLE
US-09-764-762-3

Sequence 3, Application US/09764762
Sequence 3, Application US/09764762
Sequence 3, Application US/09764762
Sequence 3, Application US/09764762
TITLE OF INVENTION:
APPLICANT: Hillman, Jennifer L.
Lal, Preeti
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: CA
COUNTRY: USA
ZIP: 94304
PEDIUM
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Qy         616         TGCAATGGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCTGCAAGGTCTGGTGTCC         675           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy         436 GGAACCACCTGTACCTGGCTGGGGCACTACCACGAGCCCAGATGTGACCTTTCCC	CTTTCCC 495           rphePro 160
Qy         676 TGGGGAACTTTCCCTTGCGGCCAACCCAATGACCCAGAGTCTACACTCAAGTGTGCAAG 735           Db         221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240	Qy 496 TCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCCCCAGGACTGCACGAAGGTTTAC	GGTTTAC 555           SValTyr 180
Qy         736 TTCACCAAGTGGATAAATGACACCATGAAAAAGCATCGC         774           L	Qy         556 AAGGACTTACTGGAAAATTCCATGCTGTGGCTGGCATCCCCGACTCCAAGAAAACGCC	AAACGCC 615          8A8nAla 200
ESULT 3 S-10-071-214-2 Sequence 2, Application US/10071214 Sequence 2no. US20030066099A1 GENERAL INFORMATION: APPLICANT: HANSSON, Lennart APPLICANT: EGELRUD, Torbjorn	Qy         616         TGCAATGGTGACTCAGGGGGACCGTTGGTGGAGGTACCCTGCAAGGTCTGGTGTCC           Db         201         CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer           Qy         676         TGGGGAACTTTCCCTTGCGGCCAACCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG           Db         221         TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys	HTCTGGTGTCC 675 
; Illia C F INVENTION: SOCCE MULIFIED IRANSCENIC MANMALS AND THEIR USE AS MODELS OF HUMAN; FILE REFERENCE: HANGSON=3A; CURRENT APPLICATION NUMBER: US/10/071,214; CURRENT FILING DATE: 2002-02-11; PRIOR APPLICATION NUMBER: US 60/267,422	Oy 736 TTCACCAAGTGGATAAATGACACCATGAAAAAGCATCGC 774 	
; PRIOR FILING DATE: 2001-02-09 ; PRIOR APPLICATION NUMBER: DK PA 2001 00218 ; PRIOR FILING DATE: 2001-02-09 ; NUMBER OF SEQ ID NOS: 50 ; SOFTWARE: Patentin version 3.1	RESULT 4 US-10-071-214-48 ; Sequence 48, Application US/10071214 ; Bublication No. US20030066099A1 ; GENERAL, INFORMATION	
; SEQ ID NO 2 ; LEWGTH: 25.3 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-071-214-2	,	SE AS MODELS OF HUMAN
Alignment Scores: 1.26e-118 Length: 253 Score: 1364.00 Matches: 253 Percent Similarity: 100.0\$ Mismatches: 0 Query Match: 4.6\$ Gaps: 0 DB:	; CURRENT FILING DATE: 2002-02-11 ; PRIOR APPLICATION NUMBER: US 60/267,422 ; PRIOR FILING DATE: 2001-02-09 ; PRIOR APPLICATION NUMBER: DK PA 2001 00218 ; PRIOR FILING DATE: 2001-02-09 ; NUMBER OF SEQ ID NOS: 50 ; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 48	
US-09-905-083A-30 (1-969) x US-10-071-214-2 (1-253)		
Oy 16 AIGGCAAGATCCCTTCTCCTGCCCTGCAGATCTTACTGCTATCCTTAGCCTTGGAAACT 75	<ul> <li>UKGANTANI ATLIICIAI Sequence</li> <li>FEATURE:</li> <li>OTHER INFORMATION: Deduced amino acid sequence from the C-term</li> <li>ICHER INFORMATION: homo sapiens.</li> </ul>	C-terminal part of SCCE from
Qy         76 GCAGGAGAAGAAGACCCAGGATTATTGATGATGCCCCCATGTGCAAGAGGCTCC         135	ignment Scores: 1.26e-118 Length:	
Oy 136 CACCCATGGCAGGTGGCCTGCTCAGTGGCAATCAGCTCCACTGCGGAGGCGTCCTGGTC 195	354.00 00.08 00.08 6.68	
Qy         196 AATGAGGGTGCTGACTGCCCCCACTGCAAGATGAATACACCGTGCACCTG         255           Db         61 A8nGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTyrThrValHisLeu         80	-09-905-083	
Oy 256 GGCAGTGATACGCTGGGCGACAGGAGAGCTCAGAGGATCAAGGCCTCGAAGTCATTCCGC 315	Oy 16 ATGGCAAGATCCCTTCTCCTGCCCTGCAGATCTTACTGCTATCCTTAGCCTTGGAAACT	3GAAACT 75         uGluThr 20
316 CACCCGGCTACTCCACACAGACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC	Oy 76 GCAGGAGAAGAAGCCCAGGGTGACAAGATTATTGATGGCGCCCCATGTGCAAGAGGCTCC	AGGCTCC 135         gGlySer 40
DB 101 H18FroGLYTYrSerThrGinThrH18ValA8nA8pLeuMetLeuValLy8LeuA8nSer 120 Qy 376 CAGGCCAGGCTGTCATCCATGGTGAAAGTCAGGCTGCCCTCCCGCTGCGAACCCCT 435	Qy 136 CACCCATGGCAGGTGGCCTGCTCAGTGGCAATCAGCTCCACTGCGGAGGCGTCCTGGTC	CCTGGTC 195

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                                                      GGCAGTGATACGCTGGGCGACAGGAGAGCTCAGAGGATCAAGGCCTCGAAGTCATTCCGC 315
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                            CACCCCGCTACTCCACACACACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC
                                                                                                     CAGGCCAGGCTGTCATCCATGGTGAAGAAGTCAGGCTGCCCTCCCGCTGCGAACCCCT
                                                                                                                                                                         201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer
                  GGAACCACCTGTACTGTCTCCGGCTGGGGCACTACCACGAGCCCAGATGTGACCTTTCCC
                                                                                                                                                                                                     TCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCCCCAGGACTGCACGAAGGTTTAC
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HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 90, Application US/10264283
| Publication No. US2030144494A1
| GENERAL INFORMATION
| APPLICANT: Algate, Paul A. |
| APPLICANT: Mannion, Jane | TITLE OF INVENTIONS CONSITIONS AND METHODS FOR THE THEI | TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEI | TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEI | TITLE OF INVENTION: 21012.590 | CURRENT APPLICATION NUMBER: US/10/264,283 | CURRENT FILING DATE: 2002-10-02 | NUMBER OF SEQ ID NOS: 111 | SOFTWARE: Corixa Invention Disclosure Database | SEQ ID NO 90 | LENGTH: 253
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Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Homo sapiens
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-264-283-90
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21 AlaGiyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer
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                                                                GCAGGAGAAGAAGCCCCAGGGTGACAAGATTATTGATGGCGCCCCCATGTGCAAGAGGCTCC
                                                                                                                                               CACCCATGGCAGGTGGCCCTGCTCAGTGGCAATCAGCTCCACTGCGGAGGCGTCCTGGTC
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APPLICANT: Aziz, Natasha
APPLICANT: Gishery, Wendy M.
APPLICANT: Gisheberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Howezi, Peter A.
APPLICANT: Howezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Warray, Richard
APPLICANT: Wasson, Susan R.
APPLICANT: Weston, Susan R.
APPLICANT: Weston, Susan R.
APPLICANT: Weston, Susan R.
APPLICANT: Weston, Susan R.
APPLICANT: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer,
FILE REFERENCE: 018601-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR FILING DATE: 2000-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 498, Application US/10295027; Publication No. US20030232350A1; GENERAL INFORMATION:
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RESULT 7
US-10-13-99-48

i Sequence 48, Application US/10173999

i Publication No. US20040005563A1

i GENERAL INFORMATION:

APPLICANT: Mack, Day;

APPLICANT: Gish, Kurt C.

APPLICANT: Gish, Kurt C.

TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions

TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian

TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian

TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian

TITLE OF INVENTION: Cancer

FILE REPERENCE: 018501-002420US

CURRENT FILING DATE: 2001-06-18

PRIOR APPLICATION NUMBER: US 60/299,234

PRIOR APPLICATION NUMBER: US 60/399,234

PRIOR APPLICATION NUMBER: US 60/399,234

PRIOR PILING DATE: 2001-08-27

PRIOR FILING DATE: 2001-08-27

PRIOR FILING DATE: 2001-04-12

NUMBER OF SEQ ID NOS: 163

SEQ ID NO 48

LENGTH: 253

TYPE: PAT

TYPE: PAT

TYPE: PAT

TYPE: PAT

SORJANISM: Homo sapiens
                                                                                             201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
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PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR PILING DATE: 2001-11-13
PRIOR PLING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR PLING DATE: 2001-11-29
PRIOR PLING DATE: 2001-11-29
PRIOR PLING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR PLING DATE: 2002-01-10
PRIOR PPLING DATE: 2002-01-10
PRIOR PLING DATE: 2002-02-08
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ORGANISM: Homo sapiens
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APPLICANT: KENNETH J. HILLAN
APPLICANT: RENNETH J. HILLAN
APPLICANT: PAUDEW POLSON
APPLICANT: VICTORIA SNITH
APPLICANT: UCTORIA SNITH
APPLICANT: SPENCER
APPLICANT: SPENCER
APPLICANT: THOMAS D. WU
APPLICANT: SEMIN ZHANG
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: P5026R1-US
CURRENT APPLICATION NUMBER: US 60/404,809
PRIOR APPLICATION NUMBER: US 60/404,809
PRIOR APPLICATION NUMBER: US 60/405,645
PRIOR APPLICATION NUMBER: US 60/413,192
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US-10-643-795A-95
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APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
TITLE OF INVENTION: TARGETS FOR THERABEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: 1DENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF STEVENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT PILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SEQ ID NO 639
SEQ ID NO 639
LENGTH: 253
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US-10-408-765A-639
US-10-408-765A-639
Sequence 639, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Rahy, Boin D.
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ORGANISM: Homo sapiens
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CORGANISM: Homo sapien
US-10-643-795A-95
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                                           RESULT 10

US-10-948-518-95

Sequence 95, Application US/10948518

Publication No. US20050064492A1

GENERAL INFORMATION:
APPLICANT: FREDERIC J. DESAUVAGE
APPLICANT: RENDERIC J. DESAUVAGE
APPLICANT: RENDERIC J. DESAUVAGE
APPLICANT: PAUL POLAKIS
APPLICANT: PAUL POLAKIS
APPLICANT: ANDREW POLSON
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION WHERE: US/10/948,518
CURRENT APPLICATION NUMBER: US/10/643,795
FRIOR FILING DATE: 2004-09-22
FRIOR PELLING DATE: 2002-08-21
FRIOR PELLING DATE: 2002-08-21
FRIOR PELLING DATE: 2002-08-21
FRIOR PELLING DATE: 2002-08-21
FRIOR APPLICATION NUMBER: US 60/405,645
FRIOR APPLICATION NUMBER: US 60/419,008
FRIOR APPLICATION NUMBER: US 60/426,947
FRIOR PELLING DATE: 2002-01-01
FRIOR APPLICATION NUMBER: US 60/426,947
FRIOR PELLING DATE: 2002-01-01
FRIOR APPLICATION NUMBER: US 60/426,947
FRIOR PELLING DATE: 2002-01-01
FRIOR PELLING DATE: 2002-01-01
FRIOR FILING DATE: 2003-07-02
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US-10-948-518-95
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Publication No. US2004003822341
GENERAL INFORMATION:
APPLICANT: Smithson, Glenda
APPLICANT: Peyman, John A.
APPLICANT: Peyman, John A.
APPLICANT: Peyman, John A.
APPLICANT: Li, Li
APPLICANT: Peyman, Mera
APPLICANT: Batturajan, Meera
APPLICANT: Batturajan, Meera
APPLICANT: Batturajan, Mera
APPLICANT: Batturajan, Meera
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Adherson, Linda
APPLICANT: Anderson, Linda
APPLICANT: Zerbusen, Bryan D.
APPLICANT: Zerbusen, Bayan D.
APPLICAN
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Shenoy, Suresh G.
Shimkete, Richard A.
Rothenberg, Mark E.
Leach, Martin D.
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Miller, Charles E.
Rastelli, Luca
Stone, David J.
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US-10-262-511-92
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; Sequence 1, Application US/1086841
; Sequence 1, Application No. US20050106586A1
; GENERAL INFORMATION:
    APPLICANT: Diamandis, Eleftherios
; TITLE OF INVENTION: Detection of Neurodegenerative Dis; FILE REFERENCE: 11757.96USU1
; CURRENT APPLICATION NUMBER: US/10/868,490A
; CURRENT APPLICATION NUMBER: US 60/478,486
; PRIOR FILING DATE: 2003-06-13
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
LENGTH: 253
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CORGANISM: Homo sapiens
US-10-868-490A-1
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Best Local Similarity:
Query Match:
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US-10-868-490A-1
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161 MetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyrLysAspLeu 180
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                                                                  141 CysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPheProSerAspLeu
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US-10-144-394-38

i Sequence 38, Application US/10344394

is Publication No. US20040058342A1

i GENERAL INFORMATION:

APPLICANT: Yousef, George M.

ITILE OF INVENTION: NOVEL KALLIKREIN GENE

FILE REPERRENCE: 1177-51UNO

CURRENT PEPLICATION NUMBER: US/10/344,394

CURRENT FILING DATE: 2003-02-11

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-08-11

PRIOR FILING DATE: 2000-08-11

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin version 3.1

SEQ ID NO 38

LENGTH: 257

TYPE: PATENTION HOME SAPING 
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APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
FILLE OF INVENTION: NOWEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILLE REPERENCE: 21402-462C
CURRENT PILING DATE: 2003-05-28
FRICH PRICA PILING DATE: 2001-10-28
FRICH APPLICATION NUMBER: 60/326,483
PRICH FILING DATE: 2002-04-19
PRICH FILING DATE: 2002-04-19
PRICH FILING DATE: 2002-04-19
PRICH FILING DATE: 2002-05-16
PRICH FILING DATE: 2002-06-16
PRICH FILING DATE: 2002-06-16
PRICH RELIGH DATE: 2002-06-16
PRICH PRICH APPLICATION NUMBER: 60/381,260
PRICH RILING DATE: 2002-04-17
PRICH FILING DATE: 2002-04-17
PRICH FILING DATE: 2002-04-17
PRICH FILING DATE: 2002-04-17
PRICH PRICH DATE: 2002-04-19
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ORGANISM: Homo sapiens
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Percent Similarity:
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CURRENT FILLING DATE: 2003-05-26

PRIOR PLICATION NUMBER: 60/326,483

PRIOR PLLING DATE: 2001-10-02

PRIOR APPLICATION NUMBER: 60/313,815

PRIOR APPLICATION NUMBER: 60/327,917

PRIOR FILING DATE: 2000-09

PRIOR PLING DATE: 2002-05-17

PRIOR PLING DATE: 2002-05-17

PRIOR PLING DATE: 2002-05-17

PRIOR PLING DATE: 2002-05-17

PRIOR PLING DATE: 2002-10-09

PRIOR PLING DATE: 2002-10-09

PRIOR PLING DATE: 2002-10-09

PRIOR PLING DATE: 2002-05-16

PRIOR PLING DATE: 2001-00-09

PRIOR PLING DATE: 2001-00-09

PRIOR PLING DATE: 2001-00-09

PRIOR PLING DATE: 2001-00-09

PRIOR PLING DATE: 2002-04-17

PRIOR PLING DATE: 2002-04-17

PRIOR PLING DATE: 2002-04-19

PRIOR PLING DATE: 2001-00-05

REMAINING PRIOR APPLICATION NUMBER: 60/327,435

PRIOR PLING DATE: 2001-00-05

REMAINING DATE: 2001-00-05

REMAINING DATE: 2001-00-05

REMAINING PRIOR APPLICATION NUMBER: 60/327,435

PRIOR PLING DATE: 2001-00-05

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               GATGTGACCTTTCCCTCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCCCCAGGAC
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                                                                          TCGAAGTCATTCCGCCACCCCGGCTACTCCACACAGACCCATGTTAATGACCTCATGCTC
                                                                                                                                                            GTGAAGCTCAATAGCCAGGCCAGGCTGTCATCCATGGTGAAGAAAGTCAAGGCTGCCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Age, Michiel L.
APPLICANT: Age, Michiel L.
APPLICANT: Berghs, Constance
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
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Anderson, David W.
Zhong, Mei
Catterton, Elina
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Miller, Charles E.
Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
Shimkets, Richard A.
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US-10-262-511-102
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Search completed: March 11, 2006, 02:21:02 Job time : 183 secs
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                                                                      TCAGGGGGACCGTTGGTGCAGAGGTACCCTGCAAGGTCTGGTGTCCTGGGGAACTTTC
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APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Peyman, John A.
APPLICANT: Peyman, John A.
APPLICANT: Peyman, John A.
APPLICANT: Abuse B.
APPLICANT: Ou, Jingfang
APPLICANT: Ou, Jingfang
APPLICANT: Ou, Jingfang
APPLICANT: Go, Xiaojia (Sasha)
APPLICANT: Spivek, Kimbelly A.
APPLICANT: Spivek, Kimbelly A.
APPLICANT: Spivek, Kimbelly A.
APPLICANT: Spivek, Kimbelly A.
APPLICANT: Malyankar, Unida
APPLICANT: Anderson, Landa
APPLICANT: Anderson, Bavid W.
APPLICANT: Anderson, Bavid W.
APPLICANT: Carterton, Elina
APPLICANT: Shimkets Rachall J.
APPLICANT: Shimkets Rachall J.
APPLICANT: Shimkets Rachall J.
APPLICANT: Shimkets, Elina
APPLICANT: Shimkets, Elina
APPLICANT: Carterton, Boyla G.
APPLICANT: Shimkets, Elina
APPLICANT: Shimkets, Gol319, 235
FRIOR APPLICANTON NUMBER: Gol329, 297
FRIOR PILING DATE: 2001-10-09
FRIOR PILING DATE: 2002-06-17
FRIOR PILING DATE: 2002-06-17
FRIOR PILING DATE: 2002-06-17
FRIOR APPLICANTON NUMBER: Gol329, 235
FRIOR APPLICANTON NUMBER:
                                                                                                                                                                                                                                                                          231 IleAsnAspThrMetLysLysHisArg 239
                                                                                                                                                                                                                                                     ATAAATGACACCATGAAAAAGCATCGC
                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 94, Application US/10262511; Publication No. US20040038223A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
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US-10-262-511-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 ThrValSerGlyTrpGlyThrThrTserProAspValThrPheProSerAspLeuMet 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Remaining Prior Application data removed - See File Wrapper or PALM.; NUMBER OF SEQ ID NOS: 439; SOFTWARE: CuraSeqList version 0.1; SEQ ID NO 94; LENGTH: 252; TYPE: PRT
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Matches:
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Sequence 11, Application US/10412748

Sequence 11, Application US/10412748

Publication No. US20060035219A1

GENERAL INFORMATION:
APPLICANT: Queensland University of Technology
APPLICANT: Queensland University of Technology
TITLE OF INVENTION: Aberrant Kallikrein Expression
FILE REFERENCE: DAVIJ72.003A04

CURRENT APPLICATION NUMBER: US/10/412,748

PRIOR APPLICATION NUMBER: AU PS1616/02

PRIOR FILING DATE: 2002-04-09

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin version 3.2

LENGTH: 253

TYPER: RET.
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Query Match:
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Sequence 14, Appl
Sequence 17, Appl
Sequence 98, Appl
Sequence 19, Appl
Sequence 2, Appli
Sequence 7, Appli
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Sequence 7, Appli
                                                                                                                                         March 11, 2006, 02:15:14; Search time 3.5 Seconds (without alignments) 1541.257 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*

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8: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                     GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-412-748-14
US-11-037-243-98
US-11-037-243-98
US-10-412-748-19
US-10-131-826A-456
US-10-412-748-2
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Result No.

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1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuLeuSerLeuAlaLeuGluThr 20 76 GCAGGAGAAGACCCAGGGTGACAAGATTATTGATGGCCCCCATGTGCAAGAGGCTCC 13 [	256 GGCAGTGATACGCTGGGCGACAGGAGCTCAGAGGATCAAGGCCTCGAAGTCATTCCGC 3	Oy         496 TCTGACCTCATGTGCGTGGATCTCCCCCCGGGATGCACGAGGATTAC 555           Db         161 SerAepLeuMetCysValAspValLysbLulleSerProGlnAepCysThrLysValTyr 180           Cy         556 AAGGACTTACTGGAAAATTCCATGCTGTGCGCTGGCATCCCCGACTCCCAAGAAAAACGCC 615           Db         181 LysAapLeuLeuGluAenSerMetLeuCysAlaGlyIleProAepSerLysLysAsnAla 200           Cy         616 TGCAATGGTGACTCAGGGGACCTTGGTGCAGAGGTACCCTGCAAGGTCTGGTGTCC 675           Db         201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220           Cy         676 TGGGGAACTTTCCCTTGCGGCCAACCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735           Db         221 TrGGlyThrPheProCysGlyGlyGlnProAsnAspProGlyValTyThrGlnValCysLys 240           Cy         736 TTCACCAAGTGGATAAAAGCATCGATGAAAAAGCATCGC 774	Db 241 PheThrLyGTrpIleAsnAspThrMetLySLySHisArg 253 RESULT 2 US-10-412-748-14 Sequence 14, Application US/10412748 Sequence 14, Application US/10412748 Publication No. US20060035219A1 GENERAL INFORMATION: APPLICANT: Queensland University of Technology APPLICANT: Clements, Judith A ITILE OF INVENTION: Aberrant Kallikrein Expression FILE REFERENCE: DAVILT2.003AUS CHORMAT APPLICANT NAMERE: INS/10/412 748	CURRENT FILING DATE: 2003-04-09 PRIOR APPLICATION NUMBER: AU PS1616/02 PRIOR FILING DATE: 2002-04-09 NUMBER OF SEQ ID NOS: 41 SOFTWARE: Patentin version 3.2 SAG ID NO 14 LENGTH: 253 TYPE: PRT ORGANISM: Human G-10-412-748-14 Lignment Scores: 7.13e-116 Length: 126

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Alignment Scores
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Matches:
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US-11-037-243-98
; Sequence 98, Application US/11037243
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         version 3.2
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Percent Similarity:
Best Local Similarity:
Query Match:
6
; NUMBER OF SEQ ID NOS:
; SOFWARRE: Patentin ve
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORPANISM: Human
US-10-412-748-17
                                                                Alignment Scores:
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Matches:
Conservative:
Mismatches:
Indels: US-09-905-083A-30 (1-969) x US-11-037-243-98 (1-253) Publication No. US20050287546A1
GENERAL INFORMATION:
APPLICANT: HOLOWANN, GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CAENEPEEL, SEAN
APPLICANT: MANNING, GERARD
TILES OF INVENTION: NOVEL PROTEASES
TILE REPERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/11/037,243
CURRENT FILING DATE: 2005-05-26
PRIOR FILING DATE: 2001-06-26
PRIOR PILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIN Ver: 2.1
SEQ ID NO 98
LENGTH: 253
TYPE: PRT 7.13e-116 1364.00 100.0% : 100.0% 76.6% ; ORGANISM: Homo sapiens US-11-037-243-98 Percent Similarity: Best Local Similarity: Query Match: DB: 929 181 ð

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APPLICANT: STEWART, INDECTY A.
APPLICANT: Watanabe, Colin K
APPLICANT: Mondy, William
APPLICANT: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION WABER: US/049911
PRIOR FILING DATE: 1997-06-18
PRIOR PLICATION NUMBER: 60/05914
PRIOR FILING DATE: 1997-09-17
PRIOR PLILING DATE: 1997-09-17
PRIOR PRILING DATE: 1997-09-17
PRIOR PLILING DATE: 1997-09-18
PRIOR PLILING DATE: 1997-09-19
PRIOR PLILING DATE: 1997-09-18
PRIOR PLILING DATE: 1997-09-19
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerriteen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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34.4%
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Query Match:
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; ORGANISM: Homo
US-10-131-826A-456
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US-10-131-826A-456
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US-10-412-748-19
i Sequence 19, Application US/10412748
i Publication No. US20060035219A1
i GENERAL INFORMATION:
    APPLICANT: Clements, Unith A
    TITLE OF INVENTION: Aberrant Kallikrein Expression
    FILE REFERENCE: DAVIJ2.003AUS
CURRENT APPLICATION NUMBER: US/10/412,748
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: AU PSI616/02
PRIOR PILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 41
i SOFTWARE: Patentin version 3.2
i LENGTH: 181
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Matches:
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114 PheArgValArgLeuGlyHisTyrSerLeuSerProValTyrGluSerGlyGlnGlnMet 133
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                          GCAGGAGAAGAAGCCCAGGGTGAC------AAGATTATTGATGGCGCCCCATGT 123
                                          241 TACACCGTGCACCTGGGCAGTGATACGCTGGGC-----GACAGGAGAGCTCAGAGG
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US-09-905-083A-30 (1-969) x US-10-131-826A-456 (1-293)
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Publication No. US20060035219A1

GRENERAL INFORMATION:
APPLICANT: Olements, Judith A

TITLE OF INVENTION: Aberrant Kallikrein Expression;
FILE REFERENCE: DAVI172.003AUS

CURRENT APPLICATION NUMBER: US/10/412,748

CURRENT APPLICATION NUMBER: AU PS1616/02

PRIOR APPLICATION NUMBER: AU PS1616/02

PRIOR FILING DATE: 2002-04-09

NUMBER OF SEQ ID NOS: 41

SEQ ID NO 2

LENGTH: 293
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US-10-412-748-2
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Alignment Scores:

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114 PheArgValArgLeuGlyHisTyrSerLeuSerProValTyrGluSerGlyGlnGlnMet 133
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| Publication No. US20060035219A1
| GENERAL INFORMATION:
| APPLICANT: Oucensland University of Technology
| APPLICANT: Clements, Judith A
| TITE OF INVENTION: Aberrant Kallikrein Expression
| FILE REPERENCE: DAVI172.003AUS
| CURRENT APPLICATION NUMBER: US/10/412,748
| CURRENT FILING DATE: 2003-04-09
| PRIOR RPLICATION NUMBER: AU PS1616/02
| PRIOR FILING DATE: 2002-04-09
| NUMBER OF SEQ ID NOS: 41
| SEQ ID NO 7
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                            US-09-905-083A-30 (1-969) x US-10-412-748-2 (1-293)
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                             Percent Similarity:
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114 PheArgValArgLeuGlyHisTyrSerLeuSerProValTyrGluSerGlyGlnGlnMet 133
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Sequence 456, Application US/10973115B
Sequence 456, Application US/10973115B
SEQUENCE No. US20060040351A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: DeFosige, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
                                                                                                                                      8.12e-48
612.50
66.0%
47.9%
34.4%
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Best Local Similarity:
Query Match:
DB:
                    TYPE: PRT
ORGANISM: Human
                                                                                                                      Alignment Scores:
                                                                    US-10-412-748-7
LENGTH: 293
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APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Thuse, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: STEWARTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SAGNET: 2004-10-22
PRIOR PRILING DATE: 2004-10-22
PRIOR PLILING DATE: 2001-12-19
PRIOR PLILING DATE: 2001-12-19
PRIOR PLILING DATE: 2000-12-01
PRIOR PLILING DATE: 2000-12-01
PRIOR PLILING DATE: 2000-12-01
PRIOR PLILING DATE: 2000-03-02
PRIOR PLILING DATE: 2000-03-02
PRIOR PLILING DATE: 2000-03-02
PRIOR PLILING DATE: 1999-03-05
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Gurney, Austin L.
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Best Local Similarity:
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; ORGANISM: Homo
US-10-973-115B-456
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Sequence 553, Application US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DATE: 2004-11-24
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 553
LENGTH: 267
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| ProhlaArgIleGlyArgAlaValArgProIleGluValThrGlnAlaCysAlaSerPro 155
                                                                                                                                                     556 AAGGACTTACTGGAAAATTCCATGCTGTGCGCTGGCATCCCCGACTCCAAGAAAACGCC 615
                                                                                                                                                                                                                                                                                      676 TGGGGAACTTTCCCTTGCGGCCAACCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
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Matches:
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US-10-995-561-553
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Best Local Similarity:
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US-10-995-561-553
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Pred. No.:
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19.10-995-561-552
19.10-995-561-552
Sequence 55.2, Application US/10995561
Sequence 55.2, Application US/10995561
Sequence 55.2, Application No. US20050272054A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF FILE REPERBACE: CLO01559
TITLE OF INVENTION: USPECTION AND USES THEREOF
FILE REPERBACE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FRALSEQ for Windows Version 4.0
                                                                                                                                    ::: ||| |||||||||| || 214 GlnlysArgCluAspAlaTyrProArgCluIleAspAspThrMetPheCysAlaGly 233
                                                                                                                                                                                                     592 ATCCCCGACTCCAAGAAAAACGCCTGCAATGGTGACTCAGGGGGGACCGTTGGTGTGCAGA 651
                                                                                                                                                                                                                                                  GGTACCCTGCAAGGTCTGGTGTCCTGGGGAACTTTCCCTTGCGGCCAACCCCAATGACCCA 711
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                                                                    CCCCAGGACTGCACGAAGGTTTACAAGGACTTACTGGAAAATTCCATGCTGTGCGCTGGC
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Indels:
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Matches:
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583.00
61.2%
44.0%
32.8%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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LENGTH: 267
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46 ATCTTACTGCTATCCTTAGCCTTGGAAACTGCAGGA----GAAGAAGCCCAGGGTGACAAG 102
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| 133 GlySerLysValLysPro1leSerLeuAlaAspHisCysThrGlnProGlyGlnLysCys 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACTGCAAGATGAATGAGTACACCGTGCACCTGGGCAGTGATACGCTG-----GGCGAC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277 AGGAGAGCTCAGAGGATCAAGGCCTCGAAGTCATTCCGCCACCCCGGCTACTCCACA--- 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyProGluGlnGluileProValValGlnSerlleProHisProCysTyrAsnSerSer 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HisCyslyslysProLysTyrThrValArgLeuGlyAspHisSerLeuGlnAsnLysAsp 92
PRIOR PAPLICATION NUMBER: 60/059115
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PLICATION NUMBER: 60/059184
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-19
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CysAlaGluValLysIlePheProGlnLysLysCysGluAspAlaTyrProGlyGlnIle
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1118
26
888
111
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Matches:
Conservative:
Mismatches:
Indels:
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582.50
59.3%
48.6%
32.7%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Homo US-10-131-826A-396
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Pred. No.:
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                                                                                                                                                     435
                                                                               262 GATACGCTG-----GGCGACAGGAGACTCAGAGGATCAAGGCCTCGAAGTCATTCCGC 315
                                                                                                         ||||||:::
| ProAlaArgIleGlyArgAlaValArgProIleGluValThrGlnAlaCysAlaSerPro 155
                                                                                                                                                                                                                                                                                                       496 TCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCCCCAGGACTGCACGAAGGTTTAC 555
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                             APPLICANT: Zhang, Zemin TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT APPLICATION NUMBER: US/40/49911
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 00/056974
                                                                                                                                                                                                                                 376 CAGGCCAGGCTGTCATCCATGGTGAAGAAGTCAGGCTGCCCTCCCGCTGCGAACCCCCT
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwoo, Austin L.
Sherwoor Smith, Victoria
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Wood, William
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Filvaroff, Ellen
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US-10-131-826A-396
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODINC
TITLE OF INVENTION: SAME
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                                                                                                                                                                                                                                                                                                                                                                                  448 ACTGTCTCCGGCTGGGGCACTACCACGAGCCCAGATGTGACCTTTCCCTCTGACCTCATG 507
                                                                                                                                                                          508 TGCGTGGATGTCAAGCTCATCTCCCCCCAGGACTGCACGAAGGTTTACAAGGACTTACTG 567
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CURRENT APPLICATION NUMBER: US/10/973,115B
CURRENT PILING DATE: 2004-10-22
PRIOR PILING DATE: 2004-10-27
PRIOR PILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR PILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 10/026,072
PRIOR APPLICATION NUMBER: US 09/581,742
PRIOR FILING DATE: 2000-12-01
PRIOR PILING DATE: 2000-06-16
PRIOR FILING DATE: 2000-06-16
PRIOR FILING DATE: 1999-06-16
PRIOR FILING DATE: 1999-03-05
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Sequence 396, Application US/10973115B
; Publication No. US20060040351A1
; GENERAL INFORMATION:
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Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Gao, Wei-Quiang
Gerritsen, Mary E.
Goddard, Audrey
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Wood, William I.
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Gurney, Austin L.
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; Sequence 2, Application US/10510321
; Publication No. US20050287528A1
; GENERAL INFORMATION:
; APPLICANT: Diamandis, Eleftherios P.
; APPLICANT: Kishi, Tadaaki
; TITLE OF INVENTION: Methods for Detecting Ovarian Cancer;
; FILE REFERENCE: 11757.104USWO
; CURRENT APPLICATION NUMBER: US/10/510,321
CURRENT FILING DATE: 2004-10-04
; PRIOR FILING DATE: 2003-04-04
; PRIOR FILING DATE: 2003-04-04
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 2
LENGTH: 260
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: HUMAN PROTEASE MOLECULES NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS: ADDRESSEE: Incyte Pharmaceuticals, Inc.
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580.50
59.3*
48.6*
                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                       COMPUTER READABLE FORM:
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IMMEDIATE SOURCE:
                                                         Palo Alto
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                                                         CITY: Palo
STATE: CA
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Pred. No.:
                                                                                COUNTRY:
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CysAlaGluValLysIlePheProGlnLysLysCysGluAspAlaTyrProGlyGlnIle 192
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                                                                                 US-09-905-083A-30 (1-969) x US-10-973-115B-396 (1-260)
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Matches:
Conservative:
Mismatches:
                                                Indels:
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Publication No. US20050282214A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hilman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Googler, Karl J.
APPLICANT: Googler, Karl J.
APPLICANT: Googler, Karl J.
APPLICANT: Shah, Purvi
  4.18e-45
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Matches:
Conservative:
Mismatches:
Indels:
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COMPUTER: IBM Compatible
COMPUTER: FASEES (or Windows Version 2.0
SOFTWARE: FASEES (or Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/183,914
FILING DATE: 19-UULY-2005
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271
FILING DATE: 16-Jan-1998
PRIOR APPLICATION NUMBER: CUNKNOWN-
FILING DATE: APPLICATION NUMBER: CUNKNOWN-
ATTORNEY-AGENT INPORMATION:
NAME: MODAIN-PEREFERON, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/POCKET NUMBER: 41,201
REFERENCE/P
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B: Incyte Pharmaceuticals,
3174 Porter Dr.
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508 TGCGTGGATGTCAAGCTCATCTCCCCCCAGGACTGCACGAAGGTTTACAAGGACTTACTG 567
                                                                                                                                                                                      113 AspValGluAspHisAsnHisAspLeuMetLeuLeuGlnLeuArgAspGlnAlaSerLeu 132
                   388 TCATCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAACCCCTGGAACCACCTGT 447
                                 ||| |||||| ::: |||
133 GlySerLysValLysProIleSerLeuAlaAspHisCysThrGlnProGlyGlnLysCys 152
                                                                                                                ||| :::||||||:::
173 CysAlaGluValLysIlePheProGlnLysLysCysGluAspAlaTyrProGlyGlnIle 192
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Search completed: March 11, 2006, 02:21:42 Job time : 22.5 secs .



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RESULT 1
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March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds (without alignments) 45.628 Million cell updates/sec
           GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Listing first 45 summaries
                                                          protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Human NOV Human NOV Novel hum Stratum c Stratum c Human NOV Human NOV Human NOV Human NOV ΝO Aae08294 Human str Human str Human SUMMARIES ADR68792 ADR68870 ADA05740 ADA05740 ADR23378 ADI37151 ADA05738 ADI3705738 ADA05736 ADN62900 ADN62908 ADN62908 ADN21100 ADN62908 ADN62906 ADN62906 ADN62896 ADN62896 ADN62896 ADN62896 ADN62896 AAE08236 ADR68850 AAE08294 Query Match Length DB 2222 22222 22222 2222 2220 2220 2222 2222 100.0 100.0 100.0 100.0 100.0 100.0 Score Result

Aar67888 Human str	Aaw05383 Human amy	Abb84421 Human SCC	Abb84406 Human SCC	Aau82740 Amino aci	Abu07440 Protein d	Abu07471 Protein d	Abr58471 Human str	Adb80484 Ovarian c	Adj68833 Human hea	Adn39180 Cancer/an	Adl06515 Human tum	Adn04182 Antipsori	Adr72880 Human ova	Ady67588 Human kal	Aec00353 Human kal	Aab21326 Human HSC	Abb84422 Rat SCCE	Aae08326 Human str	Adr68883 Human str	Aae08298 Human str	
AAR67888	AAW05383	ABB84421	ABB84406	AAU82740	ABU07440	ABU07471	ABR58471	ADB80484	ADJ68833	ADN39180	ADL06515	ADN04182	ADR72880	ADY67588	AEC00353	AAB21326	ABB84422	AAE08326	ADR68883	AAE08298	
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25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia. Human stratum corneum chymotrypsin enzyme peptide #59 (residues 72-80). Diagnosing cancer comprises detecting stratum corneum chymotrypsin AAE08294 standard; peptide; 9 AA 07-FEB-2001; 2001WO-US003977. 11-FEB-2000; 2000US-00502600 (first entry) (UYAR-) UNIV ARKANSAS WPI; 2001-514676/56. WO200159158-A1. Homo sapiens. 01-NOV-2001 16-AUG-2001. O'brien TJ; AAE08294; 

Disclosure, Page 115, 127pp, English. enzyme

The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCB). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCB oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide

Sequence 9 AA;

Human

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Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:89
                                                                               WO2004075723-A2
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                                                                                                                                                                                         Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia.
                                                                                                                                                                        Human stratum corneum chymotrypsin enzyme peptide #1 (residues 72-80).
                     Gaps
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 100.0%; Score 49; DB 4; Length 9; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
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                                                                                                            AAE08236 standard; peptide; 9 AA.
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Best Local Similarity 100.00
9; Conservative
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The invention relates to a novel method for vaccinating an individual against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating an individual with a SCCE peptide, which elicits an immune response in the individual with a SCCE peptide, which elicits an immune response in chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or at risk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligonucleotide is useful for treating an enoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or pancreatic cancer, and other cancers in which SCCE is overexpressed. The peptides are also useful in the monitoring and development of immunotherapies for ovarian and other malignancies. The present sequence represents a peptide fragment of serine protease SCCE (stratum corneum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
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serine protease; stratum corneum chymotrytic enzyme; SCCE;
immune response; ovarian cancer; lung cancer; prostate cancer;
pancreatic cancer; colon cancer.
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immune response; ovarian cancer; lung cancer; prostate cancer;
pancreatic cancer; colon cancer.
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09-0CT-2001;
12-0CT-2001;
12-0CT-2001;
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22-0CT-2001;
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29-OCT-2001;
01-NOV-2001;
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                                                                                                                                                                                  The invention relates to a novel method for vaccinating an individual against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating an individual with a SCCE peptide, which elicits an immune response in the individual with a SCCE peptide, which elicits an immune response in the individual A peptide of the invention acts as a stratum corneum chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or a trisk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligonucleotide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or peptides are also useful in the monitoring and development of immunocherapies for ovarian and other malignancies. The present sequence represents a peptide fragment of serine protease SCCE (stratum corneum
                                                                                                                    Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:109.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             serine protease; stratum corneum chymotrytic enzyme; SCCB;
immune response; ovarian cancer; lung cancer; prostate cancer;
pancreatic cancer; colon cancer.
                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 49; DB 8; Length 9; 100.0%; Pred. No. 2e+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                 Claim 5; SEQ ID NO 31; 117pp; English
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         20-FEB-2004; 2004WO-US005134.
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                                                                                                                                                                                                                                                                                                                                       chymotrytic enzyme)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004075723-A2
                                                                                                                                                                                                                                                                                                                                                          Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                          O'brien TJ,
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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ADR68870
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                                                                                                                                                                                                                                             against stratum corneum chymotry incurvant (SCCE), comprising inculating an individual with a SCCE peptide, which elicits an immune response in the individual with a SCCE peptide, which elicits an immune response in the individual. A peptide of the invention acts as a stratum corneum chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or at risk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligonucleotide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or peptides are also useful in the monitoring and development of immunotherapies for ovarian and other malignancies. The present sequence represents a peptide fragment of serine protease SCCE (stratum corneum
Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
                                                                                                                                                                                                                  The invention relates to a novel method for vaccinating an individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 49; DB 8; Length 9; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
                                                                                                                                             Disclosure, SEQ ID NO 109, 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human NOV18e protein SEQ ID NO:100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA05740 standard; protein; 97 AA.
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2001US - 0327435P.
2001US - 0327449P.
2001US - 0328029P.
2001US - 0328044P.
2001US - 0328046P.
2001US - 0328044P.
2001US - 03329444P.
2001US - 0329046P.
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2001US-0343629P.
2001US-0349575P.
2001US-0346357P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
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The present live and describes Nova procesus, where A can be a two so described above and a carrier; (2) a kit comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NoVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically by binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for determining the presence of or predisposition to a disease associated with altered levels of expression of the above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or above; (10) a method for identifying a potential therapeutic agent for comparing for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating or predisposition to a pathology associated with the polypeptide; (12) a method for modulating or predisposition to a pathology associated with the above polypeptide. Novx sequences have antidiabetic, anorectic, antibacterial, virucide, and manual; and (14) a method for producing the above polypeptide in a seful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic card molecule may be used to diagnose, treat or prevent metabolic card molecule may be used to diagnose, treat or prevent metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Raetelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes NOVX proteins, where X can be 1 to 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 171; 586pp; English.
               19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373817P.
19-APR-2002; 2002US-0373826P.
19-APR-2002; 2002US-037384P.
22-APR-2002; 2002US-0381037P.
16-MAY-2002; 2002US-0381038P.
17-MAY-2002; 2002US-0381642P.
28-MAY-2002; 2002US-0381642P.
28-MAY-2002; 2002US-0381642P.
28-MAY-2002; 2002US-0381642P.
28-MAY-2002; 2002US-038156P.
25-JUN-2002; 2002US-0381385P.
01-OCT-2002; 2002US-0381381P.
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N-PSDB; ADA05739
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Score 49; DB 6; Length 97; Pred. No. 0.12;
 100.0%;
100.0%;
  Query Match
Best Local Similarity
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Sequence 97 AA;

human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer: cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X; Gapa ö Indele ö Mismatches ADN62904 standard; protein; 97 AA. ö 2001US-0326483P. 2001US-0327435P. 2001US-0327449P. 2001US-0327917P. 2001US-0328029P. 2001US-0328044P. 2001US-0328056P. 2001US-0328849P. 2001US-0329414P. 2001US-0343629P. 2001US-0349575P. 2001US-0346357P. 01-OCT-2002; 2002US-00262511 2001US-0330142P 001US-0330309P 2001US-0341058P 2001US-0339266P 2002US-0373260P 2002US-0373815P 2002US-0373817P 2002US-0373826P 2002US-0373884P 2002US-0374977P 2002US-0381037P 2002US-0381038P 2002US-0381042P 2002US-0383656P 25-JUN-2002; 2002US-0391335P 2002US-0383831P 01-JUL-2004 (first entry) 9; Conservative SPYTEK K A. EDINGER S R. ELLERMAN K. MALYANKAR U M. 53 KONNEYTVHL 61 1 KMNEYTVHL 9 PATTURAJAN M. MILLET I. PEYMAN J A. KEKUDA R. SMITHSON G. wasting disorder US2004038223-A1. 05-OCT-2001; 09-OCT-2001; 09-OCT-2001; 09-OCT-2001; 17-0CT-2001; 18-0CT-2001; 22-0CT-2001; 24-0CT-2001; SUO X Homo sapiens. Human NOV18e 12-OCT-2001; 15-OCT-2001; 22-APR-2002; 16-MAY-2002; 02-OCT-2001; 29-OCT-2001; 01-NOV-2001; 17-APR-2002; 19-APR-2002; 19-APR-2002; 19-APR-2002; 19-APR-2002; 16-MAY-2002; 16-MAY-2002; 28-MAY-2002; 26-FEB-2004. ADN62904; (EDIN/) (ELLE/) (MALY/) (LILL/) (GUOX/) (PATT/) (SPYT/) (MILL/) (/LIWS) KEKU/ Matches ADN62904 셤 ð

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PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E.
LEACH M D.
                                                        AGEE M L.
BERGHS C.
DIPIPPO V A.
EISEN A.
GANGOLLI B.
RIEGER D K.
                                                                                        Millet I.
  GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
                                                                                 SPADERNA S K.
                  CATTERTON E.
                         MILLER C E.
RASTELLI L.
STONE D J.
                                                                                                                    WPI; 2004-213931/20.
                                                                                                                        N-PSDB; ADN62903.
               ZHONG M.
                                                                                                                                                                                                                                                                    Sequence 97 AA;
                                                                        (GANG/)
(RIEG/)
(SPAD/)
                              (RAST/)
(STON/)
                                                                 (DIPI/)
(RISE/)
               ZHON/)
                      (JEMMIC)
                                      (PENA/)
                                          (SHEN/)
                                              (SHIM/)
                                                      (LEAC/)
                                                         AGEE/)
                                                              (BERG/)
           ANDE/
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The invention relates to isolated NOVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the abstract expression and activity of NOVX polypeptides. For example, NOVX polypeptides and activity of NOVX polypeptides. For example, NOVX polypeptides and cour polymucleotides may be used to treat disorders associated with decreased expression or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polymetric assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may also be used as anti-low modulate NOVX polypeptide antibodies and antagonists and polymucleotide expression and activity of NOVX polypeptides antibodies may be used in this way to prevent, diagnose and treat: metabolic disorders, immune disorders, disorders, and the various dyslipidaemias, metabolic disorders, metabolic syndrome X and the various dyslipidaemias, metabolic disorders, metabolic syndrome X and the various dyslipidaemias, metabolic metabolic syndrome X and the various dyslipidaemias, metabolic metabolic metabolic syndrome X and the various dyslipidaemias, metabolic met
                                                                                                                                                                                                                                                                                         Dipippo VA;
Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Elsen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease
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Gaps

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100.0%; Score 49; DB 8; Length 97; 100.0%; Pred. No. 0.12; ive 0; Mismatches 0; Indels

9; Conservative

Query Match Best Local Similarity Matches 9; Conserv

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PRR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a cuplypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders cupolypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations creponable for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in celectronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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100.0%; Pred. No. 0.18;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID NO 53737; 103pp; English
                                                                                                                                                                                                            Novel human diagnostic protein #23369.
                                                                                                     ABG23378 standard; protein; 136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                           18-FEB-2002 (first entry)
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Best Local Similarity 100.
Matches 9; Conservative
WPI; 2001-639362/73.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS87565
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                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                 RESULT 8
ABG23378
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The invention relates to extracellular serine protease termed tumour antigen derived gene-14 (TADG-14) and its nucleic acid. Composition comprising TADG-14 peptide is useful for treating a neoplastic state in an individual. The neoplastic state is chosen from ovarian cancer, colon cancer, prostate cancer in which TADG-14 is overexpressed. The present sequence is Stratum corneum chymotryptic enzyme (scce) catalytic domain. This sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated DNA encoding tumor antigen derived gene-14 protein, useful for treating neoplastic state (such as ovarian cancer, breast cancer, lung cancer, colon cancer, prostate cancer) in an individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunomodulator, cytostatic, nootropic, neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obseity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
neoplastic state; cancer; ovary; breast; lung; colon; prostate; chymotryptic enzyme; scce; enzyme.
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98US-00137944.
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Les 9; Conservative
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                                                                                                                      US2003199010-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 144 AA;
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                                                                          Homo sapiens
                                                                                                                                                                                                                                                             21-AUG-1997;
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                                                                                                                                                                                                                                                                                  21-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dendritic cells directed toward extracellular serine protease termed tumour antigen derived gene-14 (TADG-14). The method of the invention involves exposing the immune cells to a TADG-14 protein fragment, where exposure to the TADG-14 protein fragment activates the immune cells. The invention is used for the production of activated immune T cells or dendritic cells. The invention allows screening to identify proteases overexpressed in carcinoma. The present sequence is stratum corneum chymotryptic enzyme (scce) catalytic domain. This sequence is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Production of activated immune cells or dendritic cells by exposing immune cells to tumor antigen derived gene protein fragment consisting of amino acid sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                   Immune T cell; dendritic cell; extracellular serine protease;
tumour antigen derived gene-14; TADG-14; carcinoma;
stratum corneum chymotryptic enzyme; scce.
                                                                                                                                                                                                                                                             corneum chymotryptic enzyme (scce) catalytic domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 49; DB 8; Length 144; 100.0%; Pred. No. 0.19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 4; 44pp; English.
                                                                                                                      ADI39727 standard; protein; 144 AA.
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98US-00137944.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O'brien TJ, Underwood LJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KMNEYTVHL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-118109/12
       78 KMNEYTVHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6642013-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-AUG-1998;
                                                                                                                                                                                                               15-APR-2004
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Best Local &
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ADI39727
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09-0CT-2001; 20010S-0379179.

09-0CT-2001; 20010S-0328029P.

09-0CT-2001; 20010S-0328049P.

12-0CT-2001; 20010S-0328049P.

15-0CT-2001; 20010S-0329144P.

17-0CT-2001; 20010S-0339149P.

18-0CT-2001; 20010S-0339169P.

24-0CT-2001; 20010S-0341058P.

24-0CT-2001; 20010S-0341058P.

24-0CT-2001; 20010S-0341058P.

24-0CT-2001; 20010S-0341058P.

24-0CT-2001; 20010S-034957P.

17-APR-2002; 2002US-034957P.
                                                                                                                                19-APR-2002; 2002US-0373815P.

19-APR-2002; 2002US-0373817P.

19-APR-2002; 2002US-037382F.

19-APR-2002; 2002US-037384P.

22-APR-2002; 2002US-0374977P.

16-MAY-2002; 2002US-0381037P.

16-MAY-2002; 2002US-0381042P.

17-MAY-2002; 2002US-0381642P.

28-MAY-2002; 2002US-0381642P.

28-MAY-2002; 2002US-0381642P.

29-MAY-2002; 2002US-0381642P.
                                                                                                                                                                                                                                     01-OCT-2002; 2002US-00262511
                                                                                                                                                                                                                                                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                               WPI; 2003-381626/36.
N-PSDB; ADA05737.
                                                                                                                                                                                                                                                                                                                                                                                  pharmacogenomics.
                                                                                                                                                                                                                                                                    Smithson G, M
Patturajan M,
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Shimkets RA,
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thson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; turajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; M, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; hkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; en AJ, Gangolli EA, Rieger DK, Spaderna SK; Ju J, Li L, Guc man K, Malyankar UM; w Catterton E;

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or

Claim 1; Page 171; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOVI). Also described: (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit comprising, in one or more
containers, the composition described above; (3) an isolated nucleic acid
comprising the nucleic acid molecule described above; (5) a cell.

comprising the nucleic acid molecule described above; (5) a cell.

comprising the nucleic acid molecule described above; (6) an entitody that immunospecifically
binds to the polypeptide described above; (7) methods for determining the
presence or amount of the above polypeptide or nucleic acid molecule in a
sample; (8) methods for determining the presence of or predisposition to
a disease associated with altered levels of expression of the above
comprising a nucleic acid molecule in a first mammalian subject; (9) a
method of identifying an agent that binds to the polypeptide described
above; (10) a method for identifying a potential therapeutic agent for
ca berrant physiological interactions of the polypeptide; (11) a method of
acceptance or amount of activity or of latency or predisposition to
aberrant physiological interactions of the polypeptide; (11) a method of
creening for a modulator of activity or of latency or predisposition to
compression or preventing a pathology associated with the above polypeptide in a
consecutor, cytostatic, antibacterial, virucide,
consecutors have antidiabetic, anorectic, antibacterial, virucide,
consecutors have antidiabetic, anorectic, antibacterial, The
consecutor and antilipaemic activities, and can be used in gene therapy. The

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                                                                                                                                                                                                                                                                                                                                                                                                         human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson; disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to disquose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
                                                                                                                                                                                          Gaps
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                                                                                                                                                                 6; Length 181;
                                                                                                                                                                                        0; Indels
                                                                                                                                                                 100.0%; Score 49; DB 6;
100.0%; Pred. No. 0.25;
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                                                                                                                                                                                                                                                                                                        ADN62902 standard; protein; 181 AA.
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2001US-0328029P.
2001US-0328044P.
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2001US-0328849P.
2001US-0329414P.
2001US-0330142P.
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2001US-0341058P.
2001US-034362P.
2001US-034362P.
2001US-0346357P.
2002US-0373260P.
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2002US-0381642P
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                                                                                                                                                                                                                                                                                                                                                         01-JUL-2004 (first entry)
                                                                                                                                                                           Local Similarity 100
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                                                                                                                                                                                                                 1 KMNEYTVHL
                                                                                                               present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            wasting disorder
                                                                                                                                         Sequence 181 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-0CT-2001; 2
09-0CT-2001; 2
09-0CT-2001; 2
12-0CT-2001; 2
15-0CT-2001; 2
17-0CT-2001; 2
18-0CT-2001; 2
24-0CT-2001; 2
24-0CT-2001; 2
                                                                                                                                                                                                                                                                                                                                                                                  Human NOV18d.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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Matches
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100.0%; Score 49; DB 8; Length 181; 100.0%; Pred. No. 0.25; cive 0; Mismatches 0; Indels

9; Conservative

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1 KMNEYTVHL

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disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, haematopoietic disorders, and the various dysliptdaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
 diagnose and treat: metabolic disorders, diabetes, obesity, infectious
                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 9; Conservat
                                                                                                                                                       Sequence 181 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated NOVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the abberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and activity of NOVX polypeptides associated with decreased expression or activity of NOVX by supplementing the patient our production or to recrify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX colymetric and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of calmilar sequences in samples, and so which patients may be in need of calmilar sequences in samples, and so which patients may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists may also be used as used as antibopypeptides. The anti-NOVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polymucleotides may be used in this way to prevent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM, Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenborg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated NOVX polypeptides and nucleic acids, useful for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 98; 395pp; English.
29-MAY-2002; 2002US-038331P.
25-JUN-2002; 2002US-0391335P.
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RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
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RIEGER D K.
SPADERNA S K.
                                                                                                                                                                     PATTURAJAN M.
SPYTEK K A.
EDINGER S R.
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MALYANKAR U M.
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BERGHS C.
DIPIPPO V A.
                                                                                                                                                                                                                                                                                          ZERHUSEN B D.
ANDERSON D W.
                                                                MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                              CATTERTON E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-213931/20.
                                                   SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEACH M D.
                                                                                                                                                                                                                                                                              GORMAN L.
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(LEAC/)
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                                                                                                                                                                                         (SPYT/
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immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human dieease;
metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                           human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                            ADA05736 standard; protein; 198 AA
                                                                                                                        Human NOV18c protein SEQ ID NO:96.
                                                                                                                                                                                                                                                                                                                        2001US-0327449P.
2001US-0327917P.
2001US-0328029P.
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2001US-0349575P.
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2002US-0373826P.
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2001US-0329414P
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2002US-0383656P.
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                                                                                                    06-NOV-2003 (first entry)
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53 KMNEYTVHL 61
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                                                                                                                                                                                                                                                                                                                                                                                     15-0CT-2001
17-0CT-2001
28-0CT-2001
24-0CT-2001
24-0CT-2001
29-0CT-2001
01-NOV-2001
                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                       09-OCT-2001;
09-OCT-2001;
                                                                                                                                                                                                                                                                                                                         05-OCT-2001;
                                                                                                                                                                                                                                                                                                                                              09-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                             12-OCT-2001;
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                                                                                                                                                                                                                                                                                                                  05-OCT-2001;
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                                                                                ADA05736;
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(MILL/)
(PEYM/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KEKU/)
(JUJJ/)
(LILL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SPYT/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GORM/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes NOVX proteins, where X can be 1 to 55 C (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more described above; and a carrier; (3) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule described above; (5) a cell or comprising the nucleic acid molecule described above; (5) a cell or comprising the nucleic acid molecule described above; (5) a cell or presence or amount of the above polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a disease associated with altered levels of expression of the above a polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for above; (10) a method of identifying a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator or factivity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulation or reventing a pathology associated with the above polypeptide in a sectivity or of latency or predisposition to corpression or a pathology associated with the above polypeptide or mammal; and (14) a method for producing the above polypeptide or section of a pathology associated with the above polypeptide or section of a pathology associated with the above polypeptide or section of sections or an anitial and (14) a method for producing the above polypeptide or section of a pathology associated with the above polypeptide or section of a pathology associated with a human disease. The polypeptide or the nucleic syndrome associated with a human disease. The polypeptide or pathology and disperse such as disperse or 
                                                                                                                                                                                                                                                 ng M, Catterton B;
A, Shenoy SG;
Berghs C, Dipippo VA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                 Guo X;
                                                                                                                                                                                 Li L, Guo )
Malyankar UM;
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                                                                                                                                                                  Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li Patturajan M, Spytek KA, Edinger SR, Ellerman K, Mal. Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Sh Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Bergh Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 170; 586pp; English.
25-JUN-2002; 2002US-0391335P 01-OCT-2002; 2002US-00262511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100...
-hag 9; Conservative
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                                                                                                         (CURA-) CURAGEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADA05735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmacogenomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 198 AA;
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ADN62900 standard; protein; 198 AA.

RESULT 14
ADN62900
ID ADN62
XX
AC ADN62

ઠ 셤 ADN62900

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anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
                                      human; NOVX; metabolic disorder; diabetes; obesity; infectious disease.
                                                                                                                                                    2001US-0326483P.
2001US-0327443P.
2001US-03274449P.
2001US-03274449P.
2001US-0328029P.
2001US-0328044P.
2001US-0328044P.
2001US-0330144P.
2001US-0330148P.
2001US-0330199P.
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2001US-0343629P.
2001US-0346357P.
2001US-0373260P.
2002US-0373815P.
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2002US-0373884P.
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                                                                                                                                                                                                                                                                                                                                                 2002US-0381042P.
2002US-0381642P.
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2002US-0383831P.
                                                                                                                                     01-OCT-2002; 2002US-00262511
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                                                                                                                                                                                                                                                                                                                                                                                  25-JUN-2002; 2002US-0391335P
        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                GUO X.
PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                                                                         MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATTERTON E.
                                                                                                                                                                                                                                                                                                                                                                                                 SMITHSON G.
                                                                      wasting disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GORMAN L.
                                                                                                      US2004038223-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZHONG M
                                                                                                                                                                                                                                          22-OCT-2001; 2
24-OCT-2001; 2
24-OCT-2001; 2
29-OCT-2001; 2
01-NOV-2001; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                  다.
다.
                        Human NOV18c.
                                                                                       Ното варіелв.
                                                                                                                                                                                                             12-OCT-2001;
                                                                                                                                                                                                                                                                                                   19-APR-2002;
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16-MAY-2002;
        01-JUL-2004
                                                                                                                     26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (STON/)
(PENA/)
(SHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANDE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZHON/
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Human NOV18g protein SEQ ID NO:104

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The invention relates to isolated NOVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the abserrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and corpleted to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the colls own genes and preventing their expression. NOVX polypeptic and complementary sequences may also be used as DNA probbe in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. The entil of antibodies, agonists and antagonists may also be used as anti-NOVX polypeptide antibodies, agonists and antagonists may also be used as diagnostic agonists and polymucleotide expression and activity of NOVX polypeptides. The anti-NOVX polypeptide antibodies may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, anorexia, cancer, cancer-associated achexia, neurodegenerative disorders, alzheimer's Disease, Parkinson's Dispersion and the warious dislibutions and the disorders, and the various dislibutions and activity of NOVX character associated achexia, neurodegenerative haematopoletic disorders, and the various dislibutions and activity of an anti-NOVX character associated achexia, neurodegenerative themselved and the activity of an a
                                                                                                                                                                                                                                                              Smithson G, Millet I, Peyman JA, ARALLETTON MALYANKAL ...,
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankal ...,
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E,
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Shimkets RA, Rothenberg ME, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 96; 395pp; English.
SHIMKETS R A. ROTHENBERG M E.
                                                                                                                                                         EISEN A.
GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
                                                                            AGEE M L.
BERGHS C.
DIPIPPO V A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-213931/20.
N-PSDB; ADN62899.
                                                    LEACH M D.
                                                                                                                                                         (EISE/)
(GANG/)
(RIEG/)
(SPAD/)
                                                 (LEAC/)
                                                                                                        BERG/)
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Sequence 198 AA;

Gaps ö 100.0%; Score 49; DB 8; Length 198; 100.0%; Pred. No. 0.27; ive 0; Mismatches 0; Indels Local Similarity 100. nes 9; Conservative Query Match Matches

72 KMNEYTVHL 80 σ 1 KMNEYTVHL

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ADA05744 standard; protein; 224 AA. ADA05744; RESULT 15 ADA05744

06-NOV-2003 (first entry)

immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obseity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoletic disorder; dyslipidaemia. human; NOVX; antidiabetic; anorectic; antibacterial; virucide; 2001US-0327435P. 2001US-0327449P. 2001US-0327917P. 2001US-0328044P. 2001US-0328056P. 2001US-0328849P. 2001US-0339266P. 2001US-0343629P. 2001US-0349575P. 2001US-0346357P. 2002US-0373260P. 2002US-0373817P. 2002US-0373826P. 2002US-0373884P. 2002US-0374977P. 002US-0381042P. 2001US-0329414P. 2002US-0381037P. 2002US-0381038P 2002US-0381642P. 002US-0383656P. 02-OCT-2002; 2002WO-US031373 2001US-0328029P 2001US-0330142P 2001US-0330309P 2001US-0341058P 2002US-0373815P 2002US-0383831P 2002US-0391335P WO2003029424-A2. 15-OCT-2001; 17-OCT-2001; 18-OCT-2001; Homo sapiens 09-OCT-2001; 12-OCT-2001; 22-OCT-2001; 29-OCT-2001; 01-NOV-2001; 17-APR-2002; 19-APR-2002; 19-APR-2002; 22-APR-2002; 16-MAY-2002; 16-MAY-2002; 09-OCT-2001; 17-MAY-2002; 10-APR-2003 25-JUN-2002 

(CURA-) CURAGEN CORP.

Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhueen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

WPI; 2003-381626/36. N-PSDB; ADA05743

ö

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabbetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

Claim 1; Page 172; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector

comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or above; (10) a method for identifying of the polypeptide; (11) a method of sociated with the polypeptide; (12) a method of a pathology associated with the polypeptide; (12) a method for modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (13) methods of treating or pathology associated with the polypeptide; (12) a method for modulating the above polypeptide; Novx cor preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a crivity of the polypeptide, and can be used in gene therapy. The squances have antidiabetic, anorcotic, antibacterial, virucide, immunomodulator, cytostatic, nortropic, neuroprotective, antiparkinsonian complexity and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or prevent metabolic cor disease, immune disorders such as diabetes or obesity, infections, cancer, neurodegenerative disorders under acids can also be used as hybridisation of probes, in chromosome mapphing, tissue typing, preventive medicine and probes, in chromosome mapphing, tissue typing, preventive medicine acids can also be used to be acid present invention. 

Sequence 224 AA;

Gaps ö 100.0%; Score 49; DB 6; Length 224; 100.0%; Pred. No. 0.32; ive 0; Mismatches 0; Indels Ouery Match
Best Local Similarity luv...
9; Conservative

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1 KMNEYTVHL 9

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S8 KMNEYTVHL 66

Search completed: March 11, 2006, 00:24:09 Job time : 89.6667 secs



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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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- protein search, using sw model OM protein March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds (without alignments) 61.367 Million cell updates/sec Run on:

US-09-905-083A-31 Title: Perfect score:

1 KMNEYTVHL 9 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_80:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	% Query Match Length	80	SUMMAKIES	Description
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н	49	100.0	253	0	A53968	serine proteinase
7	39	79.6	_		YVBPK3	Д
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4	37	75.5	334	~	B98019	conserved hypothet
ហ	37	75.5	393	~	D75207	hypothetical prote
9	36	73.5	627	~	T25395	
7	36	73.5	1829	~	T34239	hypothetical prote
œ	35	71.4	159	8	A11406	ρ
σ	35	71.4	159	N	A11782	spermidine/spermin
10	35	71.4	505	~	H75431	
11	35	71.4	555	~	AD1794	ise a
12	35	71.4	667	N	T09013	RING finger protei
13	35	71.4	667	N	T09482	
14	34	69.4		7	A43711	
12	34	69.4	270	~	S28682	replication protei
16		69.4	285	~	F70348	_
17		69.4	421	~	AH1120	7
18	34	69.4	421	~	AC1481	conserved hypothet
19		67.3	204	7	E95345	FixJ Transcription
20	33	67.3	204	N	B31227	nitrogen fixation
21		67.3	218	N	S53354	calflagin Tb-24 -
22	33	67.3	218	~	E83724	hypothetical prote
23	33	67.3	227	~	D83796	ent
24		67.3	229	~	S53355	calflagin Tb-1.7 -
25		67.3	233	٦	AQUI17	flagellar calcium-
56	33	67.3	407	N	\$53353	calflagin Tb-44A -
27		67.3	422	~	T11714	hypothetical prote
28	33	67.3	429	7	H70307	ansl
53	33	67.3	525	~	B84028	oligopeptide ABC t

hypothetical prote	TonB-dependent rec	pyr1-3 protein - s	probable membrane	pyrimidine synthes	50S ribosomal prot	hypothetical prote	ribosomal protein	hypothetical prote	hypothetical prote	MdaB protein homol	hypothetical prote	hypothetical prote	probable membrane-	conserved hypothet	citrate/sodium sym
C72379	A87470	523738	E71622	QZD0P3	H89908	AE2172	S24989	E97262	F71215	G81301	C90033	H75378	F97121	A89800	F82280
Ο .	~	~	~	-4	~	N	~	7	~	7	~	N	N	~	~
664	677	1042	1308	1481	49	84	116	130	144	192	228	304	339	371	448
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67.3	67.3	67.	67.	67.	65.	65	65	65	65	65	65	9	65	9	9
33 67.3	33 67.3							32 65							

## ALIGNMENTS

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C.Species: Homo sapiens (man)
C.Species: O7-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C.Species: D3-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C.Species: D3-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C.Stroes of D3-Jul-1995 #sequence 07-Jul-1995 #text_change 09-Jul-2004
C.Stroes of D3-Jul-1995 #sequence 0-Jul-1995 #text_change 09-Jul-2004
C.Stroes of D3-Jul-1995 #text_change 09-Jul-2004
C.Stroes of D3-Jul-1995
C.Stroes of D3-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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serine proteinase SCCE precursor - human
N'Alternate names: stratum corneum chymotryptic enzyme
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72 KMNEYTVHL 80 1 KMNEYTVHL 9 셤 ò

lysis protein t - phage K3 C.Species: phage K3 A,Note: host Escherichia coli C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004 C;Accesion: A27083

A.Title: Lysis gene t of T-even bacteriophages: evidence that colicins and bacteriophage A.Title: Lysis gene t of T-even bacteriophages: evidence that colicins and bacteriophage A.Title: Lysis gene t of T-even bacteriophages: A.Title: Lysis gene t of T-even bacteriophages: A.Accession: A27083
A.Accession: A27083
A.Molecule type: DNA
A.Residues: 1-218 <AIE>
A.Forestion: A.Genecies: UNIPROT:P10393, UNIPARC:UP10000138941; GB:M16812; NID:g215503; PIDN:A.Forestive: the author translated the codon CAA for residue 85 as Ile and CAG for residue 20: C.Genetics:
A.Genetics:
A.Genetics: C.Superfamily: phage T4 lysis protein t
C.Superfamily: phage T4 lysis

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C;Accession: D75207
R;anonymous, Genoscope
Bubmitted to the EMBL Data Library, July 1999
A;Bescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struct
A;Reference number: A75001
A;Accession: D75207
A;Status: preliminary
A;Molecule type: DNA
A;Redecule type: DNA
A;Residues: 1-393 <KAW>
A;Cross-references: UNIPROT: Q97291; UNIPARC: UPI0000063251; GB:AJ248283; GB:AL096836; NID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: 220027
A;Accession: T25395
A;Accession: T25395
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Redidues: 1-627 <WILL>
A;Redidues: 1-627 <WILL>
A;Cross-references: UNIPROT: Q9XU04; UNIPARC: UPI0000077722; EMBL: Z92813; PIDN: CAB07289.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F26F12.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T34239
R;Wilson, R.; Bentley, D.; Gattung, S.
Submitted to the EMBL Data Library, April 1996
A;Reference number: 221493
A;Reference number: 221493
A;Accession: T34239
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CjSpecies: Caenorhabditis elegans
CjBate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CjAccession: T25395
                                                                                                      C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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C;Superfamily: Caenorhabditis elegans hypothetical protein Y57A10A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: PAB2235
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH0196
                                                                  hypothetical protein PAB2235 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Length 393;
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1larity 66.7%; Pred. No. 29;
Conservative 2; Mismatches
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: clone T28A8 C; Genetics:
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Best Local Similarity 66.7
Matches 6; Conservative
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129 KLPEYTIHL 137
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KMNEYSIEL 70
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Matches 6; Conserv
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T34239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Molecule type: DNA
A, Residues: 1-218 cMONS
A, Residues: 1-218 cMONS
A, Cross-references: UNIPROT: P06808, UNIPARC: UPI00005CBE7; GB: Y00408, NID: g15368; PIDN: G
A, Note: the sequence is almost identical with that of the B.coli phage K3
C, Comment: At the end of the growth cycle, phage T4 expresses two genes with lysis funct about the gene product of t, although it has been suggested that it acts as a phospholi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-334 <KUR>
A;Cross-references: UNIPROT:Q8DFG2; UNIPARC:UPI00000E35EF; GB:AE007317; PIDN:AAK99982.1;
C;Genetics:
A;Gene: spr1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein spr1179 [imported] - Streptococcus pneumoniae (strain R6 C, Species Streptococcus pneumoniae C; Species Streptococcus pneumoniae C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004 C; Date: 28-Oct-2001 #text_change 09-Jul-2004 C; Date: 28-Date: 28-Date:
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                                                                                                                                                                                                                                                                                                                                                                   lysis protein t - phage T4
C;Species: phage T4
A;Note: host Escherichia coli
A;Note: host Escherichia coli
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: JF0028; S07395
R;Montea, D.; Degen, M.; Henning, U.
Nucleic Acids Res. 15, 6736, 1987
A;Fitle: Nucleotide sequence of gene t (lysis gene) of the E. coli phage T4.
A;Reference number: S07395; MUID:87316934; PMID:3628006
                                                                      Gaps
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Length 218;
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Pred. No. 2.3;
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                                                                      0; Indels
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C;Superfamily: phage T4 lyais protein t
C;Reywords: host cell lysis; transmembrane protein
P;35-49/Domain: transmembrane #status predicted <TMN>
Score 39; DB 1
Pred. No. 2.3;
                                                                      1; Mismatches
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   79.6%;
87.5%;
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87.58;
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Best Local Similarity 8/...
7; Conservative
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                                                                      7; Conservative
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139 MDEYTVHL 146
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139 MDEYTVHL 146
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Query Match
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Matches 6; Conser
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A; Molecule type: DNA
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conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O9-Jul-2004
C;Accession: H75431
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F.White, O.; Sisen, W.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mab S; Shch, H.O.; Venter, J.C.; Fraser, C.M.
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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-505 <WHI>
A;Cross-references: UNIPROT:Q9RV79; UNIPARC:UPI00000C18AC; GB:AE001964; GB:AE000513; NID
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acylase and diesterase homolog lin2898 [imported] - Listeria innocua (strain Clip11262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A,Reference number: A75250; WUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: ADI794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35; DB 2; Length 505;
Pred. No. 37;
1; Mismatches 2; Indels
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C, Superfamily: conserved hypothetical protein b0835
            Pred. No. 11;
2; Mismatches
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      75.0%;
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Best Local Similarity 66.7
Matches 6; Conservative
                                     6; Conservative
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483 KINEYTIDL 491
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|139 KMSEWTVH 146
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57 QMNBYDTHL 65
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Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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                                                                                             1 KMNEYTVH
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.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karet, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitcurnam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-159 <GLA>
A;Cross-references: UNIPROT:Q8Y419; UNIPARC:UPI000005520D; GB:NC_003210; PIDN:CAD00871.1
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo2658
A;Residues: 1-1829 <WIL>
A;Cross-references: UNIPROT:Q19815; UNIPARC:UP100000765C9; EMBL:U55373; PIDN:AAC25894.1;
A;Experimental source: strain Bristol N2; clone F26F12
C;Genetics: CSP:F26F12.7
A;Gene: CESP:F26F12.7
A;Map position: 5
A;Introns: 110/3; 441/3; 801/2; 1244/3; 1693/2; 1784/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spermidine/spermine N1-acetyl transferase homolog lmo2658 [imported] - Listeria monocytc
C;Species: Listeria monocytcgenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: Al1406
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A;Experimental source: strain Clip11262
C;Genetics:
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7
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; Pred. No. 91;
2; Mismatches
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Pred. No. 11;
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 75.0
Matches 6, Conservative
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139 KMSEWTVH 146
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A;Molecule type: DNA
A;Residues: 1-159 <GLA>
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Search completed: March 11, 2006, 00:40:44 Job time : 16.1111 secs
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152 MNEFTTHI 159
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152 MNEFTAHI 159
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A;Residues: 1-270 <ERD>
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                                                                                                                                                                                                                                                                                                                                                                                                                     A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Aolecule type: mRNA
A,Residues: 1-667 <PL>
A,FCCBS-references: UNIPARC:UPI000016C7E6; EMBL:AF026565; NID:g2589222; PIDN:AAB83986.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tigger protein FXY - human (199482 Finger protein Father) (199482 Finger protein Father) (199482 Finger protein Father) (199482 Finger protein FXY maps to chromosome Xp22.3: Implications for evolution of the A; Reference number: 216687 Finger preliminary; translated from GB/EWBL/DDBJ A; Residues: 1-667 - PER> A; Residues: 1-667 - PER> A; Cross-references: UNIPROT: 015344; UNIPARC: UPI000012F0E6; EMBL: AF035360; NID: G2827993;
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A43711
replication protein repA 32K chain - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Decies: Homo sapiens (man)
C;Decies: Homo sapiens (man)
C;Decies: Homo sapiens (man)
C;Decies: Homo sapiens
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                              RING finger protein Fxy - mouse
C;Species: Mus musculus (house mouse)
C;Dacte: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 04-Apr-2004
C;Accession: T09013
R;Palmer, S.; Perry, J.; Kipling, D.; Ashworth, A.
Proc. Natl. Acad. Sci. U.S.A. 94, 12030-12035, 1997
A;Title: A gene apans the pseudoautosomal boundary in mice.
A;Reference number: Z16531; MUID:98004518, PMID:9342357
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Pred. No. 49;
0; Mismatches 2; Indels
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S. Suberfamily: Fifth transforming protein
C; Keywords: Zinc finger
F; 6-65/Domain: RING finger homology <RRN>
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C;Superfamily: rfp transforming protein
F;6-65/Domain: RING finger homology <RRN>
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Matches 6; Conservative
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Matches 6; Conserv
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A;Cross-references: UNIPROT:P15927; UNIPARC:UPI000013379F; EMBL:J05249; NID:g337349; PIDP C;Superfamily: Schizosaccharomyces pombe single-stranded DNA binding protein 30K chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ciptication protein A 32K chain homolog - mouse
Cispecies: Mus musculus (house mouse)
Cipate: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
Cipate: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
Cipate: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
Cipatesion: S28682
Rinakagawa, M.; Tsukada, S.; Soma, T.; Shimizu, Y.; Miyake, S.; Iwamatsu, A.; Sugiyama, F.; Nucleic Acids Res. 19, 4292, 1991
A; Title: CDNA cloning of the murine 30-kDa protein homologous to the 32-kDa subunit of ha A; Reference number: S28682
A; Rolcoule: Cype: mRNA
A; Residues: 1-270 cNAG
A; Residues: 1-270 cNAG
A; Residues: 1-270 cNAG
A; Cosser-references: UNIPROT: O62193; UNIPARC: UPI0000028990; EMBL: D00812; NID: G220583; PIDP
C; Superfamily: Schizosaccharomyces pombe single-stranded DNA binding protein 30K chain
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                                                                                                              69.4%; Score 34; DB 2; Length 270; 62.5%; Pred. No. 30; tive 2; Mismatches 1; Indels
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                                                                                                                  Query Match
Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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                                                                                      March 11, 2006, 00:11:15; Search time 95.222 Seconds (without alignments) 66.684 Million cell updates/sec
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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                                                                                                                                                                                                                                                                                  2166443 seqs, 705528306 residues
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Q9G0B3 BPAR1
VLYS BPK3
VLYS BPT4
RRA4 HUMAN
Q8DPG2 STRR6
PRIL PYRAB
QSLZSB STRT1
Q4UCK5 THEAN
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06731B_ARATH
05WPT2_LUTLO
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08UV0_STRAN
08E6M8_STRAS
019815_CAEBL
061WR2_CABR
0610815_CAEBL
061082_LEIMA
080274_MUSMA
080284_MUSMA
080283_ARVTE
080283_ARVTE
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Q8Y419_LISMO
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Maximum Match 100%
Listing first 45 summaries
                                                                protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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Q92711 listeria in Q71552 cryptophleb Q4ra68 tetraodon n Q4x866 plasmodium Q4k81 pseudomonas Q4q709 leishmania Q55sa4 cryptococcu Q5kqqq mus musculu Q5hyk magnaporthe Q4h24 deinococcus Q5ry19 deinococcus Q5ry10 pongo pygma Q926z1 listeria in	Stratum corneum  Sbrata; Euteleostomi;  SBC Catarrhini; Hominidae;  PROTEIN SEQUENCE OF 23-53.  Librandt P., Carlstein A.,  Estratum corneum  Srine proteinase.";  CIPICITY, AND INDUCTION.  280-8;  Pillai A.,  Lum corneum chymotryptic  and hormonal  Lei H., McCuaig J.,  Lei H., McCuaig J.,  srine protease gene  srine protease gene  chymotryptic enzyme in  databases.  chymotryptic enzyme in  databases.  subCELLULAR LOCATION,	
092711 LISIN 077552 GVCL 04RA68 TETNG 04X8E6 PLACH 04X8E6 PLACH 04C01 PSEF5 04Q709 LEIMA 05SA4 CRYNE 05KG01 CRYNE 05KG01 CRYNE 05KG01 CRYNE 04H24 DBEIO 09RV79 DEIRA 05RF10 PONPY	COMMENTS  253 AA.  253 AA.  10 (hK7) (Strible of the content of th	
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AF332583; AAK69624.1; -; AF411214; AAN03662.1; -; AF411215; AAN03663.1; -; BC032005; AAH32005.1; -;

EMBL; EMBL; EMBL; EMBL; EMBL;

GO; GO:0008236; F:serine-type peptidase activity; TAS

sapiens

MEROPS; S01.300; -. Ensembl; ENSG0000169035; Homo

PIR; A53968; A53968.

P00760; 1EZX

H-InvDB; HIX0015373; -. HGNC; HGNC: 6368; KLK7.

604438; -.

GO; GO:0008544; P:epidermis development; TAS. InterPro; IPR001254; Peptidase\_S1\_S6. InterPro; IPR001314; Peptidase\_S1A.

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Attaubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altachul S.P., Zeeberg B., Buetow K.H., Schafer C.F., Bahat N.K.,
Altachul S.P., Zeeberg B., Buetow K.H., Schafer C.F., Bahat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soarse M.B., Bonaldo M.F., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robak S.A., McKwan P.J., McKernan R.J., Madek J.A., Gubbs R.A.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A., Garcia A.M., Rodrigues S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
C., Grimwood J., Schmutz J., Marra M.A.,
C., Schert J., Marra M.A.,
C., Schert J., Skalska U., Smailus D.E.,
C., Grimwood J., Schmutz J., Myers R.M.,
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C., Grimwood J., Schmutz J., Marra M.A.,
C., Schert J., Skalska U., Smailus D.E.,
C., Grimwood J., Schmutz J., Marra M.A.,
C., Short J., Shancka J., Shanck
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**Letter Biophys. Res. Commun. 211:589(1995).

**Letter Biophys
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Isold=P49862-1; Sequence=Displayed;
Name=2; Synonyms=Long;
Isold=P49862-2; Sequence=VSP 013581;
Isold=P49862-2; Sequence=VSP 013581;
TISSUE SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermia. Also expressed in the brain, mammary gland, cerbellum, spinal cord and kidney. Lower levels in salivary gland, uterus, thymus, thyroid, placenta, trachea and testis. Up-regulated in ovarian carcinoma, especially late-stage serous carcinoma, compared with normal ovaries and lebnign adenomas (at the protein level).
INDUCTION: By estrogens and glucocorticoids in a breast carcinoma
                            Dong Y., Kaushal A., Brattsand M., Nicklin J., Clements J.A.; "Differential splicing of KLKS and KLK7 in epithelial ovarian cancer produces novel variants with potential as cancer biomarkers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell line.
SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
                                                                                                                                                                                                                                                                        IISSUE=Skin;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                               [6]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                      Clin. Cancer Res. 9:1710-1720(2003).
MEDLINE=22623266; PubMed=12738725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse cDNA sequences."
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPF: 1.
PR05ITE; PS00134; TRYPSIN DOM; 1.
PR05ITE; PS00135; TRYPSIN JRS; 1.
Alternative splicing; Direct protein sequencing; Glycoprotein; Hydrolase; Protease; Signal; Zymogen.
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Kallikrein 7.
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opean Bioinformatics Institute. There are no restrictions on its long as its content is in no way modified and this statement is not

EMBL; L33404; AAC37551.1; -; mRNA. EMBL; AF166330; AAD49718.1; -; Genomic\_DNA.

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261 AA
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EMBL; AFF18101; AAD42661.1; -; Genomic DNA.
EMBL; X05677; CAA29164.1; -; Genomic DNA.
EMBL; M9441; AAA32481.1; -; Genomic_DNA.
PIR; JF0028; YVBPT4.
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TRANSMEM 35 49 Potent
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Mol. Cell. Biol. 15:3119-3128(1995)
                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE OF 202-218.
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218 AA; 25176 MW;
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Matches 7; Conserv
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RFA4_HUMAN
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Montag D., Degen M., Henning U.;
"Nucleotide sequence of gene t (lysis gene) of the E. coli phage T4.";
Nucleic Acids Res. 15:6736-6736(1987).
                                                                                                                                             Gaps
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T4-like viruses.
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
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                                                                                        Score 39; DB 2; Length 210;
Pred. No. 15;
1; Mismatches 0; Indels
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                      210 210 210 210 210 AA; 24348 MW; C6FF585F9FE0DF68 CRC64;
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01-MAR-1989 (Rel. 10, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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EMBL; AF208841; AAG29756.1; -; Genomic_DNA.
NON TER 210 210
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PIR; A27083; YVBPK3.
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MEDLINE=87250254; PubMed=3597316;
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                                                                                          Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
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MDEYTVHL 146
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Bacteriophage T4.
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SEQUENCE
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                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE OF 1-34.
MEDIANE=88011316; PubMed=2958637;
MONIAG D., Riede I., Eschbach M.-L., Degen M., Henning U.;
"Receptor-recognizing proteins of T-even type bacteriophages. Constant and hypervariable regions and an unusual case of evolution.";
J. Mol. Biol. 196:165-174(1987).
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
MEDLINE=22514363; PubMed=12626685; DOI=10.1128/MMBR.67.1.86-156.2003;
Miller E.S., Kutter E. Mosig G., Arisaka F., Kunisawa T., Ruger W.;
"Bacteriophage T4 genome.";
Microbiol. Mol. Biol. Rev. 67:86-156(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein.";
J. Bacteriol. 175:85-93(1993).
-!- FUNCTION: At the end of the growth cycle, phage T4 expresses two genes with lysis function, e and t. Nothing is known about the gene product of t, although it has been suggested that it acts as a phospholipase.
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Keshav K.F., Chen C., Dutta A.;
"Rpa4, a homolog of the 34-kilodalton subunit of the replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAX-2005 (Rel. 47, Last annotation update)
Replication protein A 30 KDa subunit (RP-A) (RF-A) (Replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=D;
MEDLINE=93106978; PubMed=8416914;
Orsini G., Ouhammouch M., Le Caer J.-P., Brody B.N.;
"The asiA gene of bacteriophage T4 codes for the anti-sigma 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                 ROCKENTINE SEQUENCE ILARGE SCARGE ALG. MCLAY K, MAZNY D., RANCHESTINES SEQUENCE ILARGE SCARE ALG. SCAREET S., MCLAY K, MAZNY D., RANCHEST M., SCARLAND D., SCARLAND C., SCARLAND C., SCARLAND C. S., MCLAY K., WANDY D., RANCHEST M., SCARLAND C., SCARLAND C. S., SCARLAND C., SCARCET R., SCARCE S., SCARLAND C., SCARCET R., MARITANER T.D., SCARCE C., SCARLAND C., SCARCET R., MARITANER T.D., SCARLAND C., CALLAND C., CALLAND C., CALLAND C., SCARLAND C., SCARLAND C., CALLAND C., SCARLAND C.
                                       NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT THR-33.
Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
Ozuna M., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
"NIEHS-SNB- environmental genome project, NIEHS ES15479,
"NIEHS-Schees, Seattle, WA (URL: http://egp.gs.washington.edu).";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Straubberg R.L., Feligold E.A., Grouse L.H., Derge d'G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
            Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                              [4]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Carainori P., Frange C., Brownstein M.J., Usdin T.B., Tochiyuki S., Carainori P., Frange C., Rabas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Helton B., Ketreman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse CDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-! FUNCTION: Absolutely required for simian virus 40 DNA replication in vitro. It participates in a very early step in intiation. RP-A is a single-stranded DNA-binding protein (By similarity).

-! SUBDINIT: Heterotrimer of 70, 32/30, and 14 kDa chains. The DNA-binding activity may reside exclusively on the 70 kDa subunit.
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GO; GO:000567; F:single-stranded DNA binding; TAS.
GO; GO:000567; F:single-stranded DNA binding; TAS.
GO; GO:000627; P:single-stranded DNA binding; TAS.
InterPro; IPR01240; OB NA bd sub.
InterPro; IPR011991; Wing hlx_DNA_bd.
InterPro; IPR011991; Wing hlx_DNA_bd.
Pfam; PF01316; tRNA_anti; 1.
Alternative splicing; DNA replication; Nuclear protein; Polymorphism.
Alternative splicing; DNA replication; Nuclear protein; Polymorphism.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein spril79.
OrderedLocusNames=spril79;
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EMBL, AF494047; AAM09569.1; -; Genomic_DNA.
EMBL, 286061; CA142256.1; -; Genomic_DNA.
EMBL, BC069791; AAH69791.1; -; MRNA.
EMBL, BC069808; AAH69808.1; -; MRNA.
EMBL; BC069824; AAH69824.1; -; MRNA.
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Q8DPG2;
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HGNC; HGNC:30305; RPA4.
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HSSP;
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use as long as its content is in no way modified and this statement is not
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44973 MW; 1998CF52CB40CBAC CRC64;
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Last annotation update)
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Pred. No. 76;
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TIGRFAMs; TIGR01413; Dyp perox fam; 1.
TIGRPAMs; TIGR01409; TAT signal seq; 1.
TIGRPAMs; TIGR01412; tat substrl; 1.
Complete proteome; Hypothetical protein
SEQUENCE 401 AA; 44973 MW; 1998CF52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OrderedLocusNames=str1023;
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QSLZS8;
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QSM4D9;
                                                                                                                                                                                                                                                                                                Best Local Similarity 66.7 Matches 6; Conservative
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Les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        129 KLPEYTIHL 137
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Matches
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                                                                                                 MEDLINE=21429245; PubMed=11544234;
DDI=10.1128/JB.183.19.5709-5717.2001;
HOSKING J., Alborn W.E. Jr., Arnold Jr., Blaszczak L.C., Burgett S.,
DeHoff B.S., Estrem S.T., Friz L., Fu D.-Jr., Fuller W., Geringer C.,
Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,
Norris F.H., O'Grem M., Peery R.B., Robertson G.T., Rockey P.,
Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBDATT: Heterodimer of a small subunit and a large subunit. Both participate in formation of the active center, but the ATP-binding site is exclusively located on the small subunit (By similarity). SIMILARITY: Belongs to the eukaryotic-type primase large subunit
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10-OCT-2003 (Rel. 42, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
DNA primase large subunit (EC 2.7.7.-) (DNA primase 46 kDa subunit)
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                                                                                                                                                                                                                                                                                                                                        "Genome of the bacterium Streptococcus pneumoniae strain R6.";
J. Bacteriol. 183:5709-5717(2001).
EMBL; AE0084990; AAK99982.1; -; Genomic_DNA.
PIR; B98019; B98019.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.5%; Score 37; DB 2; Length 334; 66.7%; Pred. No. 63; 2; Indels iive 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein.
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TIGRPAMs, TIGRO413; Dyp perox 1.
Complete proteome, Hypothetical prot SEQUENCE 334 AA; 38137 MW. F207F
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR006314; Dyp_peroxidase.
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Streptococcus.
NCBI_TaxID=171101;
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Q9V291;
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PRIL PYRAB

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DT 10-0CT-

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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

PubMed=15543133; DOI=10.1038/nbt1034;

Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,

Kulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D.,

A. Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,

A. Goffeau A., Hols P.;

Goffeau A., Hols P.;

"Complete sequence and comparative genome analysis of the dairy

Lacerium Streptococcus thermophilus.";

In Biotechnol. 22.1554-1558(2004).

R. EnterPro; IPR006314; Dyp peroxidase.

InterPro; IPR006311; Tat.

R. InterPro; IPR006311; Tat.

Prome T. Prome T.
EMBL; AJ248283; CAB49107.1; -; Genomic_DNA.

PIR; D75207; D75207.

InterPro; IPR001238; DNA_primase_lrg.

InterPro; IPR008918; HhHZ.

InterPro; IPR008918; HHZ.

INTERPRO; IPR008918; HTZ.

INTERPRO; IPR00
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
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Q67Z18_ARATH
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Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
Hall N., Barrell B.G.;
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In Nat. Biotechnol. 22:1554-1558 (2004).

EMBL; CP0000023; AAV60681.1; -; Genomic_DNA.

InterPro; IPR006311; Tat.

InterPro; IPR006313; Tat.—nzyme.

R Pfam; PF04261; Dyp_perox fam; 1.

R TIGRPAMS; TIGR01413; Dyp_perox fam; 1.

R TIGRPAMS; TIGR01412; tat. sugnal seq; 1.

R TIGRPAMS; TIGR01412; tat. substr. 1; 1.

R TIGRPAMS; TIGR01412; tat. substr. 1; 1.

R Complete proteome; Hypothetical protein.

O SEQUENCE 401 AA; 44973 MW; 1998CF52CB40CBAC CRC64;
                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
PubMed=15543133; DOI=10.1038/nbt1034;
Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
Kulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D.,
Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J.,
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                                                          Streptococcus thermophilus (strain ATCC BAA-250 / LMG 18311).
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The chromosome 3 genome sequence of Theileria annulata."; Submitted (MAR-2005) to the EMBL/GenBank/DBBJ databases. EMBL; CR40352; CAI75446.1; -; Genomic DNA. SEQUENCE 498 AA; 55564 WW; 9135F36Z0AC4758A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 2; Length 401;
Pred. No. 76;
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13-5EP-2005 (TrEMBLrel. 31, Last sequence update)
13-5EP-2005 (TrEMBLrel. 31, Last annotation update)
RNA 3'-terminal phosphate cyclase like-protein, putative.
ORFNammes-TAO3460,
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Best Local Similarity 66.7°,
6, Conservative
                             OrderedLocusNames=stu1023;
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Q633P6_BACCZ_PRELIMINARY;
Q633P6;
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Q4UCKS;
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447 KLNRYSVHL 455
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                                                                                                                                                 NCBI_TaxID=264199;
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Best Local &
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TOTOK! Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,
Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,
Narusaka M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.;
Hayashizaki Y., Shinozaki K.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AK176300; BAD44063.1; -; mRNA.
EMBL; AK176300; BAD44063.1; -; mRNA.
EMBL; AK176300; BAD4308.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
Hitchoock P., Jackson P., Kehm P., Longmire J., Lucae S., Okinaka R.,
Richardson P., Rubin E., Tice H.;
"Complete genome sequence of Bacillus cereus ZK.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, CP000001, AMUSJ77.1; -; Genomic_DNA.

InterPro; IPR006655; NRA_transpt.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
MRNA, partial cds, clone: RAFL23-25-J01 (MRNA, partial cds, clone:
RAFL23-09-L14) (Fregment).
Arabidopsis thaliana (Mouse-ear cress).
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Pred. No. 1.9e+02;
2; Mismatches 0; Indels
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                                                                                                                                                                         Bacillus cereus (strain ZK).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus,
Bacillus cereus group.
NCBI_TaxID=288681;
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PROSITE; PSS0978; NEAT, 5.
COMPLETE proteome; Hypothetical protein.
SEQUENCE 936 AA; 104539 MW; D05C843D8B02DF8A CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
45-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
BrNames=BCE3314292;
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Q67218;
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Best Local Similarity 66.77
Even 6; Conservative
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nes 6; Conservative
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11 KLNEYQTHL 19
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Length 603;

73.5%; Score 36; DB 2; Le: 66.7%; Pred. No. 1.9e+02; tive 1; Mismatches 2;

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GO; GO:0005096; F:GTPase activator activity; IEA.
InterPro; IPR007145; MAP65_ASE1.
Pfam, PF03999; MAP65_ASE1; I.
Hypothetical protein.
SEQUENCE 603 AA; 69060 MW; 7C2B37A23CBB889D CRC64;
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Best Local Similarity 66...
6; Conservative
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Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A.,
Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,
Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY120768; AAM53326.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
Southwick A., Karlin-Neumann G., Nguyen M., Tripp M., Miranda M., Palm C.J., Bowser L., Jones T., Banh C. Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Saki M., Shinn P., Yamada K., Shinozaki K., Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=153747479; DOI=10.1242/jeb.01185;
Valenzuela J.G., Garfield M., Rowton E.D., Pham V.M.;
Valenzuela J.G., Garfield M., Rowton E.D., Pham V.M.;
Infertification of the most abundant secreted proteins from the salivary glands of the sand fly Lutzomyia longipalpis, vector of Leishmania chagasi.";
J. Exp. Biol. 207:3717-3729(2004).
I- SIMILARITY: Belongs to the serpin family.
GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA. InterPro; IRPR000015; Prot_inh_serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryora, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantes, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnolitophyta; eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                              Lutzomyia Inogipalia (Sand fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Psychodoidea; Psychodidae; Lutzomyia; Lutzomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.5%; Score 36; DB 2; Length 446; 75.0%; Pred. No. 1.4e+02; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         446 AA; 50670 MW; 0D8F747D8A6F1E30 CRC64;
                                                                                                             25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
49 kDa salivary protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2002 (TrEWBLrel. 22, Created)
01-0CT-2002 (TrEWBLrel. 22, Last sequence update)
01-FEB-2005 (TrEWBLrel. 29, Last annotation update)
Hypothetical protein At1g14690.
                                              446 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      603 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=At1g14690;
Arabidopsis thaliana (Mouse-ear cress).
                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam, PF00079, Serpin, 1.
SMART, SM00093, SERPIN, 1.
PROSITE, PS00284; SERPIN, UNKNOWN 1.
                                       QSWPT2_LUTLO PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QBL836 ARATH PRELIMINARY;
Q8L836;
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Matches 6; Conservative
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for
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                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein T28A8.6.
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Pred, No. 2e+02;
2; Mismatches
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                                                                                                                627 AA
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Wormbase; WBGene00012112; 728A8.6.
Wormpep; T28A8.6; CE18977.
InterPro; IPR006570; SPK.
Pfam; PF04435; SPK; 2.
SMART; SMOS83; SPK; 2.
Complete protecome; Hypothetical protein.
SEQUENCE 627 AA; 71794 MW; 4A5684D3658B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                investigating biology.";
Science 2882:2012-2018(1998).
EMBL: 292813; CAB07289.1; -; Genomic_DNA.
PIR; T25395; T25395.
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                                                                                                                PRT;
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66.7%;
                                                                                 QOXUO4 CAEEL PRELIMINARY;
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Best Local Similarity 66.7
Matches 6; Conservative
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169 KLNEYOTHL 177
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62 KWNEYSIEL 70
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Sequence 1 Sequence

Sequence 2136, Ap Sequence 5100, App Sequence 5702, Ap Sequence 2, Appli Sequence 12, Appli Sequence 49, App Sequence 12375, A Sequence 12375, A Sequence 12375, A Sequence 26699, A Sequence 4628, A P Sequence 4628, A P Sequence 5895, A P Sequence

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Database :

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Sequence 89, Application US/09502600A

Patent No. 6294344

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer

TITLE OF INVENTION: Ovarian Cancer

TITLE OF INVENTION: Ovarian Cancer

FILE REFERENCE: D6232GIP-C

CURRENT FILING DATE: 2000-02-11

CURRENT APPLICATION NUMBER: 09/039,211

PRIOR FILING DATE: 03-14-1998

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 89

LENOTH: 9

TYPE: PRT

CORGANISM: Homo sapiens

FEATURE:
                                                                                                                                                                                                                                                                                                                                                          Sequence 31, Application US/09502600A
Sequence 31, Application US/09502600A
Sequence 31, Application US/09502600A
Sequence 31, Application US/09502600A
SEQUENT NO. Sequence 31, Application Sequence 31, Application Sequence 31, Application Sequence 31, APPLICANTON: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: CONTRIBUTION: CONTRIBUTION: CONTRIBUTION: DECEMBER: US/09/502,600A
SET OF TILING DATE: 03-14-1998
SEQ ID NO 31
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 49; DB 2; Length 9; 100.0%; Pred. No. 4.6e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
OTHER INFORMATION: Residues 72-80 of the SCCE protein
                         US-09-072-433-22
US-09-710-279-2136
US-09-134-001C-5502
US-08-134-001C-5502
US-08-909-954-4
US-08-909-954-2
US-09-134-001C-5184
US-09-134-001C-5184
US-09-137-55-49
US-09-091-725-49
US-09-091-725-49
                                                                                                                                                                                            US-09-248-796A-26699
US-09-949-016-10644
US-09-583-110-2714
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US-09-134-000C-5895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
   TYPE: PRT
ORGANISM: Homo sapiens
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RESULT 2
US-09-502-600-89
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 RESULT 1
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Sequence 89, Appl
Sequence 109, Appl
Sequence 89, Appl
Sequence 109, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
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Sequence 3, Appli
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Sequence 122, App
Sequence 93, Appl
Sequence 93, Appl
Sequence 2942, Ap
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                                                                                               March 11, 2006, 00:41:16; Search time 21.222 Seconds (without alignments) 35.061 Million cell updates/sec
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            GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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(cgn2_6/ptodata/1/iaa/f_COMB.pep:*
(cgn2_6/ptodata/1/iaa/H_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-918-243-109

US-09-261-416-7

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US-09-654-600A-4

US-09-18-24-3

US-09-18-24-3

US-09-18-24-2

US-09-918-24-3

US-09-918-243-122

US-09-918-243-122

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Maximum Match 100%
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Match Length DB
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Sequence 89, Application US/09918243
; Sequence 89, Application US/09918243
; Patent No. 6627401
; Patent No. 6627401
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Cannon, Martin J.
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer; TILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT FILING NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; LENGTH: 9
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APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandra.
APPLICANT: Santin, Alessandra.
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer FILE REFERENCE: D6223CIP/C/D/CIP
CURRENT APPLICATION NUMBER: US/09/918,243
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-13
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Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels
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NAME/KEY: CHAIN
OTHER INFORMATION: Residues 72-80 of the SCCE protein US-09-918-243-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Residues 72-80 of the SCCE protein US-09-918-243-89
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; Patent No. 6627403
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US-09-618-259-4
'Sequence 4, Application US/09618259
'Patent No. 6642013
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SEQ ID NO 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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US-09-918-243-89
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Sequence 109, Application US/09502600A

Jatent No. 6294144

Jatent No. 6294144

Jatent No. 6294144

JAPLICANT: O'Brien, Timothy J.

JITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of

TITLE OF INVENTION: Ovarian Cancer

TITLE OF INVENTION: Ovarian Cancer

FILE REFERENCE: D6223CIP-C

CURRENT FILING DATE: 2000-02-11

CURRENT APPLICATION NUMBER: US/09/502,600A

PRIOR APPLICATION NUMBER: 09/039,211

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 109

LENGTH: 9
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| Sequence 31, Application US/09918243
| GENERAL INCRMATION
| APPLICANT: Cannon, Martin J.
| TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
| TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
| CURRENT FILING DATE: 2001-07-30
| PRIOR PLING DATE: 2001-07-30
| RIOR FILING DATE: 2001-07-13
| NUMBER OF SEQ ID NOS: 136
| SEQ ID NO 31
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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100.0%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                  Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                              0; Indels
; OTHER INFORMATION: Residues 72-80 of the SCCE protein US-09-502-600-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Residues 72-80 of the SCCE protein US-09-502-600-109
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; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-918-243-31
                                                                           100.0%; Score 49; DB 2; I
100.0%; Pred. No. 4.6e+05;
vative 0; Mismatches 0;
                                                       Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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STEVEN D.
NOVEL SERINE PROTEASE REAGENTS
AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
OF THE PROSTATE
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US-08-557-146-12

Sequence 12, Application US/08557146

Patent No. 5834290

GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Bnzyme (SCCE)
MUMBER OF SEQUENCES:
CORRESPONDENCE ADDRES:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDLIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
SOFTWARE: VALICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
APPLICATION NUMBER: 35,441
RESERENCE/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 31,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELEPHONE: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                     TITLE OF INVENTION: NOVEL SERINE P.
TITLE OF INVENTION: NOVEL SERINE P.
TITLE OF INVENTION: OF THE PROSTATI
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park Road
CITY: Abbott Park Road
CITY: Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 33: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: No. 6232456e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 224 amino acids TYPE: amino acid
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Best Local Similarity 100.
Matches 9; Conservative
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COUNTRY: U.S.A.
ZIP: 10036-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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Sequence 1. Application US/09261416A
Sequence 1. Control 1. Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic; OTHER INFORMATION: enzyme (scce) catalytic domain US-09-618-259-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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OTHER INFORMATION: Serine protease catalytic domain of stratum corn.
OTHER INFORMATION: chymotryptic enzyme (Scce) homologous to similar
OTHER INFORMATION: domain in TADG-12
GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: O'Brien, Timothy J.

APPLICANT: O'Brien, Towell J.

TITLE OF INVENTION: No. 6442013el Extracellular Serine Protease

TITLE OF INVENTION: No. 6442013el Extracellular Serine Protease

CURRENT APPLICATION NUMBER: US/99/618,259

CURRENT APPLICATION NUMBER: US/99/618,259

FILING DATE: 2000-07-18

PRIOR FILING DATE: 1998-08-21

NUMBER OF SEQ ID NOS: 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 49; DB 2; Length 144; 100.0%; Pred. No. 0.02;
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| Patent No. 6222456
| GENERAL INFORMATION:
| APPLICANT: COHEN, MAURICE |
| APPLICANT: COLPIT'S, TRACEY L. APPLICANT: GRANADOS, EDWARD N. APPLICANT: GRANADOS, EDWARD N. APPLICANT: RUSSELL, JOHN C. APPLICANT: STEWART, KENT D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-08-944-483-33
                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 4
LENGTH: 144
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US-09-261-416-7
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease;
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease;
TITLE OF INVENTION: Overexpressed in Carcinomas
FILE REPRERENCE: D6064CIP/D
CURRENT APPLICATION NUMBER: 09/421,213
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: 09/421,213
PRIOR PLILING DATE: 1999-10-20
PRIOR PLILING DATE: 1999-10-20
PRIOR PLILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 4
LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 49; DB 1; Length 225; Best Local Similarity 100.0%; Pred. No. 0.033; Matches 9; Conservative 0; Mismatches 0; Indel8
                           COUPTRY: U.S.A.

COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA: WS/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
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100.0%; Pred. No. 0.033;
tive 0; Mismatches 0.
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REGISTRATION NUMBER: 35,372
REFERENCE/POCKET NUMBER: 1103;
RELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 354-8113
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 mino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-09-644-600-4
; Sequence 4, Application US/09644600
; Patent No. 6451500
                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: polypeptide
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Best Local Similarity 100.
Matches 9; Conservative
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STRANDEDNESS: single
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; OTHER INFORMATION: SCCE
US-09-644-600-4
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ORGANISM: Homo sapiens
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Sequence 1, Application US/09027337B

Patent No. 5972616

GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REPERENCE: D6064

CURRENT APPLICATION NUMBER: US/09/027,337B

CURRENT FILING DATE: 1998-02-20

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 4

LENGTH: 225
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Patent No. 5881256
GENERAL INFORMATION:
APPLICANT: Beal-ud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Bazyme (SCCE)
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 49; DB 1; Length 225; Best Local Similarity 100.0%; Pred. No. 0.033; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 49; DB 1; Length 225
100.0%; Pred. No. 0.033;
tive 0; Mismatches 0; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STERNEY, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELEPHONE: (212) 819-81783
TELEPHONE: (212) 819-81783
TELEPKX: (212) 819-81783
TELEPKX: (212) 849-8113
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
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Best Local Similarity
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-557-146-12
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US-09-154-344-12
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US-09-027-337-4
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Fatent No. 5834290
GENERAL INFORMATION
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CONTESSOURCES: 17
COUNTRY: U.S.A.
STREET: 1155 Avenue of the Americas
COUNTRY: U.S.A.
ZIP: 10036-278 ORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM FC compatible
OPERATION SYSTEM: US/OS/SS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/OS/57,146
FILING DATE: 14-DEC-1995
CLASSIFICATION NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
MAME: Sterner, Richard J.
RESTERRICE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPAN: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
CENTER OF SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                         | Sequence 4, Application US/09654600A
| Sequence 4, Application US/09654600A
| Patent No. 6649710.|
| GENERAL INFORMATION:
| APPLICANT: Tanimoto, Hirotoshi
| TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
| TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
| TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
| TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
| FILE REFERENCE: D6064CIP/D
| CURRENT PAPLICATION NUMBER: US/09/654,600A
| PRIOR APPLICATION NUMBER: 09/421,213
| O9/021,337
| PRIOR FILING DATE: 1999-10-20
| NUMBER OF SEQ ID NOS: 98
| SEQ ID NO 4
| LENGTH: 225
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OTHER INFORMATION: SCCE
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ORGANISM: Homo sapiens
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RESULT 14
US-09-654-600A-4
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US-08-557-146-2
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; TOPOLOGY: linear; ; MOLECULE TYPE: protein US-08-557-146-2 U
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Run on:

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Sequence 31, Appl Sequence 109, Appl Sequence 4, Appl Sequence 96, Appl Sequence 96, Appl Sequence 10, Appl Sequence 94, Appl Sequence 94, Appl Sequence 94, Appl Sequence 3, Appl Sequence 2, Appl Sequence 3, Appl Sequence 3, Appl Sequence 2, Appli Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                       March 11, 2006, 01:24:47; Search time 69.444 Seconds (without alignments) 54.151 Million cell updates/sec
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L: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

1: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-905-083-31

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US-09-905-083-89

US-09-905-083-109

US-10-372-521-89

US-10-372-521-109

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US-10-372-521-109

US-10-372-521-109

US-10-831-075-89

US-10-831-075-89

US-10-831-075-109

US-10-62-511-96

US-10-262-511-96

US-10-262-511-96

US-10-262-511-96

US-10-262-511-96

US-10-262-511-96

US-10-262-511-96

US-10-262-511-97

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US-10-262-511-97

US-10-262-511-97

US-10-262-511-97

US-10-262-511-97
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                                                                                                                                                                                                                                                                                                                                                                1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq length: 0
seq length: 200000000
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Match Length
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Perfect score:
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                                                                                    OM protein
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Result No.

28	Sequence 48, Appl Sequence 90, Appl Sequence 498, App Sequence 639, Appl Sequence 639, Appl Sequence 95, Appl Sequence 194726, Sequence 194726, Sequence 122, App Sequence 132, App Sequence 132, App Sequence 15592, App Sequence 5592, App Sequence 93, Appl	of ovarian cancer	Length 9; Indels 0; Gaps 0;	of ovarian cancer
28 49 100. 31 49 100. 31 49 100. 32 49 100. 32 49 100. 33 49 100. 34 49 100. 35 49 100. 36 49 100. 37 49 100. 38 49 100. 38 49 100. 39 79 49 100. 39 79 49 100. 39 79 79 49 100. 39 79 79 79 49 100. 39 79 79 79 79 79 79 79 79 79 79 79 79 79	253 4 US-10-071-214-48 253 4 US-10-264-283-90 253 4 US-10-264-283-90 253 4 US-10-173-999-48 253 4 US-10-173-999-48 253 5 US-10-643-765A-659 253 5 US-10-643-765A-95 253 5 US-10-643-795A-95 253 5 US-10-918-218-95 257 4 US-10-344-394-38 257 4 US-10-344-394-38 257 4 US-10-344-394-38 258 5 US-10-314-39 259 4 US-10-314-39 26 4 US-10-31-1214-9 27 US-09-918-243-122 28 1 US-09-918-243-122 29 4 US-10-424-599-17518 26 5 US-10-424-599-17518 26 5 US-10-424-599-17518	IGNMENTS early diagnosis 18,243 of the SCCE prote	100.0%; Score 49; DB 3; Le 100.0%; Pred. No. 1.7e+06; vative 0; Mismatches 0; 9	early diagnosis 18,243
	8 0 0 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	RESULT 1 US-09-918-243-31 Sequence 31, Appli Patent No. US20020 GENERAL INFORMATIO APPLICANT: Canno APPLICANT: Canno APPLICANT: Canno TITLE OF INVENTIO FILE REPERENCE: D CURRENT APPLICATION FILE REPERENCE: D CURRENT APPLICATION FILE REPERENCE: D CURRENT FILING DATE NUMBER OF SEQ ID SEQ ID NO 31 LENGTH: 9 TYPE: PRT ORGANISM: HOMO 8 FRATURE: PRT ORGANISM: HOMO 8 FRATURE: PRT ORGANISM: HOMO 8 FRATURE: PRT ORGANISM: HOMO 9 FRATURE: FRT ORGANISM: HOMO 9 FRATURE: NEATURE: CHAIN OTHER INFORMATIO	Query Match Best Local Simi Matches 9; 1 KWN 1 KWN	RESULT 2 US-09-918-243-89 Sequence 89, Appli Sequence 89, Appli Patent No. USJ0020 GRERAL INFORMATIO APPLICANT: Canno APPLICANT: Canno APPLICANT: Canno APPLICANT: Canno CURRENT SAITI TITLE OF INVENTIO FILE REFERENCE: D CURRENT APPLICANT CURRENT APPLICANT PRIOR PILING DATE NUMBER OF SEQ ID SEQ ID NO 89 LENGTH: 9

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Indels

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Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 9; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Homo sapiens
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US-09-905-083-89
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Fatent NO. US20020142317A1

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: Cannon, Martin J.

APPLICANT: Santin, Alessandro.

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

FILE REFERENCE: D6223CIP/C/D/CIP

CURRENT APPLICATION NUMBER: US/09/918,243

CURRENT FILING DATE: 2001-07-30

PRIOR PILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 31, Application US/09905083

Sequence 31, Application US/09905083

Batent No. US20020146708A1

GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer File Reference: D6223CIP/C/Div CURRENT APPLICATION NUMBER: US/09/905,083

CURRENT FILING DATE: 2001-07-13

PRIOR FILING DATE: 2000-02-11

FIGH FILING DATE: 2000-02-11

SEQ ID NO 31

LENGTH: 9
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100.0%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                      FEATURE:

NAME/KEY: CHAIN

OTHER INFORMATION: Residues 72-80 of the SCCE protein US-09-918-243-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CHAIN
CTHER INFORMATION: Residues 72-80 of the SCCE protein US-09-918-243-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-905-083-31
TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-918-243-109
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US-09-905-083-31
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Sequence 89, Application US/09905083

Patent No. US20020146708A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer;

FILE REPERRNCE: D6223CIP/C/Div

CURRENT FILING DATE: 2001-07-13

PRIOR PELING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 136

LENGTH: 9
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Fatent No. US20020146708A1

GENERAL INFORMATION:
FATENCE OF INVENTION:
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer
FILE REFERENCE: DS223CIP/C/Div
CURRENT FILING DATE: 2001-07-13
FRIOR APPLICATION NUMBER: US/9905,083
FRIOR APPLICATION NUMBER: US 09/502,600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-905-083-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-905-083-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 49; DB 3; I
100.0%; Pred. No. 1.7e+06;
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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RESULT

100.0%; Score 49; DB 3; Length 9;

Query Match

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RESULT 10
US-10-831-075-31
; Sequence 31. Application US/10831075
; Publication No. USZ0040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Marthy J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer; FILE REPERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US,10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US,10/372,521
; RIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer FILE REFERENCE: D6223CIP/C/D/CIP2
CURRENT APPLICATION WOMBER: US/10/372,521
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/918,243
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 109
LENGTH: 9
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Publication No. US20040224891A1
EMBERRAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
TITLE OF INVENTION: Methode for the early diagnosis of ovarian cancer File Reference: D6223CIP/C/D/CIP3
CURRENT APPLICATION NUMBER: US/10/831,075
CURRENT APPLICATION NUMBER: US 10/372,521
PRIOR APPLICATION UNBER: US 10/372,521
PRIOR SPECIAL OF SEQ ID NOS: 140
                                                                                                                                                                                                                                                                                                                                                                 Length 9;
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                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Residues 72-80 of the SCCE protein US-10-372-521-109
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; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-10-831-075-31
                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 49; DB 4; L 100.0%; Pred. No. 1.7e+06; tive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0;
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Best Local Similarity 100..
Best Local 9; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Homo sapiens
FEATURE:
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              Sequence 31, Application US/10372521

Publication No. US20030223973A1

GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Methods for the early diagnosis of ovarian cancer;
FILE REFERENCE: D6223CIP/C/D/CIP2
CURRENT APPLICATION NUMBER: US/10/372,521

CURRENT FILING DATE: 2003-02-21

PRIOR PILING DATE: 2001-07-30

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Sequence 89, Application US/10372521
| Sequence 89, Application US/203973A1
| Publication No. US20030223973A1
| GENERAL INFORMATION:
| APPLICANT: O'Brien, Timothy J.
| APPLICANT: Cannon, Martin J.
| APPLICANT: Santin, Alessandro:
| TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer:
| FILE REFERENCE: Do223CIP/C/D/CIP2
| CURRENT APPLICATION NUMBER: US 10/372,521
| PRIOR FILING DATE: 2003-02-21
| PRIOR FILING DATE: 2001-07-30
| SEQ ID NO 89
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; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-10-372-521-89
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Publication No. US20030223973A1
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
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Matches 9; Conserv
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US-10-372-521-109
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US-10-372-521-89
    US-10-372-521-31
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Gaps

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APPLICANT: Ratefuli, Lucales E.
APPLICANT: Ratefuli, Lucales E.
APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: Shanders, Richard A.
APPLICANT: Shanders, Richard A.
APPLICANT: Agee, Michale L.
APPLICANT: Agee, Michale L.
APPLICANT: Agee, Michale L.
APPLICANT: Berghs, Contance
FILE APPLICANT: Berghs, Contance
FILE REFERENCE: 21402-462.28
FILE REFERENCE: 21402-462.28
FILE REFERENCE: 2003-062.28
FRIOR APPLICATION NUMBER: 60/326,483
FRIOR APPLICATION NUMBER: 60/326,483
FRIOR FILING DATE: 2001-10-09
FRIOR FILING DATE: 2002-04-19
FRIOR FILING DATE: 2002-10-09
FRIOR FILING DATE: 2002-04-17
FRIOR APPLICATION NUMBER: 60/313,805
FRIOR FILING DATE: 2002-04-17
FRIOR APPLICATION NUMBER: 60/313,805
FRIOR APPLICATIO
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Catterton, Elina
Ji, Weizhen
Miller, Charles E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
nes 9; Conservative
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CORGANISM: Homo sapiens
US-10-262-511-100
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Publication No. US20040224891A1
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
TITLE OF INVENTION: Methods to the early diagnosis of ovarian cancer;
FILE REFERENCE: D62221P/C/D/CIR3
CURRENT APPLICATION NUMBER: US/10/831,075
CURRENT FILING DATE: 2004-04-23
FRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 140
SEQ ID NO 109
LENGTH: 9
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                                                                                                                                ; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-10-831-075-89
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Spytek, Kimberly A.
Bdinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
Ort, Tatiana
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
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Anderson, David W.
Zhong, Mei
                                                                                                                                                                                                                                                                                                 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
                                                    TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 9; Conserv
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US-10-831-075-109
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  SEQ ID NO 89
LENGTH: 9
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Gaps

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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (61)..(78)
OTHER INFORMATION: Serine proteases trypsin family, histidine proteins. domain
OTHER INFORMATION: 1dentified by eMATRIX, accession number BL00134A, p-value=6.143e-
PRATURE:
NAME/KEY: DOMAIN
LOCATION: (36)..(133)
                                                                                                                                                                                                                   ; LOCATION: (36)...(133)
; OTHER INFORMATION: Trypsin domain identified by PFam, accession name trypsin, E-
; OTHER INFORMATION: value=3.2e-31, PFam score of 101.0
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100.0%; Score 49; DB 5; Length 136;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09796294
; Patent No. US20020037581A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Extracellular Serine Protease; FILE REFERENCE: D6020CIP3
; CURRENT APPLICATION NUMBER: US/09/796,294
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/618,259
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 72
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ORGANISM: unknown
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NAME/KEY: DOMAIN
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LENGTH: 136
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US-09-796-294-4
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Search completed: March 11, 2006, 01:37:21 Job time : 70.4444 secs

9 KMNEYTVHL 17

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Query Match
Best Local Similarity 100.
Matches 9; Conservative
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1730
1730
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ORGANISM: Human
US-10-412-748-11
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Sequence 14, Appl
Sequence 17, Appl
Sequence 19, Appl
Sequence 6304, Ap
Sequence 2136, Appl
Sequence 215, Appl
Sequence 215, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 2480, Appl
Sequence 2239, Appl
Sequence 2239, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 9628, Ap
Seguence 34, Appl
Seguence 18, Appl
                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                             March 11, 2006, 01:27:17; Search time 8 Seconds (without alignments) 31.314 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
        GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-793-626-2136

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US-10-793-626-2136

US-11-13-424-49

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US-11-13-743-626

US-11-129-741-2480

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US-11-129-741-2480

US-11-096-5684-10287

US-11-096-5684-10287

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US-11-096-5684-9629

US-11-096-5684-9629
                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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US-11-021-441-18
                                                                                                                                                                  161667 segs, 27834885 residues
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                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
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                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                    1 KMNEYTVHL 9
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26, Appl
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Sequence 283
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Sequence 2
Sequence 2
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Sequence 2
Sequence 1
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; Sequence 11, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INPORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2002-04-09
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin version 3.2
; LENGTH: 23
; TYPE: PRIOR TIPLICATION UND CONTROL C
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VESULT:

Sequence 14, Application US/10412748

Sequence 14, Application US/10412748

Publication No. US20060035219A1

GENERAL INFORMATION:

APPLICANT: Clements, Judith A

TITLE OF INVENTION: Aberrant Kallikrein Expression

FILE REFERENCE: DAVI172.003AUS

CURRENT FILING DATE: 2003-04-09

PRIOR APPLICATION NUMBER: US/10/412,748

CURRENT APPLICATION NUMBER: AU PS1616/02

PRIOR APPLICATION NUMBER: AU PS1616/02

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn version 3.2

LENGTH: 253
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US-10-511-273-1
US-11-233-796-2
US-11-072-175-138
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US-11-193-715-4
US-10-986-501-283
US-10-986-501-281
                                                US-11-021-441-20

US-10-966-483-42

US-11-021-443-42

US-11-022-490A-4

US-11-022-490A-4

US-11-021-441-24

US-11-021-441-24
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US-11-021-441-4
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67.3%;
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; ORGANISM: Neurospora crassa
US-11-087-099-6304
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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72 KMNEYTVHL 80
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34 RMNDYEAHL 42
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US-11-087-099-6304
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                                                   100.0%; Score 49; DB 6; Length 253; 100.0%; Pred. No. 0.011;
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                                                                                         0; Indels
                                                                                                                                                                                                                                   US-10-412-748-17

Sequence 17, Application US/10412748

Sequence 17, Application US/10412748

Publication No. US20060035219A1

GENERAL INFORMATION:
APPLICANT: Queensland University of Technology
APPLICANT: Clements, Judith A
TILE OF CHENTY APPLICATION NUMBER: US/10/412,748

CURRENT APPLICATION NUMBER: US/10/412,748

CURRENT FILING DATE: 2003-04-09

PRIOR APPLICATION NUMBER: AU PSIG16/02

PRIOR APPLICATION NUMBER: AU PSIG16/02

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn version 3.2

LENGTH: 253
                                                                                         0; Mismatches
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CURRENT APPLICATION NUMBER: US/11/037,243
CURRENT FILING DATE: 2005-05-26
PRIOR APPLICATION NUMBER: US/9/888,615
PRIOR FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 98
TYPE: PRI
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APPLICANT: CAENEBEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: WANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
ITLE OF INVENTION: NOVEL PROTEASES
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                                  Query Match
Best Local Similarity 100.
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Matches 9; Conservative
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; ORGANISM: Human
US-10-412-748-14
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ORGANISM: Human
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; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-159
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US-11-113-424-49
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Publication No. US20050255478A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KIMMERIY.
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 1909-111-09
PRIOR FILING DATE: 1999-111-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                      TYPE: PRT ORGANISM: Artificial Sequence PEATURE: ORCANISM: Artificial Sequence: GTHER INFORMATION: Description of Artificial Sequence: synthetic US-10-793-626-2136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amino acid sequence
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Pred. No. 29;
                                                                                                                                                                                                      6; Length 358
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Publication No. US200502562991
GENERAL INFORMATION:
APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
APPLICANT: Biosynexus Incorporated
APPLICANT: Boster, Simon
APPLICANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
TITLE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: P100629W0
CURRENT APPLICATION NUMBER: US/10/485.517
CURRENT PILING DATE: 2001-09-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR APPLICATION NUMBER: GB 020349.9
PRIOR FILING DATE: 2001-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: Patentin version 3.1
SEQ ID NO 159
LENGTH: 137
                                                                                                                                                                                                      Score 33; DB
Pred. No. 29;
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85.7%;
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LENGTH: 365
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                     Query Match
Best Local Similarity 85.
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2136
LENGTH: 358
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Best Local Similarity 85.7
Local 6; Conservative
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US-10-793-626-470
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US-10-485-517-159
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                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                               Sequence 49, Application US/11113424

j Sequence 49, Application US/11113424

j Bublication No. US20050260713A1

general Information:
    APPLICANT: Gangoli et al.
    TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
    TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
    TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
    TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
    FILE REFERENCE: 21402-225

    CURRENT APPLICATION NUMBER: 60/256,704

    PRIOR APPLICATION NUMBER: 60/251,314

PRIOR APPLICATION NUMBER: 60/257,314

PRIOR APPLICATION NUMBER: 60/257,314

PRIOR APPLICATION NUMBER: 60/311,613

PRIOR PILING DATE: 2001-08-10

PRIOR PILING DATE: 2001-08-10

PRIOR PILING DATE: 2001-08-20

PRIOR APPLICATION NUMBER: 60/302,358

PRIOR APPLICATION NUMBER: 60/302,358

PRIOR APPLICATION NUMBER: 60/224,075

PRIOR APPLICATION NUMBER: 60/224,075

PRIOR APPLICATION NUMBER: 60/228,153

PRIOR PILING DATE: 2001-05-14

PRIOR FILING DATE: 2001-05-02

PRIOR FILING DATE: 2001-05-05

PRIOR FILING DATE: 2001-05-07
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Fublication No. US20060029983A1
GENERAL INFORMATION:
APPLICANT: OAKLEY, COBERT H.
TITLE OF INVENTION:
FILE REFERENCE: NRK.108
CURRENT APPLICATION NUMBER: US/11/040,218
CURRENT FILING DATE: 2005-01-21
FRIOR PELLING DATE: 2005-01-21
FRIOR PELLING DATE: 2004-02-26
FRIOR APPLICATION NUMBER: US/10/788,197
FRIOR APPLICATION NUMBER: PCT/US03/14581
FRIOR APPLICATION NUMBER: PCT/US03/14581
   Score 32; DB 6; Length 137;
Pred. No. 16;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.3%; Score 32; DB 7; Length 688; 71.4%; Pred. No. 95;
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Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
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SEQ ID NO 49
LENGTH: 688
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188 MNEFSVH 194
                                                                                                                                  1 KMNEYTVH 8
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152 KLNNHTVH 159
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US-11-129-741-2480
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; Sequence 268, Application US/10330773
; Publication No. US20060040262A1
; GARERAL INFORMATION:
    APPLICANT: David W Morris
; APPLICANT: David W Morris
; TILE OF INVENTION: Novel Compositions and Methods in Cancer; FILE REFERENCE: 529452001300
; CURRENT APPLICATION UNDRER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SEQ ID NO 268
; SEQ ID NO 268
; LENGTH: 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 65.3%; Score 32; DB 6; Length 1051; Best Local Similarity 62.5%; Pred. No. 1.5e+02; Matches 5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 265, Application US/10330773
Publication No. US20060040262A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 52452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT PILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FRRESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.3%; Score 32; DB 6; Length 1027; 62.5%; Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                               2; Mismatches
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PRIOR APPLICATION NUMBER: 60/379,986
PRIOR FILING DATE: 2002-05-13
PRIOR PILING DATE: 2002-08-07
PRIOR FILING DATE: 2002-08-07
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 25
LENGTH: 688
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Best Local Similarity 62.5
....hea 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Mus musculus
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161 KLNNHTVH 168
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US-10-330-773-268
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188 MNEFSVH 194
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US-10-330-773-268
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Sequence 2480, Application US/10895064
Publication No. US20060018923A1
GENERAL INFORMATION:
APPLICANT: PEIRIS, JOSEPH S.M.
APPLICANT: POON, LIT MAN
APPLICANT: CHAN, XWOK HUNG
APPLICANT: CHAN, XWOK HUNG
APPLICANT: LEUNG, FREDERICK C.
TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: V0690.0031
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Publication No. US20060034853A1

Sequence 2480, Application US/11129741

Publication No. US20060034853A1

SERNERAL INFORMATION:

APPLICANT: WOO, CHUU YAT PATRICK

APPLICANT: CHAN, KMOK HUNG

APPLICANT: CHAN, KMOK HUNG

APPLICANT: CHAN, KMOK HUNG

APPLICANT: CHAN, TIT MAN

APPLICANT: CHAN, TIT MAN

APPLICANT: PEIRIS, JOSEPH S.M.

APPLICANT: PEIRIS, JOSEPH S.M.

APPLICANT: PEIRIS, JOSEPH S.M.

APPLICANT: PEIRIS, JOSEPH S.M.

APPLICANT: PEIRIS JOSEPH S.M.

APPLICANT: PEIRIS, JOSEPH S.M.

APPLICANT: PINGBONON A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT

TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT

CURRENT APPLICATION NUMBER: US/11/129,741

CURRENT APPLICATION NUMBER: 10/895,064

PRIOR APPLICATION NUMBER: 10/895,064

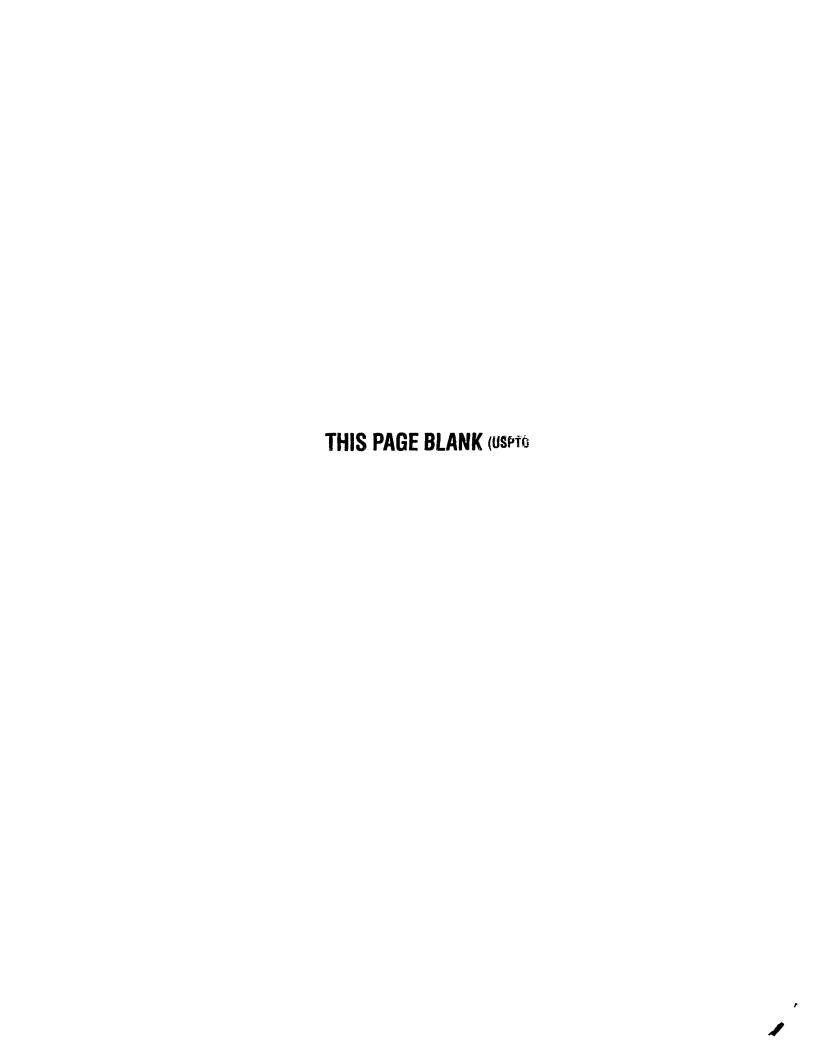
PRIOR PEILING DATE: 2004-07-21

SOFTWARE: PATENTIN VERSION 3.3

SEQ ID NO 2480

LENGTH: 22
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5; Conservative 2; Mismatches 1; Indels
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Pred. No. 3.2;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/895,064
CURRENT FILING DATE: 2004-07-21
NUMBER OF SEQ ID NOS: 2918
SOFTWARE: Patentin version 3.2
SEQ ID NO 2480
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Corononavirus-HKU1
US-10-895-064-2480
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Best Local Similarity 62.5
Matches 5; Conservative
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Search completed: March 11, 2006, 01:38:38 Job time : 9 secs



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March 11, 2006, 00:10:50; Search time 86.6667 Seconds (without alignments) 45.628 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                       OM protein - protein search, using sw model
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Run on:

US-09-905-083A-32 Perfect score:

1 RLSSMVKKV 9 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2443163 seqs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 21:\* 1: genesedm199 Database :

geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp2005s:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### STIMMARTES

		dip			SUMMAKIES	
Result No.	S	Query Match	Query Match Length DB	DB	ID	Description
-	40	100.0	6	4	AAE08237	Aae08237 Human str
7	40	100.0	0	œ	ADR68793	Adr68793 Human str
٣	40	100.0	144	æ	ADI39727	Adi39727 Stratum c
4	40	100.0	144	8	ADI37151	Adi37151 Stratum c
S	40	100.0	224	9	ADA05744	Ada05744 Human NOV
9	40	100.0	224	æ	ADN62908	Adn62908 Human NOV
7	40	100.0	224	0	ADV21100	Adv21100 Human str
æ	40	100.0	225	4	AAB98502	Aab98502 Human Str
ō	40	100.0	247	9	ADA05742	Ada05742 Human NOV
10	40	100.0	247	80	ADN62906	Adn62906 Human NOV
11	40	100.0	250	9	ADA05732	Ada05732 Human NOV
12	40	100.0	250	œ	ADN62896	Adn62896 Human NOV
13	40	100.0	252	9	ADA05734	Ada05734 Human NOV
14	40	100.0	252	œ	ADN62898	Adn62898 Human NOV
15	40	100.0	253	7	AAR67888	Aar67888 Human str
16	40	100.0	253	~	AAW05383	Aaw05383 Human amy
17	40	100.0	253	വ	ABB84421	Abb84421 Human SCC
18	40	100.0	253	ß	ABB84406	Abb84406 Human SCC
19	40	100.0	253	Ŋ	AAU82740	Aau82740 Amino aci
20	40	100.0	253	φ	ABU07440	Abu07440 Protein d
21	40	100.0	253	φ	ABU07471	Abu07471 Protein d
22	40	100.0	253	9	ABR58471	Abr58471 Human str
23	40	100.0	253	7	ADB80484	Adb80484 Ovarian c
24	40	100.0	253	7	ADJ68833	Adj68833 Human hea

Adn39180 Cancer/an Ad106515 Human tum Adn04182 Antipsori Adr72880 Human ova Ady67588 Human kal Aec00353 Human kal Aec00351 Human kal Aec0366 Yeast gen Adr68871 Human str Aec0366 Yeast gen Abp52834 Anopheles Abr84477 Mosquito Add15250 African m Ady05796 Plant ful Adx79907 Plant ful Adx774001 Plant ful Adx9108 Plant ful Adx9108 Plant ful Adx9108 Plant ful	Plant Protei Human
ADN39180 ADL06515 ADL06515 ADN04182 ADN72880 ADN72880 ADN72880 AAC0353 AAC0353 AAC0353 AAC0353 AAC0353 AAC0353 AAC0350 AAC0350 AAC0350 ADN79907 ADN79907 ADN79907 ADN79907 ADN79108	ADY07861 ABU48685 AAE08292
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4 4 5 4 3

### ALIGNMENTS

Human stratum corneum chymotrypsin enzyme peptide #2 (residues 123-131). Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia. AAE08237 standard; peptide; 9 AA. (first entry) 01-NOV-2001 AAE08237; RESULT 1 AAE08237 

Homo sapiens.

WO200159158-A1.

16-AUG-2001.

07-FEB-2001; 2001WO-US003977.

11-FEB-2000; 2000US-00502600.

(UYAR-) UNIV ARKANSAS.

O'brien TJ;

WPI; 2001-514676/56.

Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.

Claim 25; Page 102; 127pp; English.

The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide

Sequence 9 AA;

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The present invention relates to novel activated immune T cells or dendritic cells directed toward extracellular serine procease termed tumour antigen derived gene-14 (TADG-14). The method of the invention involves exposing the immune cells to a TADG-14 protein fragment, where exposure to the TADG-14 protein fragment activates the immune cells. The invention is used for the production of activated immune T cells or dendritic cells. The invention allows screening to identify proteases overexpressed in carcinoma. The present sequence is stratum corneum chymotryptic enzyme (scce) catalytic domain. This sequence is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Production of activated immune cells or dendritic cells by exposing immune cells to tumor antigen derived gene protein fragment consisting of
                                                                                                                                                                                              Immune T cell; dendritic cell; extracellular serine protease;
tumour antigen derived gene-14; TADG-14; carcinoma;
stratum corneum chymotryptic enzyme; scce.
                                                                                                                                                       Stratum corneum chymotryptic enzyme (scce) catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID NO 4; 44pp; English.
                         ADI39727 standard; protein; 144 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADI37151 standard; protein; 144 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-00137944.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-AUG-1997;
                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                   US6642013-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAY-2004
                                                                                                              15-APR-2004
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                                                                  AD139727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       against stratum corneum chymotrytic enzyme (SCCE), comprising incollating an individual with a SCCE peptide, which elicits an immune response in the individual with a SCCE peptide, which elicits an immune response in the individual. A peptide of the invention acts as a stratum corneum chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or at risk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligonucleotide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or peptides are also useful in the monitoring and development of immunocherapies for ovarian and other malignancies. The present sequence represents a peptide fragment of serine protease SCCE (stratum corneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
                                                                                                                                                                                                                                                                                                                                                                                                   Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel method for vaccinating an individual
                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                          serine protease; stratum corneum chymotrytic enzyme; SCCE; immune response; ovarian cancer; lung cancer; prostate cancer; pancreatic cancer; colon cancer.
                    100.0%; Score 40; DB 4; Length 9; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 40; DB 8; Length 9; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; SEQ ID NO 32; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Santin A;
                                                                                                                                                                                                                                                                  ADR68793 standard; peptide; 9 AA.
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Query Match
Best Local Similarity luu...
Best Local 9; Conservative
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYAR-) UNIV ARKANSAS
                                                                                                              1 RLSSMVKKV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004075723-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                       02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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ADRESULT 2
ADRES 8793
ADRES 8793
ADRES 8793
ADRES 8793
ADRES 9793

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                                                                                                                                                                                                                                                                                                        Serine protease; tumour antigen derived gene-14; TADG-14; neoplastic state; cancer; ovary; breast; lung; colon; prostate; chymotryptic enzyme; scce; enzyme.
                                                                                                                                                                                                                                                                             Stratum corneum chymotryptic enzyme (scce) catalytic domain.
100.0%; Score 40; DB 8; Length 144;
100.0%; Pred. No. 1.9;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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1D AD1

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AC AD1

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DE Str

XW Ser

XW RW neo,

XW Chy,

XX

XX Chy
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RESULT 3 ADI39727

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The invention relates to extracellular serine protease termed tumour antigen derived gene-14 (TADG-14) and its nucleic acid. Composition comprising TADG-14 peptide is useful for treating a neoplastic state in an individual. The neoplastic state is chosen from ovarian cancer, cancer, lung cancer, colon cancer, prostate cancer in which TADG-14 is overexpressed. The present sequence is Stratum corneum chymotryptic enzyme (scce) catalytic domain. This sequence is used in the envention.
                                                                                                                                                                                                                                                                           Novel isolated DNA encoding tumor antigen derived gene-14 protein, useful for treating neoplastic state (such as ovarian cancer, breast cancer, lung cancer, colon cancer, prostate cancer) in an individual.
                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 4; 46pp; English
                                                                                                  21-AUG-1997; 97US-00915659
21-AUG-1998; 98US-00137944
18-JUL-2000; 2000US-00618259
                                                                   13-JUN-2003; 2003US-00461787
                                                                                                                                                                                                        O'brien TJ, Underwood LJ;
                                                                                                                                                                       (UYAR-) UNIV ARKANSAS.
                                                                                                                                                                                                                                           WPI; 2004-141550/14.
US2003199010-A1.
                                23-OCT-2003
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## Sequence 144 AA;

Gaps ö 100.0%; Score 40; DB 8; Length 144; 100.0%; Pred. No. 1.9; .ive 0; Mismatches 0; Indels Local Similarity 100. nes 9; Conservative Query Match Matches

1 RLSSMVKKV 9

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60 RLSSMVKKV 68

ADA05744 standard; protein; 224 AA. 06-NOV-2003 (first entry) ADA05744;

Human NOV18g protein SEQ ID NO:104.

human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alaheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.

10-APR-2003.

WO2003029424-A2 Homo sapiens

02-OCT-2001; 2001US-0326483P. 05-OCT-2001; 2001US-0327435P. 05-OCT-2001; 2001US-03279449P. 09-OCT-2001; 2001US-0327917P. 09-OCT-2001; 2001US-0328044P. 02-OCT-2002; 2002WO-US031373 RESULT 5
ADA05744
ADA05744
ADA05744
AC ADA0
AX ADA0
AX ADA0
BY Human
KW AUMAN
KW AUMIN
KW AUM

20010S-0329414P 20010S-0330142P 20010S-0343039P 20010S-034362P 20010S-034362P 20010S-034363P 20010S-0343315P 20020S-0373815P 20020S-0373817P 20020S-0373817P 20020S-0373817P 20020S-0373817P 20020S-0373817P 2002US-0381037P. 2002US-0381038P. 2002US-0381042P. 2002US-0381642P 2002US-0383656P 2002US-0383831P. 2002US-0391335P. 2002US-00262511 18-OCT-2001; 2 22-OCT-2001; 2 24-OCT-2001; 2 24-OCT-2001; 2 29-OCT-2001; 2 01-NOV-2001; 17-APR-2002; 19-APR-2002; 19-APR-2002; 19-APR-2002; 22-APR-2002; 16-MAY-2002; 16-MAY-2002; 16-MAY-2002;

# (CURA-) CURAGEN CORP.

Dipippo VA; Catterton E; Guo X; Kekuda R, Ju J, Li L, Guo X SR, Ellerman K, Malyankar UM; Berghs C, T, Gorman L, Corman L, Stone LV, Miller CE, Rastelli L, Stone LV, Leach MD, Agee ML, Imkets RA, Rothenberg ME, Leach MD, Agee ML, Aleger DK, Spaderna SK; Smithson G, Millet I, Peyman JA, nexuwa Patturajan M, Spytek KA, Edinger SR, Ell Ort T, Gorman L, Zerhusen BD, Anderson I T, Gorman E, Rastelli L, Stone DJ, ... Miller CE, Rastelli L, Stone DJ, Shimkets RA, Eisen AJ,

WPI; 2003-381626/36.

N-PSDB, ADA05743

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New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics

# Claim 1; Page 172; 586pp; English.

The present invention describes NoVX proceins, where X can be 1 to 55

(e.g. NOV1). Also described: (1) a composition comprising a polypeptide

CC described above and a carrier; (2) a kit comprising, in one or more

CC containers, the composition described above; (3) an isolated mucleic acid

CC comprising the nucleic acid molecule described above; (5) a cell

CC comprising the nucleic acid molecule described above; (5) a cell

CC comprising the bove vector; (6) an antibody that immunospecifically

CC comprising the above polypeptide or nucleic acid molecule in a

Sample; (8) methods for determining the presence of or predisposition to

CC sample; (8) methods for determining the presence of or predisposition to

CC a disease associated with altered levels of expression of the above

CC a disease associated with altered levels of expression of the polypeptide described

CC comprising a nagent that binds to the polypeptide described

CC method of identifying a potential therapeutic agent for

Use in treating a pathology that is related to an aberrant expression or

above; (10) a method for identifying a potential therapeutic agent for

CC above; (10) a method gor identifying a potential therapeutic agent for

CC a pathology associated with the polypeptide; (11) a method of

CC screening for a modulator of activity or of latency or predisposition to

CC a pathology associated with the polypeptide; (12) a method for modulating

CC or preventing a pathology associated with the above polypeptide. Novx

CC a pathology associated with the polypeptide in a

CC mammal; and (14) a method for producing the above polypeptide. Novx

CC sequences have antidiabetic, anorectic, antibacterial, virucide,

CC immunomodulator, cytostatic, noorropic, and above polypeptide in an antilipaemic activities, and can be used in gene therapy. The

CC polypeptide is useful in manufacturing a medicament for treating a

CC acid molecule map be used to diagnose, treat or prevent metabolic

CC disorders such as diabetes or obesity, infections, c

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                                                                                                                                                                                                                                                                                                                                                                             human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
disease, immune disorders, haematopoietic disorders and various dyslighdaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
                                                                                                                                         Gaps
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                                                                                                           100.0%; Score 40; DB 6; Length 224; 100.0%; Pred. No. 3.1; o; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  ADN62908 standard; protein; 224 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-2001; 2001US-0326483P.
05-OCT-2001; 2001US-0327435P.
05-OCT-2001; 2001US-0327449P.
09-OCT-2001; 2001US-0327917P.
09-OCT-2001; 2001US-0328024P.
09-OCT-2001; 2001US-0328044P.
09-OCT-2001; 2001US-0328044P.
12-OCT-2001; 2001US-0328044P.
17-OCT-2001; 2001US-0328044P.
17-OCT-2001; 2001US-0330142P.
18-OCT-2001; 2001US-0330309P.
24-OCT-2001; 2001US-0343652P.
24-OCT-2001; 2001US-0343629P.
25-OCT-2001; 2001US-0343629P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-APR-2002; 2002US-0373E1SP.
19-APR-2002; 2002US-0373B17P.
19-APR-2002; 2002US-0373B26P.
19-APR-2002; 2002US-0373B4P.
22-APR-2002; 2002US-0374977P.
16-MAY-2002; 2002US-0381037P.
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2001US-0346357P.
2002US-0373260P.
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16-MAY-2002; 2002US-0381042P.
17-MAY-2002; 2002US-0381642P.
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25-JUN-2002; 2002US-0391335P.
                                                                                                                                                                                                                                                                                                                        01-JUL-2004 (first entry)
                                                                                                                         Best Local Similarity 100 Matches 9; Conservative
                                                                                                                                                                                              109 RLSSMVKKV 117
                                                                                                                                                                  1 RLSSMVKKV 9
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MILLET I.
                                                        present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                      wasting disorder.
                                                                                  Sequence 224 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2004038223-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                     Human NOV189
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                                                                                                                                                                                                                                                                                              ADN62908;
                                                                                                            Query Match
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ADN62908
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The invention relates to isolated NOVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the abbrrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and activity of NOVX polypeptides. For example, NOVX polypeptides and current associated with decreased expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polypeptides and complementary sequences may also be used as DNA probbs in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of capture to the production of antibodies and in assays to identify modulators to the production of antibodies and in assays to identify of NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists and capturity of NOVX.

Colypeptides and polynucleotide expression and activity of NOVX polypeptides may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, anorexia, cancer, cancer-associated cachexia, neurodegenerative disorders, all the waithous dyslipidaemias, metabolic shorders, and the various dyslipidaemias, metabolic disorders, haematopoletic disorders, and the various dyslipidaemias, metabolic disorders, and the waith obesity, the metabolic syndrome X and

Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease

WPI; 2004-213931/20.

N-PSDB; ADN62907.

Claim 1; SEQ ID NO 104; 395pp; English.

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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                      SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
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                                                                                                                        STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
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BERGHS C.
DIPIPPO V A.
                                                                            ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                (RIEG/) RIEGER D K.
(SPAD/) SPADERNA S K.
                               PATTURAJAN M.
                                                                                               CATTERTON E.
                                                                                                            MILLER C E.
RASTELLI L.
PEYMAN J A
KEKUDA R.
                                                                      GORMAN L.
                                                                                         ZHONG M.
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(RAST/)
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Gaps

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diseases or conditions of the prostate such as prostatic cancer. The present sequence is the human stratum corneum chymotrypsin protein. This sequence is used to align with PS133 consensus protein.
                                                                                                                                                                                                                                                            Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.
                                                                                                                                                                                                                                                                                 Human, TADG-15; cytostatic; vaccine; ovarian tumour; cancer; tumour antigen-derived gene 15; serine protease; Stratum Corneum Chymotryptic Enzyme; SCCE.
                                                                 100.0%; Score 40; DB 9; Length 224; 100.0%; Pred. No. 3.1; ive 0; Mismatches 0; Indels
                                                                                                                                                                                           AAB98502 standard; protein; 225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                20-OCT-2000; 2000WO-US029095.
                                                                                                                                                                                                                                      (first entry)
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tanimoto H;
                                                                                                                                 94 RLSSMVKKV 102
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                                                                                                               1 RLSSMVKKV
                                                                             Local Similarity
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                                             Sequence 224 AA;
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                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                     20-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polypeptides, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining predisposition to diseases or conditions of the prostate such as prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to PS133 protein, a member of the human serine protease family and its corresponding nucleic acid sequence. PS133 polypeptide is useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to
                                                                                                                                                                                                                                                                                Protein purification; PS133 protein; serine protease; prostate disease; andrology; genitourinary disease; prostatic cancer; cytostatic; protein therapy; chymotrypsin; enzyme.
   cancers.
                                                                                          Gaps
wasting disorders associated with chronic diseases and various cand. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
                                                                                          ô
                                                                  8; Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Granados E, Klass MR,
                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                          /note = Catalytically functional motif
                                                                                                                                                                                                                                                                                                                                                                                   /note = Catalytically functional
174. .179
                                                                                                                                                                                                                                                                                                                                                                                                                     /note = Catalytically functional
                                                                 100.0%; Score 40; DB 8
100.0%; Pred. No. 3.1;
iive 0; Mismatches
                                                                                                                                                                                                                                                            Human stratum corneum chymotrypsin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; SEQ ID NO 33; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Friedman PN,
Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                         ADV21100 standard; protein; 224 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-FEB-2001; 2001US-00789210.
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                                                                                                                                                                                                                                      (first entry)
                                                                          Local Similarity 100
                                                                                                                                   RLSSMVKKV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COHEN M.
COLPITTS T L.
FRIEDMAN P N.
GRANADOS E.
KLASS M R.
KLASS M R.
STEWART K D.
STROUPE S D.
                                                                                                             σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-011614/01,
                                                                                                             1 RLSSMVKKV
                                             Sequence 224 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENBANK; L33404.
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                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-OCT-1997;
                                                                                                                                                                                                                                      24-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-DEC-2004
                                                                                                                                   109
                                                                 Query Match
                                                                                                                                                                                                                ADV21100;
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(KLAS/)
(RUSS/)
(STEW/)
(STRO/)
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(COLP/)
(FRIE/)
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Matches
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                                                                                                                                                                                                                                                                           The present invention relates to human tumour antigen-derived gene 15 (TADG-15) protein and coding sequence (see AAH23601 and AAB98500). TADG-15 is an extracellular serine protease. It was found that TADG-15 is over-expressed in ovarian tumours. TADG-15 protein or its fragments of 9-20 residues that lack TADG-15 protein or its fragments of 9-20 an individual against TADG-15, having, suspected of having or at risk of getting cancer. Purthermore, the TADG-15 gene can be used as a diagnostic or therapeutic target in cancer. The present sequence was used in a sequence homology alignment with the catalytic domain of TADG-15
Novel extracellular serine protease, termed tumor antigen-derived gene 15 protein overexpressed in carcinomas and DNA encoding it, for diagnosis, treatment, prevention of cancer, particularly breast, ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Similarity 100.0%; Score 40; DB 4; Length 225;
9; Conservative 0; Mismatches 0: Indela
                                                                                                                                                                                            Example 10; Fig 1; 130pp; English
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New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Shongy SG;
                                                                                                                                                         immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                          human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
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ADA05742
ID ADA05742 standard; protein; 247 AA.
                                                                                                           Human NOV18f protein SEQ ID NO:102,
                                                                                                                                                                                                                                                                                                                                                                             02-OCT-2001; 2001US-0326483P.
05-OCT-2001; 2001US-0327435P.
09-OCT-2001; 2001US-0327449P.
09-OCT-2001; 2001US-0327917P.
09-OCT-2001; 2001US-0328029P.
09-OCT-2001; 2001US-0328044P.
12-OCT-2001; 2001US-0328044P.
15-OCT-2001; 2001US-0328049P.
15-OCT-2001; 2001US-0339144P.
17-OCT-2001; 2001US-03498P.
22-OCT-2001; 2001US-0349578P.
24-OCT-2001; 2001US-0349578P.
24-OCT-2001; 2001US-03463578P.
25-OCT-2001; 2001US-03463578P.
17-APR-2002; 2002US-0373860P.
17-APR-2002; 2002US-0373860P.
19-APR-2002; 2002US-0373860P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-APR-2002; 2002US-0373884P.
22-APR-2002; 2002US-034937P.
16-WAY-2002; 2002US-0381037P.
16-WAY-2002; 2002US-0381038P.
17-WAY-2002; 2002US-0381042P.
17-WAY-2002; 2002US-0381642P.
28-WAY-2002; 2002US-0383656P.
                                                                                                                                                                                                                                                                                                                                                    32-OCT-2002; 2002WO-US031373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002US-0383831P.
2002US-0391335P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002; 2002US-00262511
                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2003-381626/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADA05741.
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                                                                             06-NOV-2003
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Shimkets RA,
                                                                                                                                                                                                                                                                                                                      10-APR-2003
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                                              ADA05742;
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C The present Invention describes NoVX proteins, where X can be 1 too 35 containers, the composition described above; (1) an isolated nucleic acid described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector containers, the composition described above; (3) an isolated nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (6) a cell comprising the above vector; (6) an antibody methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for method of identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of secreting for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method of or preventing a pathology associated with the above polypeptide; nover a pathology associated with the above polypeptide or mammal; and (14) a method for producing the above polypeptide in a activity of the polypeptide described above; (13) method for indiabetic, anorectic, antibacterial, virucide, and antilipaemic activities, and can be used an opypaptide or the nucleic syndome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to disease or obesity, infections, cancering cylaberial and altabetes or obesity, infections, cacherial cacherial and pathology acids and antilipaemic ö present invention describes NOVX proteins, where X can be 1 to 55 Gape ö 100.0%; Score 40; DB 6; Length 247; 100.0%; Pred. No. 3.4; 0; Indels tive 0; Mismatches 0; Indels Local Similarity 100. present invention. Sequence 247 AA; Query Match Matches 

109 RLSSMVKKV 117 σ 1 RLSSMVKKV ð 셤

RESULT 10

ADN62906 standard; protein; 247 AA. ADN62906

ADN62906;

(first entry) 01-JUL-2004

Human NOV18f.

human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer: sasociated cachexia; neurodegenerative disorder; Alzheimer; s disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X; 

wasting disorder

Dipippo VA;

Homo sapiens.

US2004038223-A1.

26-FEB-2004.

01-OCT-2002; 2002US-00262511

02-OCT-2001; 2001US-0326483P. 05-OCT-2001; 2001US-0327435P.

Claim 1; Page 172; 586pp; English.

pharmacogenomics

09-OCT-2001; 2001US-0328029F.
09-OCT-2001; 2001US-0328044P.
09-OCT-2001; 2001US-0328044P.
12-OCT-2001; 2001US-0328044P.
15-OCT-2001; 2001US-0328144P.
17-OCT-2001; 2001US-033030402P.
18-OCT-2001; 2001US-033030402P.
24-OCT-2001; 2001US-0343629F.
24-OCT-2001; 2001US-0343629F.
25-OCT-2001; 2001US-0343629F.
10-NOV-2001; 2001US-0343657F.
17-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373815P.

16-MAY-2002; 2002US-0381037P. 16-MAY-2002; 2002US-0381038P. 16-MAY-2002; 2002US-0381042P. 17-MAY-2002; 2002US-0381642P. 28-MAY-2002; 2002US-038365F. 29-MAY-2002; 2002US-038361P. 25-JUN-2002; 2002US-038331P.

22-APR-2002; 2002US-0374977P

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The invention relates to isolated NOVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and activity of NOVX by supplementing the patient our polynucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators canti-NOVX polypeptides and antagonists and antagonists may also be used to modulate NOVX polypuncleotide expression and activity of NOVX polypeptides antibodies, agonists and antagonists may also be used as attivity of NOVX polypeptides antibodies, agonists and antagonists may also be used as diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, ancer, and the various dyslipidaemias, metabolic disorders associated with obesity, the metabolic syndrome X and discusses, anorexia, cancer, cancer associated cachexia, metabolic cancer, and the various dyslipidaemias, metabolic disorders, and the various dyslipidaemias, metabolic wasting disorders associated with obesity, the metabolic syndrome X and chereting disorders associated with chronic diseases and various cancers.

They may also be used as antibacterial agents. The present sequence
                         diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obseity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
  for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 40; DB 8; Length 247; 100.0%; Pred. No. 3.4; cive 0; Mismatches 0; Indels
Isolated NOVX polypeptides and nucleic acids, useful
                                                                     Claim 1; SEQ ID NO 102; 395pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA05732 standard; protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human NOV18a protein SEQ ID NO:92.
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05-0CT-2001; 2001US-0327435P.
05-0CT-2001; 2001US-0327449P.
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Best Local Similarity 100.
اتام 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 RLSSMVKKV 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 247 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
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SHIMKETS R A.
ROTHENBERG M E
LEACH M D.
AGEE M L.
BERGHS C.
DIPIPPO V A.

(SHIM/) (ROTH/) (LEAC/) (AGEE/)

GANGOLLI E A. RIEGER D K. SPADERNA S K.

(EISE/) (GANG/) (RIEG/) (SPAD/)

EISEN A.

WPI; 2004-213931/20

N-PSDB; ADN62905

ZERHUSEN B D. ANDERSON D W. ZHONG M.

(ANDE/) (ZHON/)

GORMAN L.

(GORM/)

CATTERTON E.

CATT/) JIWW/) MILL/) RAST/)

JI W.
MILLER C E.
RASTELLI L.
STONE D J..
PENA C E A.
SHENOY S G.

(STON/)

SHEN/)

ELLERMAN K. MALYANKAR U M.

(ELLE/) (MALY/)

GUO X. PATTURAJAN M.

다. 다.다.

(KEKU/) (JUJJ/) (LILL/) (GUOX/)

MILLET I. PEYMAN J A. KEKUDA R.

(MILL/)

SMITHSON G.

SMIT/)

SPYTEK K A. EDINGER S R.

(SPYT/)

PATT/

acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslighdaemlas. The nuclèic acids can also be used as hybridiation probes, in chromsome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the

°,

Gaps

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0; Indels

0; Mismatches

9; Conservative

Matches

Query Match Best Local Similarity

present invention.

88888888888888

Sequence 250 AA;

0

1 RLSSMVKKV

ò

100.0%; Score 40; DB 6; Length 250; 100.0%; Pred. No. 3.5;

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09-0CT-2001; 2001US-0328029F.
09-0CT-2001; 2001US-0328044P.
09-0CT-2001; 2001US-0328044P.
12-0CT-2001; 2001US-0328144P.
15-0CT-2001; 2001US-0328144P.
17-0CT-2001; 2001US-03303039.
18-0CT-2001; 2001US-034303P.
24-0CT-2001; 2001US-0343629F.
24-0CT-2001; 2001US-0343629F.
25-0CT-2001; 2001US-0343629F.
17-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373816P.
19-APR-2002; 2002US-037384P.
19-APR-2002; 2002US-037384P.
19-APR-2002; 2002US-037384P.
19-APR-2002; 2002US-037384P.
19-APR-2002; 2002US-037384P.
19-APR-2002; 2002US-037384P.
16-MAY-2002; 2002US-037384P.
                                                                                                                                                        2002US-0381642P.
                                                                                                                                                  2002US-0381042P
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N-PSDB; ADA05731.
                                                                                                                                                                                                                                                                                                            pharmacogenomics
                                                                                                                                                   16-MAY-2002;
                                                                                                                                                           L7-MAY-2002;
                                                                                                                                                                              25-JUN-2002;
                                                                                                                                                                       29-MAY-2002
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The present live forestibles Nova process.

(e.g. NOVI). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containmers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential described above; (11) a method of a method for identifying a potential therapeutic agent for abortant physiological interactions of the polypeptide; (11) a method of a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating cor preventing a pathology associated with the above polypeptide. Novx sequences have antidiabetic, anorectic, antibacterial, virucide, mammal; and (14) a method for producing the above polypeptide. Novx sequences have antidiabetic, anorectic, antibacterial, virucide, and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manna disease. The polypeptide or the nucleic syndrome associated with a human disease. The polypeptide or the nucleic Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK; obesity, Kekuda R, Ju J, Li L, Guo A, RR. Ellerman K, Malyankar UM; The present invention describes NOVX proteins, where X can be 1 to 55 9 New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing Claim 1; Page 169-170; 586pp; English.

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human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
                                                 ADN62896 standard; protein; 250 AA
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2001US-0349575P.
2001US-0346357P.
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2001US-0328044P.
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                                                                                       01-JUL-2004 (first entry)
120 RLSSMVKKV 128
                                                                                                                                                                      wasting disorder
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                                                                                                                                                                                                                                                                                                                                09-OCT-2001;
12-OCT-2001;
15-OCT-2001;
                                                                                                                                                                                          Homo sapiens.
                                                                                                          Human NOV18a
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18-OCT-2001;
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25-JUN-2002;
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01-NOV-2001;
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                                                                    ADN62896;
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2002US-0391335P

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The invention relates to isolated NOVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polypeptides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypetides may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polymucleotide expression and activity of NOVX.

C polypeptides. The anti-NOVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX c polypeptides and polymucleotides may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious diagnose and creat, cancer, cancer-associated cachexia, neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
n L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo
Jolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 92; 395pp; English
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jan M, Spytek KA,
Gorman L, Zerhuge
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GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
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RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
                                                                                                   GUO X.
PATTURAJAN M.
SPYTEK K A.
                                                                                                                                                                                MALYANKAR U M.
                                                                                                                                                                                                           GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
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BERGHS C.
DIPIPPO V A.
                                                                                                                                                EDINGER S R.
ELLERMAN K.
                          MILLET I.
PEYMAN J A.
KEKUDA R.
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              SMITHSON G.
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Ort T, Gorman L,
Ji W, Miller CE,
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N-PSDB; ADN62895.
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Shimkets RA,
Eisen A, Gang
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(PENA/)
(SHEN/)
(SHIM/)
(ROTH/)
(LEAC/)
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(DIPI/)
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(RAST/)
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(LILL/)
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Dipippo VA;

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disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, haematopoietic disorders, and the various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
                                                                                                                                                                                                                                                                                                                                                  human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
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                                                                                                             100.0%; Score 40; DB 8; Length 250; 100.0%; Pred. No. 3.5;
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0; Mismatches
                                                                                                                                                                                                                                                     ADA05734 standard; protein; 252 AA.
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2001US-0328029P
2001US-0328044P
2001US-0328044P
2001US-0329144P
2001US-03329414P
2001US-03329414P
2001US-03339266P
2001US-0343529P
2001US-034537P
2001US-034537P
2001US-0373866P
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2002US-037382F.
2002US-0374977P.
2002US-03381037P.
2002US-0381037P.
2002US-0381043P.
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                                                                                                                                       9; Conservative
                                                                                                                                                                                     120 RLSSMVKKV 128
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                                                                                                                         Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                1 RLSSMVKKV
                                                                                       Sequence 250 AA;
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09-OCT-2001; 2
12-OCT-2001; 2
15-OCT-2001; 2
17-OCT-2001; 2
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29-OCT-2001;
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                                                                                                                                                                                                                           RESULT 13
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01-OCT-2002;

Human NOV18b

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ADN62898 standard; protein; 252 AA.
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Matches 9; Conservative
                                                                                                                                                                                                                                              122 RLSSMVKKV 130
   (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                       1 RLSSMVKKV 9
                                     2003-381626/36
                                                                                                                                                                                                        present invention.
                                         N-PSDB; ADA05733
                                                            pharmacogenomics
                                                                                                                                                                                                               Sequence 252 AA;
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ADN62898
ID ADN62
XX
AC ADN62
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12-OCT-2001;
15-OCT-2001;
17-OCT-2001;
18-OCT-2001;
22-OCT-2001;
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16-MAY-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOV1). Also described: (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit composition or none
containers, the composition described above; (3) an isolated nucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
comprising the nucleic acid molecule described above; (5) a cell
comprising the nucleic acid molecule described above; (5) a cell
comprising the nucleic acid molecule described above; (6) a cell
comprising the above vector; (6) an antibody that immunospecifically
binds to the polypeptide described above; (7) methods for determining the
presence or amount of the above polypeptide or nucleic acid molecule in a
ample; (8) methods for identifying a potential therapeutic agent for
comprising the above polypeptide or nucleic acid molecule in a
polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
method of identifying an agent that binds to the polypeptide described
above; (10) a method for identifying a potential therapeutic agent for
use in treating a pathology that is related to an aberrant expression or
aberrant physiological interactions of the polypeptide; (11) a method of
acreening for a modulator of activity or of latency or predisposition to
compression of activity or of activity or of latency or predisposition to
a pathology associated with the polypeptide; (12) a method for modulating
the activity of the polypeptide described above; (13) methods of treating
or preventing a pathology associated with the above polypeptide in a
mammal; and (14) a method for producing the above polypeptide in a
mammal; and (14) a method for producing the above polypeptide in a
mammal; and (14) a method for producing the above polypeptide in a
mammal; and (14) a method for producing the above polypeptide or the nucleic
acid molecule may be used to diagnose, treat or prevent metabolic
disorders such as diabetes or obesity, infections, cachexia, cancer
alsorders such as 
Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Corturajan L, Zerhusen BD, Anderson DW, Zhong M, Catterton E, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                         New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
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human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopojetic disorder; dyslipidaemia; metabolic syndrome X;
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2001US-0327435P.
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2001US-0327917P.
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EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
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STONE D J.
PENA C E A.
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SHIMKETS R A.
ROTHENBERG M E
                                                                                                                                                                                                                                                                                                                                                                                                                             PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                                               MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZHONG M.
CATTERTON E.
                                                                                                                                                                                                                                                                                                                                                                         SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MILLER C E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GORMAN L.
                                                     wasting disorder
                                                                                   US2004038223-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SHEN/)
(SHIM/)
(ROTH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MALY/)
(ORTT/)
(GORM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZHON/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RAST/)
(STON/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ZERH/)
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Gaps

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0; Indels

01-JUL-2004 (first entry)

Human stratum corneum chymotrophic recombinant enzyme (SCCE).

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The invention relates to isolated NoVX polypeptides and polymucleotides.

NoVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the abstract expression and activity of NoVX polypeptides. For example, NoVX polypeptides and activity of NoVX by supplementing the patient our polymucleotides may be used to treat disorders associated with decreased to polymucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of crestorative therapy. NoVX polypeptides may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of crestorative therapy. NoVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NoVX. The anti-NoVX polypeptide antibodies, agonists and antagonists may also be used as anti-NoVX polypeptides. The anti-NoVX polypeptide antibodies, diabetes, obesity, infectious diagnose and treat: metabolic disorders, diabetes, obesity, infectious diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, haematopoietic disorders, and the various dyslipidaemias, metabolic creased with obesity, the metabolic syndrome X and disorders associated with obesity, the metabolic syndrome X and contexting disorders associated with obesity, the metabolic syndrome X and contexting disorders associated with obesity, the metabolic syndrome X and contexting disorders associated vith chosents and probable of a human NoVX protein.

They may also be used as antibacterial agents. The present sequence of a human NoVX protein.
                                                                                                                                                                                                                                                                                                                              Dipippo VA;
                                                                                                                                                                                                                           Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 94; 395pp; English.
                  AGEE M L.
BERGHS C.
DIPIPPO V A.
EISEN A.
GANGOLLI E A.
RIEGER D K.
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-213931/20.
LEACH M D.
                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADN62897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 252 AA;
                                                                                                                        (GANG/)
(RIEG/)
(SPAD/)
                                                                           (DIPI/)
(EISE/)
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Query Match
             Best Loc
Matches
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                                                                                                                                                                                                                                       0; Indels
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Matches 9; Conservative
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                                                                                                                                                                                                                Query Match
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AAR67888 standard; protein; 253 AA.

122 RLSSMVKKV 130

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(revised)
(first entry)

25-MAR-2003 09-AUG-1995 AAR67888;

RESULT 15
AAR67888
ID AAR67;
XX
AC AAR67;
DT 25-MAJ
DT 09-AU

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Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and related vectors, transformed cells and polypeptides, useful for treating skin disorders, e.g. acne or psoriasis, and for identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The enzyme encoded by this sequence is used in pharmaceutical, cosmetic and skin care products, especially to treat and prevent acne, xeroderma, or other hyperkeratotic conditions (e.g. callosities or keratosis pilaris), ichthyoses, psoriasis, eczema, etc. It is produced recombinantly following mammal, insect, plant, or microorganism transformation with plasmid pS507. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                              Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis; callosities; keratosis pilaris; ichthyoses; eczema.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 97; 137pp; English
                                                                                                                                                                           94WO-IB000166
                                                                                                                                                                                                           93DK-00000725
                                                                                                                                                                                                                                                                           Egelrud T, Hansson L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 RLSSMVKKV 131
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                                                                                                                                                                                                                                                                                                          WPI; 1995-052088/07.
                                                                                                                                                                                                                                                                                                                                                                                                        specific inhibitors.
                                                                                                                                                                                                                                           (SYMB-) SYMBICOM AB
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                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ81203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 253 AA;
                                                                                                                                                                         20-JUN-1994;
                                                                                                                                                                                                           18-JUN-1993;
                                                                               Homo sapiens
                                                                                                                                            05-JAN-1995.
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds (without alignments) 61.367 Million cell updates/sec

US-09-905-083A-32

1 RLSSMVKKV 9 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pir 80:\*
1: pir1:\*
1: pir2:\*
2: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	serine proteinase	probable endo alph	para-hydroxybenzoa	hypothetical prote	ABC transporter (1	biotin synthase (b	para-hydroxybenzoa	arginine-tRNA liga				hypothetical prote	hypothetical prote	0	vitamin D receptor	hypothetical prote	cytochrome P450 li	glycine hydroxymet	hemagglutinin homo	transcription fact	isoleucine-tRNA sy	chromosome segrega	hypothetical prote	TATA-binding prote	S-adenosylmethioni	GTP-binding protei	membrane lipoprote	Deinococcus radiod	threonine synthase
	ID	A53968	O)	S20056	S50401	C70009	D90264	T38914	A71277	T50316	H85470	T05012	T02473	T32363	156519	JC5402	G75073	D85429	T01759	A49218	A47528	E90220	A82543	T33079	JC5511	A97255	E69214	AH2591	B97374	F90194
	DB	~	N	~	N	П	N	N	~	~	7	~	0	~	~	~	~	~	~	7	~	~	N	~	~	~	N	N	~	~
	Match Length	253	282	372	260	350	351	358	589	664	915	925	239	240	318	319	373	457	532	647	833	986	1167	1846	253	285	3	337	337	4
9	Match	100.0	82.5	82.5	82.5	80.0	80.0	80.0	80.0	80.0	77.5	77.5	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	72.5	72.5	72.5	ς.	72.5	•
	Score	40	33	33	33	32	32	32	32	32	31	31	30	30	30	30	30	30	30	30	30	30	30	30	29	29	29	29	29	29
Regult	No.	-	7	m	4	S	9	7	8	σı	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

hypothetical prote	probable lipoprote	membrane lipoprote	hypothetical prote	phytoene desaturas	hypothetical prote	phytoene dehydroge	phytoene dehydroge	hypothetical prote	probable beta-gluc	hypothetical prote	hypothetical prote	hypothetical prote	dynein beta heavy	hypothetical prote	hypothetical prote
F84246	D96986	H75318	A72228	865060	H82872	829314	A45381	T23338	E70906	862963	F96596	T17484	T14914	G71376	AH2565
7	~	7	~	~	7	N	~	~	~	~	~	~	~	N	0
349	357	379	553	571	578	582	583	959	691	839	1360	4077	4589	41	63
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72.5	72.	72	72.	72	72	72.	72	72	72	72.	72	72	72.	70.	70.
29	29	29	29	29	53	59	29	29	29	29	29	29	29	28	28
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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C;Accession: A53968
R;Hansson, L.; Stroemqvist, M.; Bacckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
J. Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Reference number: A53968, MUID:94308225; PMID:8034709
A;Accession: A53968
A;Cross-references: UNIPROT:P49862; UNIPARC:UPIO00001BC4; GB:L33404; NID:g521214; PIDN:}C;Genetios: TGB:PRSS6; SCCE
A;Cross-references: GDB:PRSS6; SCCE
A;Cross-references: GDB:377730
A;Wap position: 7435-7435
C;Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                C.Species: Homo sapiens (man)
C.Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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serine proteinase SCCE precursor – human
N;Alternate names: stratum corneum chymotryptic enzyme
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probable endo alpha-1,4 polygalactosaminidase - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: OS-Nov-1999 #sequence\_revision OS-Nov-1999 #text\_change O9-Jul-2004 C;Accession: T35294 B;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999 A;Recession: T35294 A;Accession: T352

Score 33; DB 2; Length 282; Pred. No. 13; 82.5%; Query Match Best Local Similarity ~

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ABC transporter (lipoprotein) homolog yufN - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: C70009
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterc
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
A; Bhrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler,
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, R.; Lapidus, A.; Lardinois,
A,Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Mandud, S.; Mandel,
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Poth, T.M.; Potherelle,
Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A,Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sakiguchi, J.; Sekowska, A.; Sato,
T.; Winters, D.; Wipat, A.; Yamamoto, H.; Yamamoto, K.; Yasumoto,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamamoto, K.; Yasumoto,
A,Authors: Voshikawa, H.F.; Zumstein, B.; Yoshikawa, H.; Danchin, A.
A,Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A,Rocession: C70009
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Rocession: Mandor, Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:O05252; UNIPARC:UPI00006609A4; GB:Z99120; GB:AL009126; NID:g;
A;Experimental source: strain 168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q97226; UNIPARC:UPI0000064360; GB:AE006641; NID:g13814305; PJ
C;Genetics:
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Cispecies Sulfoldous Bolfataricus
Cipace: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
Cipace: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
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C;Superfamily: ABC transporter yufN
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A; Residues: 1-351 < KUR>
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Matches 6; Conser
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269 LTSMVKKV
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                                                                                                                                                                                                                                                                                                  para-hydroxybenzoate polyprenyltransferase (EC 2.5.1.-) precursor - yeast (Saccharomyces N.Alternate names: 4-hydroxybenzoate hexaprenyltransferase; protein N3419; protein YNR04 (Species: Saccharomyces cerevialae C;Species: Saccharomyces cerevialae C;Accession: S2.3Apr-1993 #sequence revision 23-Apr-1993 #text_change 09-Jul-2004 C;Accession: S20056; S63372; JC2317 R;Ashby, M.N.; Kutsunai, S.Y.; Ackerman, S.; Tzagoloff, A.; Edwards, P.A. A;Title: COG. is a candidate for the structural gene encoding para-hydroxybenzoate:polypty. A;Reference number: S20056; MUID:92156158; PMID:1740455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-372 <ASH>
A;Residues: 1-372 <ASH>
A;Residues: UNIPROT:P32378; UNIPARC:UPI0000127EF7; EMBL:M81698; NID:g171252; PID
R;Pohl, T.M.
submitted to the Protein Sequence Database, April 1996
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A;Residues: 1-372 <POH>
A;Cross-references: UNIPARC:UP10000127EF7; EMBL:Z71656; NID:g1302546; PID:e239832; PID:g
A;Experimental source: strain S288C
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A;Molecule type: DNA
A;Residues: 1-560 eBAD>
A;Cross-references: UNIPROT:P40215; UNIPARC:UPI00001388C3; EMBL:Z47071; NID:g606429; PIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Keywords: 1soprenoid biosynthesis, mitochondrion; transferase; transmembrane protein C,Keywords: 1soprenoid biosynthesis, mitochondrion) #status predicted <TRP>
F;17-212/Domain: transmembrane #status predicted <TMD>
F;172-188/Domain: transmembrane #status predicted <TMC>
F;172-188/Domain: transmembrane #status predicted <TMC>
F;203-225/Region: polyprenyl diphosphate binding #status predicted
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C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan.1995 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C;Accession: S50401
R;Badcock, K; Churcher, C.
Rspadcock, K; Churcher, C.
Bubmitted to the EMBL Data Library, December 1994
   Gaps
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Pred. No. 17;
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    yeast (Saccharomyces cerevisiae)

   Indels
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   Mismatches
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A;Cross-references: SGD:S0005324; MIPS:YNR041c
   1;
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77.8%;
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A,Cross-references: SGD:S0004753
A,Map position: 13R
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Best Local Similarity 77.0
Best Local 7; Conservative
   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: S63346
A;Accession: S63372
                                                                                                                                      265 RLSSMLKK 272
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C; Keywords: 1sonrenc
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C;Genetics:
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Residues: 1-664 <MCD>
A;Cross-references: UNIPROT:Q9P7W7; UNIPARC:UPI00006B097; EMBL:AL136536; PIDN:CAB66447.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein AT4g39750 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accesson, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Status; preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9LDK6; UNIPARC:UP100000A9562; GB:NC_001268; NID:g7270959; PJ
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R;Bevan, M.; Monfort, A.; Casacuberta, B.; Puigdomenech, P.; Hoheisel, J.; Mewes, H.W.; N
submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T19P19.140 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
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A; Molecule type: DNA
A; Residues: 1-925 <BEV>
A; Residues: 1-925 <BEV>
A; Cross-references: UNIPROT: Q9LDK6; UNIPARC: UPI000017AFB3; EMBL: AL022605
A; Experimental source: cultivar Columbia; BAC clone T19P19
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Pred. No. 1.2e+02;
3; Mismatches 1; Indels
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55.6%; Pred. No. 1.2e+02;
iive 3; Mismatches 1;
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Pred. No. 51;
2; Mismatches
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55.6%;
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Best Local Similarity 66.7
Matches 6; Conservative
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A;Introns: 142/3; 193/1; 551/1
A;Note: T19P19.140
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Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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624 RLKNMVKKI 632
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A,Map position: 2
A,Introns: 43/3
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A; Residues: 1-912 <STO>
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C;Dete: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: A71277
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin rson, J.; Khalak, H.; Richardson, D.; Howell, J. X.; Chidambaram, M.; Utterback, T.; McDC they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
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A,Residues: 1-589 <COL>
A,Cross-references: UNIPROT:O83803; UNIPARC:UPI000013666B; GB:AE001253; GB:AE000520; NIT
                                                                                                                          para-hydroxybenzoate-polyprenyltransferase (EC 2.5.1.-) precursor, mitochondrial - fissi
C,Species: Schizosaccharomyces pombe
C,Date: 03-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                        A, Residues: 1-358 <PEA>
A, Residues: 1-358 <PEA>
A; Cross-references: UNIPROT:Q10252; UNIPARC:UP10000127EF6; EMBL:Z69728; PIDN:CAA93575.1;
A; Experimental source: strain 972h-; cosmid c56F8
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C;Accession: T50316
R;McDougall, R.C; Rajandream, M.A.; Barrell, B.G.; Cadieu, E.; Lelaure, V.; Galibert,
submitted to the EMBL Data Library, January 2000
A;Reference number: Z25061
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                                                                                                                                                                                                            C; Accession: T38914

R; Pearson, D; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, February 1996
A; Reference number: Z21817
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C;Superfamily: Bacillus arginine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.0%; Score 32; DB 77.8%; Pred. No. 28; tive 1; Mismatches
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Best Local Similarity 77.8'
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Best Local Similarity 60...
6, Conservative
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473 RISSLLKKV 481
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A;Gene: SPDB:SPAC56F8.04c
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Cincession: 156519
Ribodds, D.; Schlingen, A.K.; Lu, S.Y.; Perin, M.S.
J. Neurochem. 64, 2339-2344, 1995
A.; Hule. Boyd reticular calcium binding protein is purified on taipoxin columns.
A.; Reference number: 156519; MUID:95239201; PMID:7722520
A; Acession: 156519
A; Reference number: 156519; MUID:95239201; PMID:772550
A; Reference number: 156519; MUID:95239201; PMID:772550
A; Reference number: 156519; MUID:95239201; PMID:772550
A; Reference number: 156519; MUID:95239201; PMID:72550
A; Reference number: 156519; MUID:950401; repeat homology cEF1>
F; Reference number: 156519; MUID:950401; repeat homology cEF2>
F; 1877-219; Domain: calmodulin repeat homology cEF3>
F; 288-260; Domain: calmodulin repeat homology cEF5>
F; 264-296; Domain: calmodulin repeat homology cEF5>
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NiAlternate names: ERC-55 protein
Cippecies: Mus musculus (house mouse)
Cipacies: Mus musculus (house mouse)
Cipacies: Mus musculus (house mouse)
Cipacies: O7-Jul-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
Cipacession: JC5402
Rimai, T.; Matsuda, K.; Shimojima, T.; Hashimoto, T.; Masuhiro, Y.; Kitamoto, T.; Sugite Biochem. Biophys. Res. Commun. 213, 765-769, 1997
A; Title: ERC-55, a binding protein for the papilloma virus E6 oncoprotein, specifically in A; Reference number: JC5402; MUID:97312489; PMID:9168930
A; Reference number: JC5402
A; Reference number: JC5402
A; References: UNIPROT:070341; UNIPARC:UP10000177892
A; Residues: 1-319 <IMA>
A; Residues: 1-319 <IMA>
A; Residues: Lamad
C; Comment: This protein acts as a vitamin D receptor-specific cofactor modulating its fur C; Superfamily: reticulocalbin; calmodulin repeat homology <EFI>F; 53-55, Domain: calmodulin repeat homology <EFI>F; 1188-220/Domain: calmodulin repeat homology <EFI>F; 1188-220/Domain: calmodulin repeat homology <EFI>F; 229-261/Domain: calmodulin repeat homology <EFI>F; 229-261/Domain: calmodulin repeat homology <EFI>F; 255-297/Domain: calmodulin repeat homology <EFI>F; 265-297/Domain: calmodulin repeat homology <EFI>F; 265-297/Domain: calmodulin repeat homology <EFI
                                                                                                                                  taipoxin-associated calcium binding protein-49 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
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66 RLQSIIKKI 74
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                                                                                                                                                           hypothetical protein At2945740 [imported] - Arabidopsis thaliana
NyAlternate names: hypothetical protein F4118.28
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T02473; C84894
C;Accession: T02473; C84894
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaulsubmitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC F4118 genomic sequence.
A;Reference number: Z14674
A;Accession: T02473
A;Status: translated from GB/EMBL/DDBJ
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A; Residues: 1-239 <ROU>
A; Residues: 1-239 <ROU>
A; Cross-references: UNIPROT: O80845; UNIPARC: UPI000017AF99; EMBL: AC004665; NID: G3386593;
A; Experimental source: cultivar Columbia
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
B; Lin, X.; Kaul, S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Uniter 402, 761-768, 1999
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Atatus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-240 <MIL>
A;Cross-references: UNIPROT:O17203; UNIPARC:UPI000007F654; EMBL:AF025457; PIDN:AAB70970.
A;Experimental source: strain Bristol N2; clone C08B3
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A,MOLecule type: DNA
Residues: 1-239 «STO»
A,Cross-references: UNIPARC:UP1000017AF99; GB:AE002093; NID:g3386621; PIDN:AAC28551.1;
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A;Accession: C84894
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T32363
R;Miller, N.; Kramer, J.; Keppler, D.
submitted to the RMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid COBE3.
A;Reference number: Z21155
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2; Mismatches 1; Indels
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A;Map position: 2
A;Introns: 65/3; 90/3; 115/3; 142/3; 167/3
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                                                                                                                                                       March 11, 2006, 00:11:15; Search time 95.222 Seconds (without alignments) 66.684 Million cell updates/sec
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P32378
Q6Bwfs 7
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                      GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                              2166443 seqs, 705528306 residues
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KLK7 HÜWAN
QOSVPMS_ANOGA
Q7Q1V3_ANOGA
Q7Q1V3_ANOGA
Q9S2QB_STRCO
Q7P141_CRRVO
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Q5K028_ORYLA
Q8W607_9CAUD
Q7XS95_ORYSA
Q72M04_LEPIC
Q8EYH8_LEPIN
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1: uniprot_sprot:*
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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G The German CDNA Consortium;

A Kochrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,

A Kochrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,

B Cobo G., Han M., Wiemann S.;

I. Submitted (INOV-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; CR860999; CAH93099.1; -; mRNA.

GO; GO:0006233; F:peptidase activity; IEA.

R GO; GO:0006295; F:trypsin activity; IEA.

InterPro; IPR001254; Peptidase_31_S6.

InterPro; IPR001254; Peptidase_31_S6.

InterPro; IPR001254; Peptidase_31_S6.

R SMART; SM00020; Trypsin; 1.

R ROSITE; PS00135; TRYPSIN_DOM; 1.

R PROSITE; PS00135; TRYPSIN_DOM; 1.

R PROSITE; PS00135; TRYPSIN_DOM; 1.
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Kallikrein 7 precursor (BC 3.4.21.-) (hK7) (Stratum corneum chymotryptic enzyme) (hSCCE).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 140;
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SEQUENCE 140 AA; 15127 MW; 8DD6280252A39311 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein DKFZp459E0918.
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Pred. No. 1.7;
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                                     08RUQ1_MAIZE
08RUQ1_MAIZE
0931M3_ARATH
0931W83_ARATH
08BF39_MOUSE
0851X1_ORYSA
073E11_BACC1
08045_ARATH
0173E11_BACC1
080945_ARATH
051723_CAREL
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QSR567;
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   10 RLSSMVKKV 18
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MEDLINE=95314630; PubMed=7794273;
 TISSUB-Skin;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METARUBDER R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

DA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

DA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Schalska U., Smailus D.E.,

B. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. M. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                              TISSUB-Keratinocyte;
PubMed=10974542; DOI=10.1016/S0378-1119(00)00280-8;
Yousef G.M., Socilas A., Magklara A., Soosaipillai A.,
Diamandis E.P.;
"The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic enzyme is a new member of the human kallikrein gene family - genomic characterization, mapping, tissue expression and hormonal
                                                                                                           Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A.,
                                                                                                                                                                                   [2]
NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dong Y., Kaushal A., Brattsand M., Nicklin J., Clements J.A.; "Differential splicing of KLK5 and KLK7 in epithelial ovarian cancer produces novel variants with potential as cancer biomarkers.";
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NUCLEOTIDE SEQUENCE [GENOMIC DNA].
NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Malbrandt D., Backman A., Ny A., Edlund M., Edholm E., Tornell J.,
Wallbrandt P., Egelrud T.;
"Epidermal overexpression of stratum corneum chymotryptic enzyme in
mice; a model for chronic ithchy dermatitis.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [GENOMIC DNA].
PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
Moss P., Paeper B., Wang K.;
"Sequencing and expression analysis of the serine protease gene
cluster located in chromosome 19q13 region.";
Gene 257:119-130(2000).
                                                            NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF
                                                                                                                                     "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase."; J. Biol. Chem. 269:19420-19426(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[7]
CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clin. Cancer Res. 9:1710-1720(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Ovarian carcinoma;
MEDLINE=22623266; PubMed=12738725;
                                                                                         MEDLINE=94308225; PubMed=8034709;
                                                                                                                                                                                                                                                                                                                                          Gene 254:119-128(2000)
                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                               regulation."
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isold=P49862-2; Sequence=VSP_013581;
Isold=P49862-2; Sequence=VSP_013581;
TISSUE SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermis. Also expressed in the brain, mammary gland, cerebellum, spinal cord and kidney. Lower levels in salivary gland, cerebellum, spinal cord and kidney. Lower levels in salivary glands, uterus, thymus, thyroid, placenta, trachea and testis. Up-regulated in ovarian carcinoma, especially late-stage serous carcinoma, compared with normal ovaries and benign adenomas (at the protein level).
INDUCTION: By estrogens and glucocorticoids in a breast carcinoma
                                                           chymotryptic enzyme. For the control of the control of the continuous blookys. Res. Commun. 211:586-589(1995).

-i- FUNCTION: May catalyze the degradation of intercellular cohesive structures in the cornified layer of the skin in the continuous shedding of cells from the skin surface. Specific for amino acid residues with aromatic side chains in the Pl position. SCCE cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-Phe-|-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the activation of precursors to inflammatory cytokines.
Skytt A., Stroemgvist M., Egelrud T.; "Primary substrate specificity of recombinant human stratum corneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (By similarity).
(By similarity).
(By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                        also observed at the apical membrane and in cytoplasm at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Intertro; irro; irro; ..., ..., Pfam; PF00089; Trypein; 1.
PRINTS; PR0072; CHYMOTRYPSIN.
SWART; SM00020; Tryp SPc; 1.
SPROSITE; PS50240; TRYPESIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
Alternative splicing; Direct protean sequencing; Glycoprotein; Hvdrolase; Protease; Serine protease; Signal; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 5044138; -.
GO; 60008246; F:serine-type peptidase activity; TAS.
GO; GO:0008544; P:sepidermis development; TAS.
InterPro; IPR001254; Peptidase_S1_S6.
InterPro; IPR001314; Peptidase_S1Ã.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Activation peptide.
Kallikrein 7.
Peptidase SI.
Charge relay system (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=Long;
IsoId=P49862-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Contains 1 peptidase $1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, L33404, AAC37551.1; -; mRNA.
EMBL, AF16630, AAD497181; -; Genomic_DNA.
EMBL, AF23527; AAG33360.1; -; Genomic_DNA.
EMBL, AF332583; AAK69624.1; -; Genomic_DNA.
EMBL, AF411214, AAN033662.1; -; mRNA.
EMBL, AF411215; AAN03663.1; -; mRNA.
EMBL, EMBL, AA4132005.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENSG0000169035; Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H-InvDB; HIX0015373; -.
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HSSP; P00760; 1EZX.
MEROPS; S01.300; -
Ensembl; ENSG00001690
                                                                                                                                                                                                                                                                                                                                                                                                                                               invasive front
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MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a; Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S., Rabbinowitsch B., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                       Neoptera; Endopterygota; Diptera; Nematocera; Culicoldea; Culicidae;
Anophelinae; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
                                                                                                                                                                                                                                                                        The Anopholes gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
        Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.5%; Score 33; DB 2; Length 259; 66.7%; Pred. No. 1.1e+02; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 82.5%; Score 33; DB 2; Length 282; Similarity 87.5%; Pred. No. 1.2e+02; 7; Conservative 1; Mismatches 0; Indels
                                                                                                                                                 The Anopheles gambiae Sequence Committee, "Anopheles gambiae re-annotation.", Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 AA; 28975 MW; EFB47C010FDEF6A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282 AA; 30789 MW; BEECFE1743703A33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2004 (TrEMBLrel. 26, Last amnotation update)
Putative endo alpha-1,4 polygalactosaminidase.
OrderedLocusNames=SCO2178; ORFNames=SC5F7.23c;
                                                                                                                                                                                                                                                                                                                                                        EMBL, AAAB01008807; EAA04012.2; -; Genomic_DNA.
InterPro; IPR001611; LRR.
InterPro; IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 417.141-147 (2002).
EMBL; AL939111; CAB51262.1; -; Genomic_DNA.
PIR; T35294; T35294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00560; LRR 1; 5.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00369; LRR TYP; 5.
Leucine-rich repeat; Repat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9S2Q8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
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77 RVASMVKKI 85
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                                                                                        [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
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STRAIN=A3(2) / M145;
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 6; Conserv
                                                                   NCBI_TaxID=180454
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SEQUENCE 282 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hopwood D.A.;
                                                                                                                                                                                                                                                        STRAIN=PEST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Anopheles gambiae (African malaria mosquito).
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
      . .) (Potential)
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N-linked (GlcNac. ..) (Potenti
By similarity.
By similarity.
By similarity.
By similarity.
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Missing (in isoform 2).
Arral-vsp. 01381.
C -> W (in Ref. 6; AAH12005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-SIZE TO COUNTER, Yacurde, and L3-5;
MOTIAIS I., PONCON N., Simard F., Cohuet A., Fontenille D.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX334006; AAR01131.1; -; Genomic_DNA.
REMBL; AX334005; AAR01132.1; -; Genomic_DNA.
REMBL; AX334005; AAR01130.1; -; Genomic_DNA.
ROS GO:0005549; F:odcrant binding; IEA.
ROS GO:0005549; F:odcrant binding; IEA.
ROS GO:0004984; F:olfactory receptor activity; IEA.
ROS GO:0007608; P:odcrant binding; RA.
                                                                                                                                                                                                                                                    100.0%; Score 40; DB 1; Length 253; 100.0%; Pred. No. 2.9; ive 0; Mismatches 0; Indels
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Pred. No. 85;
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202 AA; 23639 MW; E4F6334A7FC8EEA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                 27525 MW;
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORFNames=ENSANGG0000008607;
Anopheles gambiae str. PEST.
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                                                                                                                                                                                                                                                                            Local Similarity 100.
1es 9; Conservative
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nes 7; Conservative
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                                                                                                                                                                                                               253 AA;
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                                                                                                                         STRAIN=ATCC 12472 / DSM 30191;
MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                             Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
Neisseriaceae, Chromobacterium.
                                                                                                                                                                                                                                                                                                                                                   82.5%; Score 33; DB 2; Length 297; 77.8%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                        297 AA; 32462 MW; FC0D2708DB087690 CRC64;
                                                                                                                                                                                                                                                                                              le and exploitable bacterial adaptability.";
:1. Acad. Sci. U.S.A. 100:11660-11665(2003).
                                                                Last sequence update)
Last annotation update)
                                             297 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   COQ2_YEAST STANDARD; PRT; 372 AA P3.275; Q6BLI3; 01-0CT-1993 (Rel. 27, Last sequence update)
                                                                                                                                                                                                                                                                                                          EMBL; AE016911; AAQS8051.1; -; Genomic_DNA.
InterPro; IPR002790; DUF88.
                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                         Probom; PD010896; DUF88; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 297 AA; 32462 MW: FC0D270RD
                                             PRT;
                                                         Created)
                                                        01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                 OrderedLocusNames=CV0373;
Chromobacterium violaceum.
                                             Q7P141 CHRVO PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01936; DUF88;
                265 RLSSMLKK 272
                                                                            Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                           1 RLSSMVKKV 9
                                                                                                                    NUCLEOTIDE SEQUENCE.
     1 RLSSMVKK 8
                                                                                                         NCBI_TaxID=536;
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WEDLINE=97313269; PubMed=9168073;

WEDLINE=97313269; PubMed=9168073;

WHIDDEED P., Kleine K., Poehlmann R., Duesterhoeft A., Hamberg K., Hegemann J.H., Obermaier B., Urrestarazu L.A., Aert R., Albermann K., Altmann R., Andre B., Baladron V., Ballesta J.P.G., Becam A.-M., Altmann R., Andre B., Baladron V., Ballesta J.P.G., Becam A.-M.;

Beinhauer J.D., Boskovic J., Buitrago M.J., Bussereau F., Coster F., Crouzet M., D'Angelo M., Dal Pero F., De Antoni A., del Rey F., Coster F., Dongion F., Domdey H., Dubois B., Fielder T.A., Fleig U., Floeth M., A Fritz C., Gaillardin C., Garcia-Cantalejo J.M., Glansdorff N., Gandoner U., Herbert C.J., Heumann K., Heuss-Neitzel D., A Hibbert H., Hinni K., Iraqui Houssaini I., Jacquet M., Jimenz A., Jimenz A., Johniau Y., Messenguy F., Mayes H.-W., Moestl L., Naurer C.T.C., Niedenthal R.K., Pandolfo D., Pierard A., Piravandi E., Planta R.J., Niedenthal R.K., Pandolfo D., Pierard A., Piravandi E., Planta R.J., A Niedenthal R.K., Pandolfo D., Pierard A., Piravandi E., Planta R.J., A Salz-Mira A., Urbanus V.H.M., Valle G., Van Dyck L., Verhasselt P., Wambutt R., Wedler H., Zollner A., Hani J.;

Wambutt R., Wedler H., Zollner A., Hani J.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=S288C;
Marsischky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher B.,
Hu Y., Vannberg F., Weger J., Kramer J., Moreira D., Kelley F.,
Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
10-MAY-2005 (Rel. 47, Last annotation update)
Para-hydroxybenzoate--polyprenyltransferase, mitochondrial precursor (RC 2.5.1.-) (PHB:polyprenyltransferase).
Mamme=COO2; OrderediocusMames=YNRO41C; ORFNames=N3419;
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Creation of the YFLEX clone resource: cloning of Saccharomyces cerevisiae ORFs in the Gateway recombinational cloning system."; Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: Catalyzes the prenylation of para-hydroxybenzoate with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE-22156158; PubMed=1740455; AmbbiNos-22156158; PubMed=1740455; Ashby M.N., Kutsunai S.Y., Ackerman S., Tzagoloff A., Edwards P.A.; "COQ2 is a candidate for the structural gene encoding para-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                          Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inner membrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IntAct; P32378; -.
GermOnline; 143386; -.
Ensembl; YNRO41C; Saccharomyces cerevisiae.
SGD; S000005324; COQ2.
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EMBL; Z71656; CAA65321.1; -; Genomic_DNA.
EMBL; AY6931097; AAT93116.1; -; Genomic_DNA.
PIR; S20056; S20056.
IntAct; P32378; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hydroxybenzoate:polyprenyltransferase.";
J. Biol. Chem. 267:4128-4136(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4932;
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                                                                                                 Complete proteome; Isoprene biosynthesis; Mitochondrion; Transferase;
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Culicidae,
Anophelinae, Anopheles.
NCBI_TaxID=7165,
                                                                                                                                                                                                           Allylic polyprenyl diphosphate-binding site (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLECTIDE SEQUENCE, FUNCTION, INDUCTION, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                      82.5%; Score 33; DB 1; Length 372; 77.8%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=14724626; DOI=10.1038/427212a; Hallem B.A., Fox A.N., Zwiebel L.J., Carlson J.R.; "Offaction: mosquito receptor for human-sweat odorant."; Nature 427:121-213 (2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anopheles genome sequencing consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                        -> T (in Ref. 3).
4D9738CE248B4AD6 CRC64;
                                                                                                                    Mitochondrion (Potential)
GO:0005743; C:mitochondrial inner membrane; TAS.
                                                                                                                               Para-hydroxybenzoate--
polyprenyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 98:14693-14697(2001).
       GO; GO:0005386; F:carrier activity; TAS.
GO; GO:0019840; F:isoprenoid binding; TAS.
GO; GO:0004659; F:prenyltransferase activity; IMP.
GO; GO:0006743; P:ubiquinone metabolism; IMP.
InterPro; IPR000537; UbiA_prenyltrans.
Pfam; PF01044; UbiA, J.
TIGREMMs; TIGR01474; ubiA_proteo; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=12364795; DOI=10.1126/science.1076196;
                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                         (Potential).
(Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anopheles gambiae (African malaria mosquito)
                                                                                                                                                                                                                                                                                                                                                                                 417 AA
                                                                                                                                                   (Potential).
                                                                                                                                                                                                  (Potential).
                                                                                                                                                                                                                                                                                         1; Mismatches
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IDENTIFICATION, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                Ser-rich
                                                                                                     Transit peptide; Transmembrane.
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(Rel. 43, Last seq
                                                                                                                                                                                                                                                   41001 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Odorant receptor Orl (AgOrl).
                                                                                      PROSITE; PS00943; UBIA; 17
                                                                                                                                                                                                                                                                             Local Similarity 77.8
                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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191
210
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                                                                                                                                                                                                                                                  372 AA;
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29-MAR-2004 (Re)
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13-SEP-2005
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FUNCTION,
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CONFLICT
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                                                                            solutine 230:170-178(2002).
-!- FUNCTION: Plays a critical role in the anthropophilic host-seeking behavior; establishes the host preference to transmit malaria. May participate in the phenomenon of decreased host-seeking behavior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
    Chrystal M.A.,
                                                                                                                                                         în disease vector mosquitoes after blood feeding.
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
TISSUB SPECIFICITY: Female-specific antennae and maxillary palp
                                                                                                                                                                                                                                                                                                                                                                                  DATABASE: NAME-Protein Spotlight; NOTE-Issue 44 of February 2004
WWW="http://www.expasy.org/spotlight/back_issues/sptlt044.shtml"
                                                                                                                                                                                                                                               INDUCTION: Strong response to the odorant 4-methylphenol, a component of human sweat, when expressed in odorant receptor deficient Drosophila. In vivo, decreased expression in antennae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LARITY: Belongs to the G-protein coupled receptor Dr-or
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QFRS8;

O5-UL-2004 (TrEMBLrel. 27, Created)
O5-UL-2004 (TrEMBLrel. 27, Last sequence update)
O5-UL-2004 (TrEMBLrel. 27, Last annotation update)
Similar to sp|P40215 Saccharomyces cerevisiae YMR145c NDH1.
OrderedLocusNames=CAGL0100748g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 1; Length 417;
Pred. No. 1.7e+02;
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6 (Potential).
Extracellular (Potential).
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Extracellular (Potential).
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Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential).
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Cytoplasmic (Potential).
4 (Potential).
Hill C.A., Fox A.N., Pitts R.J., Kent L.B., Tan P.L., Cravchik A., Collins F.H., Robertson H.M., Zwiebel L.G protein-coupled receptors in Anopheles gambiae.", Science 298:176-178(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.76
1; Mismatches
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77.8%;
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hes 7, Conservative
                                                                                                                                                                                                                                                                                                                after a blood meal
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318
339
417 AA;
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=S288c / AB972;

BOWNELNE-$7313268; PubMed=9169872;

BOWNEN S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
Rice P., Skelton J., Walsh S.V., Whitehead S., Barrell B.G.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Hypothetical 62.8 kDa protein in RP616A-TIF34 intergenic region.
OrderedLocusNames=YMR145C; ORFNames=YM9375.14C;
Saccharomyces cerevisiae (Baker's great).
Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes;
                 Eukaryotā; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.5%; Score 33; DB 2; Length 530; 77.8%; Pred. No. 2.1e+02; ative 1; Mismatches 1; Indels
Candida glabrata (Yeast) (Torulopsis glabrata).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  560 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [GENOMIC DNA].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 387:90-93(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RLSSMVKKV 9
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Best Local Similarity
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
"Creation of the YFLEX clone resource: cloning of Saccharomyces cerevisiae ORFs in the Gateway recombinational cloning system."; Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0003739; C:mitochondrion; IDA.
GO; GO:0003954; F:NADH debydrogenase activity; IDA.
GO; GO:0019655; P:ethanol fermentation; IMP.
GO; GO:0006116; P:NADH oxidation; IDA.
GO; GO:0006116; P:NADH oxidation; IDA.
FIREPEro; IPRO01137; FAD pyr_redox.
Pfan; PF00070; Pyr_redox!
Complete proteome; FAD; Flavoprotein; Hypothetical protein; NAD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.5%; Score 33; DB 1; Length 560; 77.8%; Pred. No. 2.2e+02; ive 1; Mismatches 1; Indels
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB182370; BAD24124-1; -; Genomic_DNA.
Hypothetical protein; Plaemid.
SEQUENCE 107 AA; 12021 MW; 1E128007B7367B5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome; FAD; Flavoprotein; Hypothetical prot
Oxidoreductase; Ubiquinone.
SEQUENCE 560 AA; 62774 MW; 10B1795E12E29C34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 AA.
                                                                                                                                                                                                                                                                                                                                                                                       IntAct; P40215; -.
Germonline; 142815; -.
Ensembl; YMR145C; Saccharomyces cerevisiae.
SGD; S000004753; NDE1.
                                                                                                                                                                                                                                                                                            EMBL, Z47071; CAA87359.1; -; Genomic DNA.
EMBL, AY692785; AAT92804.1; -; Genomic_DNA
PIR; S50401; S50401.
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906 CLOTE
QB9906_CLOTE PRELIMINARY;
QB9906;
01-JUN-2003 (TREMBLE). 24,
01-JUN-2004 (TREMBLE). 24,
01-MAR-2004 (TREMBLE). 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Query Match
Best Local Similarity 77.8%,
7; Conservative
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Q616B7;
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Matches 7; Conservative
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Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chromobacterium violaceum.
                                                                                                                                                                                                                                                                                                         Q7NVJS CHRVO PRELIMINARY;
Q7NVJS;
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Matches 7; Conservative
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184 RLSSMVEK 191
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247 LTSMVKKV 254
                                                                                                                                 1 RLSSMVKK 8
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YUFN_BACSU
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TRAINELSUS 4 / DSM 12343.

PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;

Rabus R., Ruepp A., Frickey T., Rattel T., Fartmann B., Gellner K.,

Rabus R., Ruepp A., Frickey T., Becker I., Amann J., Gellner K.,

Rabus R., Loubardot T., Becker I., Amann J., Gellner K.,

Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,

The genome of Desulforalea psychrophila, a sulfate-reducing bacterium from permanently cold Arctic sediments.";

The genome of Desulforalea psychrophila, a sulfate-reducing bacterium from permanently cold Arctic sediments.";

BML: CR522871; CAG37932.1; -; Genomic_DNA.

GO: GO:0016301; F:Kinase activity; IEA.

GO: GO:0016301; F:UDP-glucose-1-phosphate uridylyltransferase. ..; IEA.

GO: GO:0000508; P:Diosynthesis, IEA.

GO: GO:0000508; P:Diosynthesis, IEA.

InterPro; IPRO05771; Galu trans.

Ro; GO:0000608; NuP transferase.

Fam; PPO0483; NuP transferase.

Pfam; PPO0483; NuP transferase.

TIGRFAM9; TIGR01099; galu; 1.

TORPAM9; TIGR01099; galu; 1.

TORPAM9; TIGR01099; galu; 1.

TORPAM9; TIGR01099; galu; 1.
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EMBL, AEDIS936; AAO34903.1; -; Genomic DNA.

R GO; GO:0005806; F:iron ion binding; IEA.

R GO; GO:0006806; P:oxidoreductase activity; IEA.

R GO; GO:0006806; P:oxidoreductase activity; IEA.

R InterPro: IPR001989; Radical activat.

R InterPro: IPR001999; Radical activat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Anaerobic ribonucleoside-triphosphate reductase activating protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OrderedLocusNāmes=DPPB68;
Desulfotalea psychrophila.
Bacteria; Proteobacteria. Deltaproteobacteria; Desulfobacterales;
Desulfobulbaceae; Desulfotalea.
                                                                           Clostridium tetani.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.0%; Score 32; DB 2; Length 169
75.0%; Pred. No. 1.2e+02;
w.:mmatches 0; Indels
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PROSTIE; PS01087; RADICAL ACTIVATING; 1.
Complete proteome; Oxidoductae.
SEQUENCE 169 AA; 19292 MW; CC7AB2511D3844C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Probable UTP-glucose-1-phosphate uridylyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                      OrderedLocusNames=CTC00258;
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QGAIBS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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                                                                                                                                                       NCBI_TaxID=1513;
                                                                                                                                 Clostridium.
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OGAIBS DES
10 06A1BS DES
10 06A1B DE 25-0C
DT 25-0C
DT 25-0C
DT 25-0C
DE Proba
GN DESUL
ON DESUL
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RR NT [1] -
RR BADES
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R. Rebl., Arologue P. Panton. 
                                                                                                 Gaps
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STRAIN=ATCC 12472 / DSM 30191;
MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
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Neisseriaceae; Chromobacterium.
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Score 32; DB 2; Length 288; Pred. No. 2e+02;
                                                                                                 0; Indela
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SEQUENCE 330 AA; 35382 MW; 2AFAB050961AF87F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330 AA
                                                                                            1; Mismatches
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us-09-905-083a-32.rup

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                                                                                                                                                                                                                                                                                                                                                                                                     (Potential). SIMILARITY: Belongs to the BMP lipoprotein family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; 293937; CAB07936.1; -; Genomic_DNA.
EMBL; 299120; CAB15143.1; -; Genomic_DNA.
PIR; C70009; C70009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Subcilist; EG12349; YufN.
InterPro; IPR003760; Bmp.
InterPro; IPR000437; Prok_lipoprot_S.
Pfam; PP02608; Bmp; 1.
                                                                                                                                                                                                                                                                                                                                                                                     Nature 390:249-256(1997)
                                                                          NUCLEOTIDE SEQUENCE.
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RA XUNBEL NESS BU144013, PubMed-2914377; DOI-10.10138/36/86;

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Ra Bortise R., Bourster L., Brans A., Braun M., Brighell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A., Borizot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emmerson P.T., R. Britz C., Fujita M., Pujita Y., Puma S., Galizzi A., Galleron N., Britz C., Fujita M., Pujita Y., Puma S., Galizzi A., Galleron N., R. Fritz C., Fujita M., Pujita Y., Puma S., Galizzi A., Galleron N., A. Guiseppi G., Guy B.J., Hage K., Haiech J., Harwood C.R., Henaut A., Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., A. Landine S., Honor S., Hullo M.-F., Itaya M., Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Roenter E., Koningstein G., Kobayashi Y., Koetter P., Koningstein G., Kopayashi Y., Koetter P., Koningstein G., Kopayashi Y., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Rark S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S., Rescott A.M., Presecan E., Pujic P., Purnelle B., Roche B., Roche M., Sadaie Y., Sacor T., Scanlan B., Schleich S., Schroeter R., Roserott A., Servin S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Remaru K., Takemaru K., Takenchi M., Tamakoshi A., Tarakagi T., Takahashi H., Remaru K., Yata K., Yoshida K., Yamamoto H., Yamane K., Welmonco K., Yata K., Yoshida K., Yamamoto H., Yamane K., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein E., Wellikawa H.-P., Zumstein E., Harle C., Roch E., Welmonco K., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein E., Wellikawa H.-P., Zumstein E., Wellikawa H.-P., Tongton G. the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oudega B., Koningstein G., Rodrigues L., de Sales Ramon M.,
Hilbert H., Duesterhoeft A., Pohl T.M., Weitzenegger T.;
"Analysis of the Bacillus subtilis genome: cloning and nucleotide
sequence of a 62 kb region between 275 degrees (rrnB) and 284 degrees
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ire 390:249-256(1997).
SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                  Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Hypothetical lipoprotein yuln precursor.
Names-yuln, OrderedLocusNames-BSU31540,
Bacillus subtilis.
    350 AA.
    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97419515; PubMed=9274030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Microbiology 143:2769-2774(1997).
    STANDARD;
    BACSU
YUFN BA
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                                                                      Hypothetical lipoprotein yufn.
N-palmitoyl cysteine (Probable).
S-diacyldlycerol cysteine (Probable)
16D5176A52A99284 CRC64;
PROSITE, PS00013; PROKAR LIPOPROTEIN; FALSE NEG.
Complete proteome; Hypothetical protein; Lipoprotein; Membrane;
Palmitate; Signal.
                                                                                                                                                                                                            ;
0
                                                                                                                                                                     80.0%; Score 32; DB 1; Length 350;
87.5%; Pred. No. 2.4e+02;
iive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                          Search completed: March 11, 2006, 00:38:38 Job time : 100.333 secs
                                                                                                                                 350 AA; 37349 MW;
                                                                                                                                                                                        Best Local Similarity 87.5
Matches 7; Conservative
                                                         13
350
14
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269 LTSMVKKV 276
                                                                                                                                                                                                                                                 2 LSSMVKKV 9
                                                                                                                                   SEQUENCE
                                                                                                                                                                         Query Match
                                                            SIGNAL
                                                                                                LIPID
                                                                            CHAIN
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Sequence 2, Appli Sequence 4, Appli Sequence 5333, A Sequence 7990, Ap Sequence 18044, A Sequence 3154, Ap Sequence 4867, Ap Sequence 4737, Ap Sequence 5154, Ap Sequence 5156, Ap Sequence 5156, Ap Sequence 5166, Ap Sequence 2462, Ap Sequence 2462, Ap Sequence 2462, Ap Sequence 2462, Ap

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Sequence 32, Application US/09502600A
Patent No. 629434
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
COMPOSITION:
TITLE OF INVENTION:
TITLE OF INVENTION WIMBER:
TITLE OF THE OF SEQ ID NOS:
TITLE OF SEQ ID NOS:
TITLE OF INVENTION:
TITLE OF THE OF SEQ ID NOS:
TI
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US-09-918-243-32
i Sequence 3.2 Application US/09918243
j Patent No. 667403
j Patent No. 667403
j GENERAL INFORMATION:
j APPLICANT: Comnon, Martin J.
j APPLICANT: Santin, Alessandro
j TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
fILE REFERENCE: D6232CIP/C/D/CIP
j CURRENT APPLICATION NUMBER: US
j CURRENT FILING DATE: 2001-07-30
j PRIOR APPLICATION NUMBER: US
j PRIOR APPLICATION NUMBER: US
j PRIOR PILING DATE: 2001-07-13
j NUMBER OF SEQ ID NOS: 136
j SEQ ID NO 32
LENGTH: 9
j TYPE: PRT
j ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Residues 123-131 of the SCCE protein
US-08-261-086-4
US-08-261-086-4
US-08-261-086-6
US-09-248-796A-23383
US-09-328-352-7990
US-09-583-110-3154
US-09-107-433-4867
US-09-107-532A-4737
US-09-107-532A-6154
US-09-107-532A-6154
US-09-1134-000C-5465
US-09-1134-000C-5465
US-09-9113-000C-5465
US-09-9113-000C-5465
US-09-9113-000C-5465
US-09-9113-000C-5465
US-09-9113-000C-5465
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US-09-9113-000C-5465
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100.0%; Pred. No. 4.6e+05;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RLSSMVKKV 9
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  US-09-502-600-32
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Sequence 15, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                            March 11, 2006, 00:41:16; Search time 21.2222 Seconds (without alignments) 35.061 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                             GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued Patents AA:*

(cgn2_6/ptodata/1/iaa/5_COMB.pep:*

(cgn2_6/ptodata/1/iaa/H_COMB.pep:*

(cgn2_6/ptodata/1/iaa/H_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PGTUS.COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE.COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE.COMB.pep:*
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US-09-618-259-4

US-09-261-416-7

US-09-261-416-7

US-09-261-418-33

US-09-91-44-483-33

US-09-154-483-33

US-09-154-483-33

US-09-154-344-12

US-09-544-600-4

US-09-544-600-4

US-09-544-600-4

US-09-164-34-2

US-09-164-34-2

US-09-164-34-2

US-09-164-34-2

US-09-18-24-110

US-09-918-243-110

US-09-918-243-110

US-09-918-243-110

US-09-918-243-179

US-09-918-243-179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  572060 segs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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Score

Result No.

Database :

Sequence:

Run on:

Searched:

222222222222222224322243224432224442224423244232442324423443244324432443

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Gaps

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Length 9; Indels

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69 RLSSMVKKV 77
                       1 RLSSMVKKV 9
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Sequence 7, Application US/09261416A

Betant No. 6291663

GENERAL INFORMATION:
APPLICANT: O'BETION, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease
TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
FILE REFERENT = 16192
CURRENT APPLICATION NUMBER: US/09/261,416A

CURRENT FILING DATE: 1999-03-03

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 7

LENGTH: 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic OTHER INFORMATION: enzyme (scce) catalytic domain
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09618259
Patent No. 6642013
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Underwood, Lowell J.
APPLICANT: Underwood, Lowell J.
APPLICANT: Underwood, Lowell J.
APPLICANTION: No. 6642013el Extracellular Serine Protease
FILE REFERENCE: D602CIP2 CURRENT APPLICATION NUMBER: US/09/618,259
CURRENT FILING DATE: 1209-09-18
PRIOR APPLICATION NUMBER: US 09/127,444
PRIOR FILING DATE: 1999-08-21
NUMBER OF SEQ ID NOS: 72
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                                                                                                                   Query Match 100.0%; Score 40; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 9; Conservative 0; Mismatches 0; Indels
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 123-131 of the SCCE protein
US-09-918-243-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 RLSSMVKKV 68
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LENGTH: 144
TYPE: PRT
ORGANISM: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: DOMAIN
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US-09-618-259-4
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APPLICANT: COLPITY, MAURICE
APPLICANT: COLPITY, TRACEY L.
APPLICANT: RILEBMAN, PAULA N.
APPLICANT: RILEBMAN, PAULA N.
APPLICANT: RILASS, MICHAEL R.
APPLICANT: RUSSLIL, JOHN C.
APPLICANT: STROUPE, STEVEN D.
APPLICANT: STROUPE, STROUPE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                               APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease
TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
FILE REFERENCE: D6192
CURRENT APPLICATION NUMBER: US/09/261,416A
CURRENT FILLING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 8
LENGTH: 161
TYPE: PRT
ORRANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Serine protease catalytic domain of hepsin (Heps) OTHER INFORMATION: homologous to similar domain in TADG-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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OPERATING SYSTEM: DOS
CUPTURER: PastsED for Windows Version 2.0
SUGNEMY APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
RESULT 5
US-09-261-416-8
; Sequence 8, Application US/09261416A
; Patent No. 6291663
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Best Local Similarity 100.
Matches 9; Conservative
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CLASSIFTCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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0; Mismatches
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NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
                                                                                                                             Sequence 4, Application US/09027337B
Patent No. 5972616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
    95 RLSSMVKKV 103
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                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-09-154-344-12
                                                                                            RESULT 8
US-09-027-337-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/08557146
Patent No. 5834290
GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Brayme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 40; DB 1; Length 225; 100.0%; Pred. No. 1.7; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATION PATA:
APPLICATION NUMBER: US/08/557,146
FILLING DATE: 14-DEC-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION UNBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
NAME: BECKET, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEPHONE: 847/938-2623
                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6232456e
US-08-944-483-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: polypeptide
US-08-557-146-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 225 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 RLSSMVKKV 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RLSSMVKKV 9
                                                                                                                                                                                                                                                                                    linear
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US-08-557-146-12
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1 RLSSMVKKV 9

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GENERAL INFORMATION:
APPLICANT: O'BRIEA, Timothy J.
APPLICANT: Tanimoto, Hirotosh.
APPLICANT: Tanimoto, Hirotosh.
APPLICANT: Tanimoto, Hirotosh.
TITLE OF INVENTION: PAGG-15: An Extracellular Serine Protease Overexpressed in TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REFERENCE: D6064
CURRENT APPLICATION NUMBER: US/09/027,337B
CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 4
LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to OTHER INFORMATION: similar domain in TADG-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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| Sequence 12, Application US/09154344
| Patent No. 5981256
| GENERAL INFORMATION
| APPLICANT: Egelrud, Torbjorn
| APPLICANT: Hansson, Lennart
| TITLE OF INVENTION: Enzyme (SCCE)
| NUMBER OF SEQUENCES: 17
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: White & Case, Patent Department
| STREET: 1155 Avenue of the Americas
| CITY: New York | STREET: New York | STREET: New York | STREET: STREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 12:
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; OTHER INFORMATION: SCCE US-09-654-600A-4
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| Sequence 4, Application US/09654600A
| Patent No. 6649741
| GENERAL INFORMATION:
| APPLICANT: O'Brien, Timothy J. APPLICANT: Tanimoco, Hirotoshi TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease; TITLE OF INVENTION: Overexpressed in Carcinomas; TITLE OF INVENTION: Overexpressed in Carcinomas; TITLE OF INVENTION NUMBER: US/09/654,600A; CURRENT APPLICATION NUMBER: US/09/654,600A; PRIOR PILING DATE: 1999-10-20
| PRIOR FILING DATE: 1999-10-20
| NUMBER OF SEQ ID NOS: 98
| SEQ ID NO 4.
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                                                                                                             100.0%; Score 40; DB 1; Length 225; 100.0%; Pred. No. 1.7; tive 0; Mismatches 0; Indels
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                            TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
US-09-154-344-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.vv
Pronective
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acids
                                                                                                   Query Match
Best Local Similarity 100.0
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US-09-644-600-4
                                                                                                                                                                                         95 RLSSMVKKV 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                       1 RLSSMVKKV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-654-600A-4
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US-09-644-600-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hanseon, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Brayme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 40; DB 1; Length 253; Best Local Similarity 100.0%; Pred. No. 1.9; Matches 9; Conservative 0; Mismatches 0; Indels
DB 2; Length 225; 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: ITEM: FLORY TIED:
COMPUTER: IEM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 1-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: White & Case, Patent Department STREET: 1155 Avenue of the Americas CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10036-2787

ZIP: 10036-2787

MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Incyte Pharmaceuticals, Inc.
  100.0%; Score 40; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-00-824-874-3
Sequence 3, Application US/08824874
Patent No. 5962300
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Freeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         Sequence 2, Application US/08557146
Patent No. 5834290
                                                .
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TELEFAX: (212) 854-8113
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYEE: amino acids
  Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-557-146-2
                                                                                                                                      95 RLSSMVKKV 103
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterrer, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103:
TELECHONE: (212) 819-8783
TELEPHONE: (212) 819-8783
TELERAX: (212) 819-8783
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08930188
Patent No. 6093397
                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1: 253 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-09-154-344-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 RLSSMVKKV 131
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-08-930-188-2
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Sequence 2, Application US/09154344

Patent No. 5981256

GENERAL INFORMATION:
APPLICANT: Bellrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Browne (SCCE)
NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 40; DB 1; Length 253; 100.0%; Pred. No. 1.9;
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CITY: New York
STRTE: 1155 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER: ENDADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PREADABLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: PREADABLE FORM:
MEDIUM TYPE: PLOPS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION TO THE PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-6555
TELEPA: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
LYPE: amino acids
TYPE: amino ac
: 3174 Porter Drive
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
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                                                                                                             USA
                                                                                                                                               ZIP: 94304
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GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Dixon, Eric P.
APPLICANT: Little, Sheilar P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPENDENCE ADDRESS:
ADDRESSEE: Elilily and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STREET: Lilly Corporate Center
CONDUTRY: United States of America
COUNTRY: United States of America
CONDUTER: LILLY COMPALIBLE FORM:
MEDIUM TYPE: FLODEY Misk
COMPUTER: BADABLE FORM:
MEDIUM TYPE: FLODEY MISSE
COMPUTER: DATE: US/08/930,188
FILING DATE: US/08/930,188
FILING DATE: US-ARPE: 195
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION NUMBER: US/08/930,188
TELEPHONE: BIALOCK, DORNA
REGISTRATION NUMBER: 38,082
ATTORNEY/AGENT INFORMATION:
TELEPHONE: 317-277-1090
TELEPHONE: 317-277-1090
TELEPHONE: 117-277-1090
TELEPHONE: SOURCET NUMBER: SEQUENCE CHARACTERICES:
FRUNCHISC CHARACTERICTICS:
FRUNCHISC CHARACTERICTICS:
FRUNCHISC CHARACTERICTICS:
FRUNCHISC CHARACTERICTICS:
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100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels
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1103326-181
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0; Gaps

0; Indels

Matches 9; Conservative 0; Mismatches 1 RLSSMVKKV 9 ||||||||| 123 RLSSMVKKV 131 රු සි

Search completed: March 11, 2006, 01:24:24 Job time: 22.2222 secs

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1 RLSSMVKKV
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US-09-905-083-32
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Sequence 13, Appl
Sequence 4, Appli
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Sequence 104, Appl
Sequence 104, Appli
Sequence 4, Appli
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48, Appl
639, App
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92, Appl
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98, Appl
3, Appli
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48, Appl
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38, Appl
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                                                   March 11, 2006, 01:24:47; Search time 69.444 Seconds (without alignments) 54.151 Million cell updates/sec
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: /cgn2 6/ptodata/1/pubpaA/USG07_PUBCOMB.pep:*
2: /cgn2 6/ptodata/1/pubpaA/USG08_PUBCOMB.pep:*
3: /cgn2 6/ptodata/1/pubpaA/USG08_PUBCOMB.pep:*
//cgn2 6/ptodata/1/pubpaA/USGA_PUBCOMB.pep:*
5: /cgn2 6/ptodata/1/pubpaA/USGB_PUBCOMB.pep:*
6: /cgn2 6/ptodata/1/pubpaA/USGB_PUBCOMB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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-10-643-795A-95
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US-09-905-083-110
                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -10-948-518-95
-10-868-490A-1
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Maximum Match 100%
Listing first 45 summaries
                                     OM protein - protein search, using sw model
                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                      US-09-905-083A-32
40
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                                            1 RLSSMVKKV 9
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Perfect score:
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Sequence 4, Appli
Sequence 1, Appli
Sequence 1611, A
Sequence 61611, A
Sequence 49273, A
Sequence 53862, A
Sequence 53750, A
Sequence 63676, A
Sequence 750, A
Sequence 750, A
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Sequence 32, Application US/09905083

Patent No. US2002014670841

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer TITLE OF INVENTION: Ovarian Cancer TITLE OF INVENTION: Ovarian Cancer CURRENT APPLICATION NUMBER: US/09/905,083

CURRENT APPLICATION NUMBER: US 09/502,600

PRIOR PAPLICATION NUMBER: US 09/502,600

PRIOR PLING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 32

LENGTH: 9

TYPE: PRT
                                                                                                                                                                                                                                                                                                        US-09-918-243-32
US-09-918-243-32

IS-09-918-243-32

Sequence 32, Application US/09918243

Patent No. US20020142317A1

GENERAL INPORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: Santin, Alessandro

TITLE OF INVENTION: Methods

TITLE DOE INVENTION: Methods

CURRENT FILING DATE: 2001-07-30

PRIOR PLICATION NUMBER: US/09/918,243

CURRENT FILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-30

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 32

LENGTH: 9
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100.0%; Score 40; DB 3; Length
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CHAIN
OTHER INFORMATION: Residues 123-131 of the SCCE protein
                                                              US-10-056-405-4
US-10-056-778-1
US-10-425-114-49273
US-10-425-114-49273
US-10-425-114-43367
US-10-425-114-53750
US-10-425-114-53750
US-10-282-122A-76609
US-09-918-243-79
US-09-918-243-79
US-09-905-003-79
                          US-10-424-599-244024
US-10-437-963-155539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 137, Application US/10831075
Fublication No. US20040224891A1
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Methods for the early diagnosis of ovarian cancer;
TITLE OF INVENTION NUMBER: US/10/613
CURRENT APPLICATION NUMBER: US/10/831,075
CURRENT PILING DATE: 2004-04-23
FRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 140
SEQ ID NO 137
LENGTH: 30
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                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 40; DB 5; Length 30; Best Local Similarity 100.0%; Pred. No. 0.4; Matches 9; Conservative 0; Mismatches 0; Indels
                        Indels
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CTHER INFORMATION: Residues 110-139 of the SCCE protein

US-10-831-075-137
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Sequence 4, Application US/09796294

Sequence 4, Application US/09796294

Sequence 4, Application US/09796294

Sequence 4, Application US/09796294

GENERAL INFORMATION: US-01

APPLICANT: Underwood, Lowell J.

TITLE OF INVENTION: Extracellular Serine Protease

FILE REPERBRICE: D6020CIP3

CURRENT APPLICATION NUMBER: US/09/796,294

CURRENT PILING DATE: 2001-02-28

PRIOR FILING DATE: 2000-07-18

SEQ ID NO 4

SEQ ID NO 4

TYPE: PRT

TYPE: PRT

CORANISM: unknown
100.0%; Fred. No. 1.7e+06; tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 9; Conserv
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NAME/KEY: DOMAIN
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Sequence 32, Application US/10831075

Sequence 32, Application No. US20040224891A1

Sequence 32, Application No. US20040224891A1

SEQUENCE OF SET TIME No. US20040224891A1

APPLICANT: Cannon, Martin J.

APPLICANT: Cannon, Martin J.

APPLICANT: Santin, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

TILE REFERENCE: DS232CIP/C/D/CIP3

CURRENT APPLICATION NUMBER: US/10/831,075

CURRENT FILING DATE: 2004-04-23

PRIOR FILING DATE: 2003-02-21

NUMBER OF SEQ ID NOS: 140
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APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Jacabandro.
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer FILE REFERENCE: D6223CIP/C/D/CIP2
CURRENT APPLICATION NUMBER: US,10/372,521
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/918,243
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 32
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                                                                                                                                       Query Match 100.0%; Score 40; DB 3; Length 9; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 9; Conservative 0; Mismatches 0; Indels
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                           NAME/KEY: CHAIN
COTHER INFORMATION: Residues 123-131 of the SCCE protein US-09-905-083-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CHAIN
OTHER INFORMATION: Residues 123-131 of the SCCE protein
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; OTHER INFORMATION: Residues 123-131 of the SCCE protein
US-10-831-075-32
                                                                                                                                                                                                                                                                                                                                                                                                       , Sequence 32, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-372-521-32
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LENGTH: 9
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Gaps
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IITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 40; DB 3; Length 224; 100.0%; Pred. No. 3.3; tive 0; Mismatches 0; Indels
                                                                          6183.US.01
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; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-789-210-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REPERENCE/DOCKET NUMBER: 6183
TELECOMMUNICATION INFORMATION:
TELEPONE: 847/938-1623
TELERA: 847/938-2623
TELERA: CURLOWN:
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
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PRIOR PAPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR APPLICATION NUMBER: 60/373,917
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2001-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 104, Application US/10262511
Publication No. US20040038223A1
BENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Railet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Rewan, John A.
APPLICANT: Rekuda, Ramesh
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PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
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Li, Li
Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
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Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
Shimkets, Richard A.
Rothenberg, Mark E.
Leach, Martin D.
Agee, Michele L.
                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Ort, Tatiana
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Zerhusen, Bryan D.
Anderson, David W.
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Miller, Charles E.
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                             Sequence A Application US/10461787

Sequence No. US20030199010A1

Sequence No. US20030199010A1

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: Underwood, Lowell J.

FILE OF INVENTION: No. US20030199010A1e1 Extracellular Serine Protease

FILE REFERENCE: D6020CIP2

CURRENT APPLICATION NUMBER: US/10/461,787

CURRENT FILING DATE: 2003-06-13

PRIOR APPLICATION NUMBER: US/09/618,259

PRIOR APPLICATION NUMBER: US/09/618,259

PRIOR FILING DATE: 2000-07-18

NUMBER OF SEQ ID NOS: 72

SEQ ID NO 4

LENGTH: 144
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| Publication No. US20040241646A1
| GENERAL INFORMATION:
| APPLICANT: COHEN, MAURICE
| COLPITTS, TRACEY L. FRIEDMAN, PAULA N. GRANADOS, EDWARD N. KLASS, MICHAEL R. RUSSELL, JOHN C. STEWART, KENT D. STEWART, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTENCE for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/789,210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: 11
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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Matches 9; Conservative
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ORGANISM: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: DOMAIN
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US-09-789-210-33
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FILE REPERENCE: 21402-462C

CURRENT APPLICATION: NOWEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERENCE: 21402-462C

CURRENT FILING DATE: 2003-05-28

PRIOR FILING DATE: 2001-10-02

PRIOR FILING DATE: 2001-10-03

PRIOR FILING DATE: 2001-10-09

PRIOR FILING DATE: 2002-05-16

PRIOR PLICATION NUMBER: 60/381, 68

PRIOR FILING DATE: 2002-04-17

PRIOR PLICATION NUMBER: 60/373, 260

PRIOR PLICATION NUMBER: 60/373, 435

PRIOR FILING DATE: 2002-04-17

PRIOR PLICATION NUMBER: 60/373, 626

PRIOR PLICATION NUMBER: 60/373, 636

PRIOR PLICATION NUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Berghs, Constance TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
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US-10-262-511-92
, Sequence 92, Application US/10262511
; Publication No. US20040038223A1
, GENERAL INFORMATION:
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
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Shimkete, Richard A.
Rothenberg, Mark E.
Leach, Martin D.
Agee, Michele L.
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Catterton, Elina
Ji, Weizhen
Miller, Charles E.
Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
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Anderson, David W.
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Best Local Similarity 100.
Matches 9; Conservative
                            Ju, Jingfang
Li, Li
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Gorman, Linda
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CORGANISM: Homo sapiens
US-10-262-511-102
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PRIOR FILING DATE: 2002-10-09

PRIOR APPLICATION NUMBER: 60/381,038

PRIOR FILING DATE: 2002-05-16

PRIOR FILING DATE: 2002-05-16

PRIOR FILING DATE: 2001-10-09

PRIOR FILING DATE: 2002-04-17

PRIOR FILING DATE: 2002-04-17

PRIOR FILING DATE: 2002-04-19

PRIOR FILING DATE: 2002-04-19

PRIOR FILING DATE: 2002-04-19

PRIOR FILING DATE: 2002-04-19

NUMBER: 60/373,826

PRIOR FILING DATE: 2001-10-05

NUMBER: 05 SEQ ID NOS: 439

SOFTWARE: CuraSeqList version 0.1

SEQ ID NO 104

LENGTH: 224
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| Bublication No. US20040086910A1
| GENERAL INFORMATION:
| APPLICANT: O'Brien, Timothy J. |
| APPLICANT: Tanimoto, Hirotoshi |
| TILLE OF INVENTION: TADG-15: An Extracellular Serine Protease |
| TILLE OF INVENTION: Overexpressed in Carcinomas |
| FILE REFERENCE: 10604-118/D |
| CURRENT APPLICATION NUMBER: US/10/600,187 |
| CURRENT APPLICATION NUMBER: US/09/654,600A |
| PRIOR APPLICATION NUMBER: US/09/654,600A |
| PRIOR APPLICATION NUMBER: 09/421,213 |
| PRIOR PRIING DATE: 1999-10-20 |
| PRIOR PRIING DATE: 1999-10-20 |
| NUMBER OF SEQ ID NOS: 98 |
| SEO ID NO 4
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100.0%; Score 40; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels
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Sequence 102, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
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Best Local Similarity 100.
Matches 9; Conservative
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95 RLSSMVKKV 103
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CORGANISM: Homo sapiens
US-10-262-511-104
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ORGANISM: Homo sapiens
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Patturajan, Meera
Spytek, Kimberly A.
Bdinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
Ort, Tatiana
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Zerhusen, Bryan D.
Anderson, David W.
Zhong, Mei
Catterton, Elina
                                                                                         APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
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ORGANISM: Homo sapiens
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APPLICANT: Shimkets, Richaed A.
APPLICANT: Beach, Mark E.
APPLICANT: Beach, Mark E.
APPLICANT: Beach, Markin D.
APPLICANT: Beach, Markin D.
APPLICANT: Beach, Machele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOWEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERBNCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2002-05-17
PRIOR PLING DATE: 2002-05-17
PRIOR PLING DATE: 2002-05-17
PRIOR PLING DATE: 2002-06-17
PRIOR PLING DATE: 2002-04-17
PRIOR PLING DATE: 2001-00-05
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                                                                                                                                                                                                                      Patturajan, Meera
Spytek, Kimberly A.
Bdinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
Ort, Tatiana
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Catterton, Elina
Ji, Weizhen
Miller, Charles E.
Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
Smithson, Glennda
Millet, Isabelle
Peyman, John A.
Kekuda, Ramesh
Ju, Jingfang
Li, Li
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Zerhusen, Bryan D.
Anderson, David W.
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Best Local Similarity 100.
Matches 9; Conservative
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; IENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-92
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1 RLSSMVKKV 9 |||||||| 120 RLSSMVKKV 128

RESULT 13 US-10-262-511-94

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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILING DATE: 16.Jan.2001
CLASSIFICATION SATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY DATE: 09/210,084
FILING DATE: cUnknown ATTORNEY/GANT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
VESOLI 18-615-98

Sequence 98, Application US/0988615
Sequence 98, Application US/0988615
Sequence 98, Application US/0988615
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GENA
APPLICANT: SUDANSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REPERBUCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT PILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PARENTING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PARENTING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
LENGTH: 253
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Patent No. US20020068341A1
GENERAL INFORMATION:
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Sequence 14, Appl
Sequence 17, Appl
Sequence 29743, A
Sequence 29742, A
Sequence 32412, A
Sequence 32411, A
Sequence 32410, A
Sequence 11, Appl
Sequence 11, Appl
Sequence 21, Appl
Sequence 24167, A
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Sequence 24166, A
Sequence 2520, Ap
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                                                                                                                                       March 11, 2006, 01:27:17 ; Search time 8 Seconds
    (without alignments)
    31.314 Million cell updates/sec
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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
GenCore version 5.1.7
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15-11-098-686-10100
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Listing first 45 summaries
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Sequence 4, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 4958, Ap
Sequence 330, Appl
Sequence 29, Appl
Sequence 1985, Ap
Sequence 11516, A
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Sequence 11, Application US/10412748
Sequence 11, Application US/10412748
Publication No. US20060035219A1
GENERAL INFORMATION:
APPLICANT: Queensland University of Technology
APPLICANT: Clements, Judith A
TITLE OF INVENTION: Aberrant Kallikrein Expression
FILE OF INVENTION: Aberrant Kallikrein Expression
FILE OF INVENTION WUMBER: US/10/412,748
CURRENT APPLICATION WUMBER: US/10/412,748
FRIOR FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
SEQ ID NOS: 41
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US-10-412-748-19
Sequence 19, Application US/10412748
Sequence 19, Application US/10412748
Publication No. US20060035219A1
GENERAL INFORMATION:
APPLICANT: Queensland University of Technology
TITLE OF INVENTION: Aberrant Kallikrein Expression
FILE REFERENCE: DAVIT/2.003AUS
CURRENT APPLICATION NUMBER: US/10/412,748
CURRENT FILING DATE: 2003-04-09
PRIOR PELICATION NUMBER: US/10/412,748
SOFTWARE: PAPELICATION NUMBER: US/10/412,748
SOFTWARE: PAPELICATION NUMBER: US/10/412,748
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TENGTH: 181
TENGTH: 181
TYPE: RT
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US-11-192-219-2
US-11-087-099-4958
US-11-087-099-330
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US-11-102-240-106
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US-11-096-568A-30776
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  51 RLSSMVKKV 59
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                                                           100.0%; Score 40; DB 6; Length 253; 100.0%; Pred. No. 0.24; cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                         Sequence 14, Application US/10412748

publication No. US20060035219A1

GENERAL INFORMATION:
APPLICANT: Queensland University of Technology
APPLICANT: Clements, Judith A
TITLE OF INVENTION: Aberrant Kallikrein Expression
FILE REFERENCE: DAVI72.003AUS
CURRENT APPLICATION NUMBER: US/10/412,748

CURRENT APPLICATION NUMBER: US/10/412,748

PRIOR APPLICATION NUMBER: 3002-04-09

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn version 3.2

LENGTH: 253
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US-10-412-748-17
Sequence 17, Application US/10412748
Sequence 17, Application US/10412748
Publication No. US20060035219A1
GENERAL INFORMATION:
APPLICANT: Clementand University of Technology
APPLICANT: Clements, Undith A
ITILE OF INVENTION: Aberrant Kallikrein Expression
FILE REFERENCE: DAVIAT2.003A08
CURRENT APPLICATION NUMBER: US/10/412,748
CURRENT FILING DATE: 2003-04-09
PRIOR PILING DATE: 2003-04-09
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.2
LENGTH: EAST
                                                                               Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                   123 RLSSMVKKV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 RLSSMVKKV 131
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ORGANISM: Human
; ORGANISM: Human
US-10-412-748-11
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                                                                Query Match
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RESULT 5

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Sequence 29743, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REPERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 29443
LENGTH: 220
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; Publication No. US20060048240A1
; GENERAL INFORMATION:
APPLICANT: ALEXANDEROY, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I
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LOCATION: (1)..(220)

CTHEN INFORMATION: Ceres Seq. ID no. 4927738

US-11-096-5588-29743
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OS-11-03-1243-98, Application US/11037243
FUDDICATION NO. US20050287546A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: PLOWMAN, GREGORY
APPLICANT: CARENEEEL, SEAN
APPLICANT: CARENEEEL, SEAN
APPLICANT: CHARVOCZAK, GLEN
APPLICANT: GUDARSANAM, SUCHA
ITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/10/9/888,615
PRIOR APPLICATION NUMBER: US/09/888,615
PRIOR PILING DATE: 2001-06-26
PRIOR PILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 98
LENGTH: 253
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RLSSMVKKV 9
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US-11-096-568A-29743
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Sequence 32410, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Thecby
TITLE OF INVENTION: Thecby
TITLE OF INVENTION: Thecby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 32410
LENGTH: 390
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| Sequence 13, Application US/11208308
| Publication NO. US20660041952A1
| GENERAL INFORMATION: US20660041952A1
| TITLE OF INVENTION: P450 Polymuclectides, Polypeptides, and TITLE OF INVENTION: USES Thereof
| FILE REPERBUCE: 18207-0066001
| CURRENT APPLICATION NUMBER: US/11/208,308
| CURRENT FILING DATE: 2005-08-19
| PRIOR PILING DATE: 2004-08-20
| NUMBER OF SEC ID NOS: 35
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEC ID NO 13
| LENGTH: 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.0%; Score 30; DB 7; Length 390; 85.7%; Pred. No. 52; 1: Mismatches 0; Indels
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                                                                                                7; Length 385;
                                                                                                                                            0; Indels
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NAME/KEY: misc feature

LOCATION: (1).7(390)

OTHER INFORMATION: Ceres Seq. ID no. 13592962

US-11-096-568A-32410
       i LOCATION: (1)...(385)
i OTHER INFORMATION: Ceres Seq. ID no. 13592963
US-11-096-568A-32411
                                                                                                Score 30; DB
Pred. No. 52;
1; Mismatches
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NAME/KEY: misc_feature
COCATION: (1)...(457)
OTHER INFORMATION: Public GI no. 4006922
US-11-208-308-13
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                                                                                             Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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ORGANISM: Glycine max
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US-11-096-568A-32410
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Sequence 32412, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1522PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT PILIG DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471
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Sequence 32411, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

FILE REFERENCE: 2750-1522F032

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 32411
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Pred. No. 44;
1; Mismatches 0; Indels
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i LOCATION: (1)..(334)
i OTHER INFORMATION: Ceres Seq. ID no. 13592964
US-11-096-568A-32412
                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (1). (236)
OTHER INFORMATION: Ceres Seq. ID no. 4927737
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILLING DATE: 2005-04-01
NUMBER OF SEQ 1D NOS: 34471
SEQ 1D NO 29742
LENGTH: 236
                                                                                                                                                                                  ORGANISM: Arabidopsis thaliana
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ORGANISM: Arabidopsis thaliana
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Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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316 LSSMIKK 322
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FEATURE
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TITLE OF INVENTION: Gene participating in the synthesis of brassinosteroid
FILE REFERENCE: 25352U (FS03-311PCT)
CURRENT APPLICATION NUMBER: US/10/507,106
CURRENT FILING DATE: 2004-09-10
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 524
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US-11-208-308-11

Sequence 11, Application US/11208308

Sequence 11, Application US/11208308

Publication No. US20060041952A1

GENERAL INFORMATION:
TITLE CAPITY: CONC. Zhihong C.
TITLE OF INVENTION: Uses Thereof
TITLE OF INVENTION: Uses Thereof
TITLE OF INVENTION: Uses Thereof
FILE REPERENCE: 18207-006001

CURRENT FILING DATE: 2005-08-19

RIOR APPLICATION NUMBER: 60/603,533

PRIOR PELLING DATE: 2004-08-20

NUMBER OF SEQ ID NO3: 35

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11

LENGTH: 524
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Publication No. US20060041952A1
GENERAL INFORMATION:
APPLICANT: Cook. Zhihong C.
TITLE OF INVENTION: P450 Polynucleotides, Polypeptides, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
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; LOCATION: (1)..(524)

; OTHER INFORMATION: Public GI no. 13878393

US-11-208-308-11
                                                                                                                                         ; Sequence 4, Application US/10507106; Publication No. US20050246797A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-507-106-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Conservative
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                                       199 ŘLIKMVKKV 207
1 RLSSMVKKV 9
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Best Local Similarity
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US-11-096-568A-24167

US-11-096-568A-24167

Sequence 24167, Application US/11096568A

Sequence 24167, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
THEORY INVENTION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 24167

LENGTH ....
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Pred. No. 73;
0; Mismatches 2; Indels
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Pred. No. 38;
1; Mismatches 2; Indels
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| DOAGTION: (1)..(187)

| OTHER INFORMATION: Ceres Seq. ID no. 12419624

US-11-096-5688-24167
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 18207-006001
CURRENT APPLICATION NUMBER: US/11/208,308
CURRENT FILING DATE: 2005-08-19
PRIOR APPLICATION NUMBER: 60/603,533
PRIOR FILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 524
                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
PEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(524)
OTHER INFORMATION: Public GI no. 18419825
US-11-208-308-12
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Best Local Similarity 77.8%;
Matches 7; Conservative (
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66.7%;
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Best Local Similarity 66.7
Matches 6; Conservative
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March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds (without alignments) 45.628 Million cell updates/sec Run on:

US-09-905-083A-33 Title: Perfect score:

1 LLLPLQILL 9 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2443163 segs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp2005s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\* A Geneseq 21:\* 1: geneseqp1980s:\* 2: geneseqp1990s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aae08238 Human str	Adr68794 Human str	Abg23378 Novel hum	Ada05736 Human NOV	Adn62900 Human NOV	Ada05732 Human NOV	Adn62896 Human NOV	Aar67888 Human str	Aaw05383 Human amy	Abb84421 Human SCC	Abb84406 Human SCC	Aau82740 Amino aci	Abu07440 Protein d	Abu07471 Protein d	Abr58471 Human str	Adb80484 Ovarian c	Adj68833 Human hea	Adn39180 Cancer/an	Adl06515 Human tum	Adn04182 Antipsori	Adr72880 Human ova	Ady67588 Human kal	Aec00353 Human kal	Aab21326 Human HSC
SUMMARIES	в ір	4 AAE08238	B ADR68794	4 ABG23378	5 ADA05736	9 ADN62900	6 ADA05732	8 ADN62896	2 AAR67888	2 AAW05383	5 ABB84421	5 ABB84406	S AAU82740	6 ABU07440	6 ABU07471	6 ABR58471	7 ADB80484	7 ADJ68833	7 ADN39180	8 ADL06515	8 ADN04182	8 ADR72880	9 ADY67588	9 AEC00353	3 AAB21326
	Query Match Length DB	6	0	136	198 (	198	250	250				253	253	253	253	253	253	253	253	253	253	253	253	253	257
dŧ	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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Klebsi	Ade08241 Human BLF Adr68796 Human Btr Adr68797 Human Btr	Human Human	Aab63578 Human gas Aab63582 Human qas	Peptic	Aam37771 Peptide # Aam64837 Human bra				ADD/8636 Rat OSTIO Ad191113 Bovine lu	Ad191117 Bovine lu	Ad191127 Bovine lu	Aar75642 Bovine co
ABO65558 AAE08240	AAEU8241 ADR68796 ADR68797	AAO12472 AAB63580	AAB63578 AAB63582	ABB43858	AAM37771 AAM64837	ABG59233	ABG46617 ADF59165	ADX94464	ABB78636 ADL91113	ADL91117	ADL91127	AAR75642
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## ALIGNMENTS

RESULT 1 AAE08238

AAE08238 standard; peptide; 9 AA.

AAE08238;

01-NOV-2001 (first entry)

Human stratum corneum chymotrypsin enzyme peptide #3 (residues 5-13).

Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia. 

Homo sapiens,

WO200159158-A1.

16-AUG-2001.

07-FEB-2001; 2001WO-US003977.

11-FEB-2000; 2000US-00502600.

(UYAR-) UNIV ARKANSAS.

O'brien TJ;

WPI; 2001-514676/56.

Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme

Claim 25; Page 102; 127pp; English.

The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide

Sequence 9 AA;

Novel human diagnostic protein #23369.

18-FEB-2002

ABG23378;

ABG23378 standard; protein; 136 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:33.
                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              serine protease; stratum corneum chymotrytic enzyme; SCCE; immune response; ovarian cancer; lung cancer; prostate cancer; pancreatic cancer; colon cancer.
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100.0%; Score 40; DB 4; Length 9; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      ADR68794 standard; peptide; 9 AA.
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Best Local Similarity 100.
                                                                       9; Conservative
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Query Match
Best Local Similarity
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed control of (II) or to treat disease states involving (II). (II) is activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a cupypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein espression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations creponable for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in all patent did not appear in the printed specification, but was obtained in
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                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                    WO200175067-A2.
                                                                                                                                                                                                                 Homo sapiens.
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RESULT 3 ABG23378

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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B;
Ji W, Miller CE, Rasclelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
                                                                                        human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antipaemic; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alaheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 170; 586pp; English.
                                                            Human NOV18c protein SEQ ID NO:96
                                                                                                                                                                                                                                                                                                                                           05-0CT-2001; 20010S-0327435P.
05-0CT-2001; 20010S-0327449P.
09-0CT-2001; 20010S-0327449P.
09-0CT-2001; 20010S-0328054P.
12-0CT-2001; 20010S-0328054P.
15-0CT-2001; 20010S-0328054P.
17-0CT-2001; 20010S-0328144P.
17-0CT-2001; 20010S-0329414P.
18-0CT-2001; 20010S-034964P.
24-0CT-2001; 20010S-034966P.
24-0CT-2001; 20010S-034966P.
25-0CT-2001; 20010S-034966P.
25-0CT-2001; 20010S-034966P.
25-0CT-2001; 20010S-034966P.
17-APR-2002; 2002US-0373816P.
19-APR-2002; 2002US-0373816P.
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22-APR-2002; 2002US-0374977P.
16-MAY-2002; 2002US-0381033P.
16-MAY-2002; 2002US-0381038P.
16-MAY-2002; 2002US-0381042P.
17-MAY-2002; 2002US-0381642P.
28-MAY-2002; 2002US-0381656P.
                           (first entry)
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                                                                                                                                                                                                      Ното варіепв
                             06-NOV-2003
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described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically brinds to the polypeptide described above; (7) methods for determining the presence of or predisposition to sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for user in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of comparison or aberrant physiological interactions of the polypeptide; (11) a method of comparison or aberrant physiological interactions of the polypeptide; (12) a method of comparison or aberrant physiological interactions of the polypeptide; (12) a method of comparison or aberrant physiological interactions of the polypeptide; (13) methods of treating cor preventing a pathology associated with the polypeptide; (13) methods of treating or mammal; and (14) a method for producing the above polypeptide; Novx sequences have antidiabetic, nortropic, neuroprotective, antiparkinsonian comparison of an antilipaemic activity of the polypeptide described above; (13) method of contracting a method for contractive, antiparkinsonian contropic polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic content metabolic disparders und antiparisial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer, cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; hamatopoietic disorder; dyslipidaemia; metabolic syndrome X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
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2001US-0327435P.
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2001US-0327917P.
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05-0CT-2001;
09-0CT-2001;
09-0CT-2001;
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09-0CT-2001; 2001US-0328056F 12-0CT-2001; 2001US-0328849F 17-0CT-2001; 2001US-0330142F 18-0CT-2001; 2001US-0330142F 18-0CT-2001; 2001US-0341058F 24-0CT-2001; 2001US-0341058F 24-0CT-2001; 2001US-034529F 25-0CT-2001; 2001US-034529F 01-NOV-2001; 2001US-034525F 01-NOV-2001; 2001US-034525F

2002US-0373826P. 2002US-0373884P. 2002US-0374977P. 2002US-0381037P. 2002US-0381038P.

2002US-0373815P.

19-APR-2002; 19-APR-2002; 19-APR-2002; 19-APR-2002; 22-APR-2002; 16-MAY-2002; 2002US-0381042P. 2002US-0381642P. 2002US-0383656P. 2002US-0383831P.

16-MAY-2002; 17-MAY-2002; 16-MAY-2002;

2002US-0391335P

29-MAY-2002; 25-JUN-2002;

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The invention relates to isolated NOVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and conjunction to the aberrant expression and polymucleotides may be used to treat disorders associated with decreased computed to five the aberiant our control or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polymucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of crestorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. polypeptides and in assays to identify with the constant and antigens in the anti-NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polypeptide expression and activity of NOVX polypeptides. The anti-NOVX polypeptide antibodies may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious collegence, anomer, and the various dyslipidaemias, metabolic disorders, disease, parkenson, and the various dyslipidaemias, metabolic disorders, and the various dyslipidaemias, metabolic wasting disorders and the various dyslipidaemias, metabolic wasting disorders and the various dyslipidaemias, metabolic wasting disorders and the various diseases and various cancers. Created with obesity, the metabolic sequence of a human NOVX protein.
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Claim 1; SEQ ID NO 96; 395pp; English
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Best Local Similarity 100...
Best Local Similarity 100...
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SR, Ellerman K, Malyankar UM;
anderson DW, Zhong M, Catterton E;
cone DJ, Pena CEA, Shenoy SG;
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ELLERMAN K. MALYANKAR U M.

(EDIN/) (ELLE/) (MALY/)

ZERHUSEN B D. ANDERSON D W.

ZERH/)

ANDE/

GORMAN

(ORTT/)

CATTERTON E.

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JIWW/ ZHON/

M SNOHZ

GUO X. PATTURAJAN M.

다. 다.

MILLET I. PEYMAN J A. KEKUDA R.

SMITHSON G.

(SMIT/) (MILL/) (PEYM/) (KEKU/) SPYTEK K A. EDINGER S R.

(PATT/) (SPYT/)

(dnox/

Zerhusen BD, Anderson DW, Zho Ramtelli L, Stone DJ, Pena CE enberg ME, Leach MD, Agee ML, EA, Rieger DK, Spaderna SK;

Peyman JA, Edinger

GOTHG...
Miller CE, Raber ME, L...
Rothenberg ME, L...

Eisen A,

WPI; 2004-213931/20. N-PSDB; ADN62899.

Jan M, Spytek KA, Gorman L, Zerhuse Millet I,

Patturajan M,

Smithson G,

EISEN A. GANGOLLI E A.

RIEGER D K. SPADERNA S K.

(RIEG/) (SPAD/)

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MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHENOY S G.
SHENOY E A.
SHENOY E A.
ELEACH M D.
ACEE M L.
BERGHS C C.
DIPIPPO V A.

(LEAC/) (AGEE/) BERG/)

(PENA/) (SHEN/)

STON/)

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09-OCT-2001; 2001US-0328056P.
15-OCT-2001; 2001US-0328849P.
15-OCT-2001; 2001US-0329144P.
17-OCT-2001; 2001US-0330142P.
18-OCT-2001; 2001US-0330309P.
24-OCT-2001; 2001US-0339266P.
24-OCT-2001; 2001US-0349575P.
01-NOV-2001; 2001US-0346357P.
17-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373817P.
19-APR-2002; 2002US-0373817P.
19-APR-2002; 2002US-0373817P.
19-APR-2002; 2002US-0373817P.
22-APR-2002; 2002US-0373817P.
                                                                                                      16-MAY-2002; 2002US-0381037P.

16-MAY-2002; 2002US-0381038P.

11-MAY-2002; 2002US-0381642P.

28-MAY-2002; 2002US-0381642P.

29-MAY-2002; 2002US-0383656P.
                                                                                                                                                                  (CURA-) CURAGEN CORP.
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Pott T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics

Claim 1; Page 169-170; 586pp; English.

The process of the composition comprising a polypeptide described above and a carrier; (2) a kit comprising in one or more containers, the composition described above; (3) an isolated nucleic acid described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a disease associated with altered levels of expression of the above comprising the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a disease associated with altered levels of expression of the above comprising an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of corrivity of the polypeptide described above; (12) a method for modulating corrective, of the polypeptide described above; (13) methods of treating or predisposition to a pathology associated with the above polypeptide. Novx correctivity of the polypeptide described above; (13) methods of treating corrective, animalial and (14) a method for producing the above polypeptide. Novx correctivity or of the polypeptide described above; (13) methods of creating corrective, animalial and antilipaemic activities, and can be used in gene therapy. The colypeptide is useful in manufacturing a medicament for treating a capture of activities and can be used in gene therapy. The colypeptide is useful in manufacturing a medicament for treating a capturing a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic. neurodegenerative disorders such as Alzheimer's disease or Parkinson's The present invention describes NOVX proteins, where X can be 1 to 55

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                                                                                                                                                                                                                                                                                                           human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; neurodegenerative disorder; Altheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
                                                                                                                  Gaps
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                                                                                         Score 40; DB 6; Length 250;
Pred. No. 26;
                                                                                                               0; Indels
                                                                                                               0; Mismatches
                                                                                                                                                                                                                  ADN62896 standard; protein; 250 AA.
                                                                                       100.0%;
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2001US - 032749P
2001US - 0328029P
2001US - 0328044P
2001US - 0328044P
2001US - 0328414P
2001US - 0329414P
2001US - 0330309P
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LLLPLQILL 10
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MILLET I.
                                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
                                              present invention.
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                                                                    Sequence 250 AA;
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09-0CT-2001; 2
09-0CT-2001; 2
09-0CT-2001; 2
12-0CT-2001; 2
15-0CT-2001; 2
18-0CT-2001; 2
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01-NOV-2001;
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AAR67888; RESULT 8 AAR67888 RESULT ន្តដូច្ចប្រជុំ ò g ઠે 셤 The invention relates to isolated NoVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NoVX polypeptides. For example, NoVX polypeptides and activity of NoVX by supplementing the patient our production or activity of NoVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NoVX polypeptides by binding with the cells own genes and preventing their expression. NoVX binding with the cells own genes and preventing their expression. NoVX polypeptides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of cretorative indiagnostic and in assays to identify modulators captured antibodies and in assays to identify of NoVX. The anti-NoVX polypeptide antibodies, agonists and antagonists and antagonists and antagonists and antagonists and antagonists and antagonist of solve to modulate NoVX polypeptide antibodies, agonists and antagonists may also be used to modulate NoVX polypeptide antibodies and presence of NoVX in samples. NoVX polypeptides and polymucleotide expression and activity of NoVX polypeptides and polymucleotides may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, anorexia, cancer, cancer, cancer associated cachexia, neurodegenerative disorders, and the various dyslipidaemias, metabolic disorders, haematopoletic disorders, parkinson's Disorder, inample and disorders, disturbances associated with obesity, the metabolic syndrome X and Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen A, Gangolli EA, Rieger DK, Spaderna SK; Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease. Claim 1; SEQ ID NO 92; 395pp; English. SPYTEK K A. EDINGER S R. ELLERMAN K. MALYANKAR U M. MILLER C E. RASTELLI L. STONE D J. STONE D J. SHENOY S G. SHENOY S G. SHENOY S G. SHENBERG M B. ROTHENBERG M D. LEACH M D. EISEN A. GANGOLLI E A. AGEE M L. BERGHS C. DIPIPPO V A. RIEGER D K. SPADERNA S K. GUO X. PATTURAJAN M. ZERHUSEN B D. ANDERSON D W. CATTERTON E. WPI; 2004-213931/20. PEYMAN J A KEKUDA R. GORMAN L. N-PSDB; ADN62895. ZHONG M. 된 다. (BISE/) (GANG/) (RIEG/) (SPAD/) (PEYM/) (KEKU/) (JUJJ/) (ROTH/) (LEAC/) (AGEE/) (PENA/) (SHEN/) (SHIM/) (RAST/) (STON/) BERG/) (ANDE/) (ZHON/) (CATT/) (ELLE/) (PATT/) ZERH/) LILL/ GUOX/ GORM/ MALY/

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The enzyme encoded by this sequence is used in pharmaceutical, cosmetic and skin care products, especially to treat and prevent acne, xeroderma, or other hyperkeratotic conditions (e.g. callosities or keratosis pilaris), ichthyoses, paoriasis, eczema, eczema, eczema, ercembinantly following mammal, insect, plant, or microorganism transformation with plasmid pSS07. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and related vectors, transformed cells and polypeptides, useful for treating skin disorders, e.g. acne or psoriasis, and for identification of specific inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stratum corneum chymotryptic enzyme; skin disorder, acne; psoriasis; callosities; keratosis pilaris; ichthyoses; eczema.
wasting disorders associated with chronic diseases and various cance
They may also be used as antibacterial agents. The present sequence
represents the amino acid sequence of a human NOVX protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human stratum corneum chymotrophic recombinant enzyme (SCCE).
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                                                                                                                                                     8; Length 250;
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                                                                                                                                                   100.0%; Score 40; DB
100.0%; Pred. No. 26;
ive 0; Mismatches
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(first entry)
                                                                                                                           Query Match
Best Local Similarity luv.
19 Conservative
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LLLPLQILL 13
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N-PSDB; AAQ81203.
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Best Local Similarity
Matches 9; Conserv
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                                                                                                   Sequence 250 AA;
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09-AUG-1995
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This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneuw chymotryptic enzyme (SCCE) or its variant, or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a cosmetic or a pharmaceutical formulation, and for the development of a diagnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an apportant dispenses scleeted from diseases consisting of epidermal hyperkeratosis, epidermal inflammator, dermal inflammator, skin diseases scleeted from diseases suth epidermal hyperkeratosis. The mammal of the invention is also useful as a model for further studies of itch mechanisms and the testing of potential compounds and compositions for relieve of various skin diseases where itch is a component. This sequence represents the N-terminal Erymonymous with human kallikrein 7 (KLKX), used in the development of the
                                                                                                                                                                                                                                                                                                                                                                                    Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; Page 37; 74pp; English
                                                                                                                          09-FEB-2001; 2001CA-02332655.
09-FEB-2001; 2001DK-00000218.
                                                                         08-FEB-2002; 2002WO-IB001300
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                     Sgelrud T, Hansson L;
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HANS/) HANSSON L.
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                     15-AUG-2002.
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ABB84406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human amyloid precursor protein protease (AAW05383) is involved in the processing or clearance of amyloid precursor protein to form beta-amyloid peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783) obtd. from a human lung library. Recombinant protease can be produced in transformed or transfected prokaryotic (partic. E. coli) or eukaryotic and testing of cods. useful for treating or develop products for the design and testing of cods. useful for treating or preventing conditions associated with beta-amyloid peptide, esp. Alzheimer's disease
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    used to develop

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human amyloid precursor protein protease - used to deve prods. for the treatment or diagnosis of associated conditions, esp. Alzheimer's disease.
                                                                                                                                                                                                                                 Amyloid precursor protein protease; Alzheimer's disease; diagnosis;
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                                                                                                                                                                              Human amyloid precursor protein protease.
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                     AAW05383 standard; protein; 253 AA.
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                                                                                                                          31-DEC-1996 (first entry)
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                                                                      AAW05383;
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SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; stransgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruittus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
                            Gaps
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 5; Length 253;
                             0; Indels
100.0%; Score 40; DB
100.0%; Pred. No. 26;
iive 0; Mismatches
                                                                                                                                                           ABB84406 standard; protein; 253 AA.
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WO200262135-A2

Homo sapiens

RESULT 10

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us-09-905-083a-33.rag

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This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a bratum corneum chymotryptic enzyme (SCCE) or its variant, coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, coperably linked to a promoter that drives expression of heterologous soce or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or tacting of a cosmetic or a pharmaceutical formulation, and for the development of a disgnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of inflammatory skin diseases selected from diseases consisting of epidermal hyperkeratosis, epidermal inflammation, dermal inflammation, erratum stopic dermatitis, eczema, acrome and inherited skin diseases with the paldermal hyperkeratosis. The mammal of the invention is also useful as a model for further studies of itch mechanisms and the testing of where itch is a component. This sequence represents the human stratum corneum chymotryptic enzyme, SCCE which is a serine protease synonymous corneum chymotryptic enzyme, SCCE which is a serine protease synonymous corneum chymotryptic enzyme, invention in the development of the
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                                                                                                                                                                                                                                                                                                                                                                                             Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 58-59; 74pp; English
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                                                                                                       08-FEB-2002; 2002WO-IB001300
                                                                                                                                                   09-FEB-2001; 2001CA-02332655.
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                     Egelrud T, Hansson L;
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                                                                                                                                                                                                                  (EGEL/) EGELRUD T.
(HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABQ76226.
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                  WO200262135-A2
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The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. restenosis and coronary thrombosis), brain or neuronal associated diseases, metabolic coronary thrombosis), brain or neuronal associated diseases, metabolic diseases, migraines, pain, sexual dysfunction, mood disorders (e.g. rheumatoid arthritis and psoriasis), central or peripheral nervous system diseases, migraines, pain, sexual dysfunction, mood disorders, attention disorders, hypotension, hypertension, psychotic disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's disease) and dyskinesias. The nucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel
                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
hypertension; psychotic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; enzyme.
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                                                                                                                                                                                                                                                                                                                    Plowman G, Whyte D, Sudarsanam S, Manning G, Caenepeel S;
Charydczak G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU07440 standard; protein; 253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human proteases of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Fig 2N; 313pp; English
                                                                                                                                                                                                      26-JUN-2001; 2001WO-US020171.
                                                                                                                                                                                                                                              26-JUN-2000; 2000US-0214047P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JAN-2003 (first entry)
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                     (SUGE-) SUGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABK31782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 253 AA;
                                                                                                                          WO200200860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Gaps .

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The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a semple comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample comprises prostate cancer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves contextention in a subject having a prostate cancer, which involves the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer. (I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer. (I) is also useful for identifying agent under conditions effective for the test agent to modulate a biological activity of the polypeptide differentially-regulated in prostate cancer cells, which involves contacting a polypeptide differentially regulated in prostate cancer cells, which involves contacting a polypeptide differentially regulated in prostate cancer cells, which involves contacting a polypeptide of the polypeptide, and determining whether the test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, subjudy determining predisposition to disease conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer e.g., in tissue sections, in blopsy sample, in total RNA, in lymph, in cell cancer its seage of development, the nature of genetic defect, etc. The polypeptide encoded by (I) can be used as target for therapy or drug of seconditic genes, and groups of genes, expressed in pathways or the polypeptide ancoded by (I) can be used as target for therapy or the polypeptide encoded by (I) can be used as target for therapy or the polypeptide encoded by (I) can be used as target for the polypeptide encoded by (I) can 
                                                                                                                                                                                                                                                                                                                                                                  Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 293-294; 416pp; English.
                                                                                                                                                                                                     (ORIG-) ORIGENE TECHNOLOGIES INC.
                                                                                                                               06-APR-2001; 2001US-0281731P.
                                                                                    08-APR-2002; 2002WO-US010824
                                                                                                                                                                                                                                                                                                   WPI; 2003-058520/05.
                                                                                                                                                                                                                                                                                                                         N-PSDB; ABX10343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 253 AA;
WO200281638-A2
                                                                                                                                                                                                                                                     Jay G;
                                           17-0CT-2002.
                                                                                                                                                                                                                                                     Sun Z,
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100.0%; Score 40; DB 6; Length 253; 100.0%; Pred. No. 26; 0; Indels 0; Mismatches 100.0%; Local Similarity 100. les 9; Conservative Query Match Matches

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ABU07471 standard; protein; 253 AA. ABU07471; RESULT 14
ABU07471
ID ABU07
XX
AC ABU07

Protein differentially regulated in prostate cancer #74.

molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer assessing; Prostate cancer; gene expression; differential regulation;

Homo sapiens.

WO200281638-A2. 

17-OCT-2002.

08-APR-2002; 2002WO-US010824.

06-APR-2001; 2001US-0281731P.

(ORIG-) ORIGENE TECHNOLOGIES INC.

ö Jay Sun Z, WPI; 2003-058520/05. N-PSDB; ABX10375. Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.

Claim 1; Page 351; 416pp; English.

The invention describes genee (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer. Which involves contering the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer. Of target genes which are differentially-regulated in prostate cancer. (C) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer. (C) activity of a polypeptide differentially-regulated in prostate cancer calls with a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, prognostical activity of the polypeptide, and conditions especially relating to prostate cancer. (I) and its expression conditions especially relating to prostate cancer. (I) and its expression conditions especially relating to prostate cancer. (I) and its expression of cancer, its stage of development, the nature of genetic defect, etc. (T) the polypeptide end diagnostic test to assay for presence of cancer of cancer, its stage of development, the nature of genetic defect, etc. (T) the polypeptide end diagnostic test to describe the type of cancer, its stage of development, the nature of genetic defect, etc. (T) the polypeptide end development, the nature of genetic defect, etc. (T) the polypeptide end groups of genes are type to development, the polypeptide and these sections in biopsy sample, in total NN, in Inyally the polypeptide end ge regulated in prostate cancer

Sequence 253 AA;

Gaps ö 100.0%; Score 40; DB 6; Length 253; 100.0%; Pred. No. 26; tive 0; Mismatches 0; Indels 9; Conservative Local Similarity Query Match Best Loca Matches

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The invention relates to a novel isolated polynucleotide. The polynucleotides of the invention have cytostatic activity, and may have a use in gene therapy, and in a vaccine. The composition and methods are useful in diagnosing and/or treating cancer, particularly ovarian cancer. The composition may also be used as a vaccine to prevent cancer. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotide and polypeptide useful for diagnosing and/or treating cancer, particularly ovarian cancer, and as a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytostatic; gene therapy; vaccine; cancer; ovarian cancer
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100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 157-158; 169pp; English
                                                                                                                                                                                                                                                                               ABR58471 standard; protein; 253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-OCT-2002; 2002WO-US031467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-OCT-2001; 2001US-0327135P.
30-MAY-2002; 2002US-0384531P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003029468-A1.
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                                                                                                                                                                                                                                                                                                                                                                    ABR58471;
                                                                                                                                                                                                       RESULT 15
ABRS8471
LD ABRS8471
XX ABRS8
XX ABRS8
XX Human
XX Human
XX Homo
XX CCRI
XX CCC The 1
CCC UBBE 2
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CCC UBBE 3
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CCC UBBE 3
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Gaps

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Search completed: March 11, 2006, 00:24:13 Job time : 88.6667 secs

|||||||||| LLLPLQILL 13

LLLPLOILL 9

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein

March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds (without alignments) 61.367 Million cell updates/sec Run on:

US-09-905-083A-33

1 LLLPLQILL 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		de			Catalana	
Result No.	Score	Query Match	댭	DB	e e	Description
	,	·	253		9	serine proteinase
7	36	90.0	146	~	H75201	hypothetical prote
m	34	85.0	277	~	H84314	cytochrome aa3 con
4	34	85.0	369	N	S33603	surfactant protein
S	34	85.0	371	-	JN0450	conglutinin precur
9	34	85.0	371	N	145878	conglutinin - bovi
7	34	85.0	754	N	AE0614	probable competenc
œ	34	85.0	845	N	D97163	cation transport P
σ	33	82.5	196	N	G65039	
10	33	82.5	282	N	E70890	
11	33	82.5	370	~	AB3334	
12	33	82.5	398	7	C91063	hypothetical prote
13	33	82.5	413	~	AC0834	д
14	33	82.5	426	~	C83103	hypothetical prote
12	33	82.5	470	~	A90083	hypothetical prote
16	33	82.5	475	-	A69149	n tra
17	33	82.5	653	N	A46362	amyloid precursor-
18	32	80.0	198	~	S25656	urface
19	32	80.0	235	Н	RWHUT8	T-cell surface gly
50	32	80.0	238	н	LNRTMA	mannose-binding le
21	32		247	Н	KYHUCM	chymase (EC 3.4.21
22	32		249	N	F91095	type III secretion
23	32	80.0	249	7	B85941	hypothetical prote
54	32	80.0	264	7	C97402	probable acyltrans
	32	80.0	264	N	AC2620	1-acyl-sn-glycerol
56	32	ö	266	~	JC7300	tax-responsive ele
27	32	•	267	~	JC4857	noge
	32	80.0	491	~	JC6197	stromelysin 3 (EC
59	32	80.0	492	N	A44399	stromelysin 3 (EC

Na+/H+-exchanging peptidyl-dipeptida	apolipoprotein C-I interleukin-2 prec	conserved hypothet	hypothetical prote	nitrate ABC transp	probable secreted	hypothetical prote	hypothetical prote	probable permease	ABC transporter, m	hypothetical prote		hypothetical prote
A12088 A31759	A38685 A31278	G75555	T43766	F69260	T35589	T38931	C84914	A98157	AH3130	D83934	C84306	A71875
7 7	0 0	9	1 (1	7	7	~	7	~	~	~	~	7
543 1306	100	159	189	244	249	269	303	372	372	392	447	493
80.0 80.0	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5
32	31 31	31	31	31	31	31	31	31	31	31	31	31
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## ALIGNMENTS

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Berline processions Such preduction - numean
NiAlternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-0ul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A5366
R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269; 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Reference number: A53968; MuID:9430825; PMID:8034709
A;Residues: 1-253 <HAN>
A;Residues: 1-253 <HAN>
A;Residues: 1-253 <HAN>
A;Residues: 1-253 <HAN>
A;Gene: GDB:PRSS6; SCCE
A;Genetics:
A;Genet
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serine proteinase SCCE precursor - human
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RESULT 2

hypothetical protein PAB0088 - Pyrococcus abyssi (strain Orsay)

Organization process abyses:
C;Species: Pyrococcus abyses:
C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004
C;Accession: H75201
A;Rescription: Pyrococcus abyses genome sequence: insights into archaeal chromosome struct
A;Rescription: Pyrococcus abyses genome sequence: insights into archaeal chromosome struct
A;Rescription: Pyrococcus abyses genome sequence: insights into archaeal chromosome struct
A;Reserince number: A75001
A;Reserince rumber: A75001
A;Residues: preliminary
A;Molecule 'type: DWA
A;Residues: 1-146 <KAM>A;Residues: 1-140 <KAMA

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A; Molecule type: mRNA
A; Residues: 1-371 <SUZ>
A; Cross-references: UNIPROT: P23805; UNIPARC: UP10000127EB3; DDBJ: D14085; NID: 9285643; PIDb
A; Experimental source: liver
R; Kawasaki, N.; Itch, N.; Kawasaki, T.
Biochem. Biophys. Res. Commun. 1994
A; Title: Gene organization and 5'-flanking region sequence of conglutinin: A C-type mamma?
A; Reference number: JC2396; MUID: 94128104; PMID: 8297370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPARC:UPI0000127EB3
A;Cross-references: UNIPARC:UPI0000127EB3
A;Cross-references: UNIPARC:UPI0000127EB3
B;Lu, J.; Laursen, S.B.; Thiel, S.; Jensenius, J.C.; Reid, K.B.M.
Biochem. J. 292, 157-162, 1993
A;Title: The cDNA cloning of conglutinin and identification of liver as a primary site of A;Reference number: S33235; MUID:93277452; PMID:7684896
A;Accession: S33235
A;Molecule type: mRNA
A;Residues: 1-172, "H, 174-217, "A', 219-271, "V', 273-371 <LUU>
A;Cross-references: UNIPARC:UPI000016C2E3; EMBL:X71774; NID:9395267; PIDN:CAAS0665.1; PII
A;Experimental source: liver
R;Lee, Y.M.; Leiby, K.R.; Allar, J.; Paris, K.; Lerch, B.; Okarma, T.B.
A;Title: Primary structure of bovine conglutinin, a member of the C-type animal lectin ft A;Reference number: A23740; MUID:91131556; PMID:1993651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Molecule type: protein
A; Residues: 21-54;75-86, X, ,88-89, X, ,91, X, ,93-94;208-209, X', ,211-227 <KAW>
A; Cross-references: UNIPARC: UP100001741A3; UNIPARC: UP100001741A4; UNIPARC: UP100001741A5
A; Experimental source: serum
R; Lu, J.; Miedemann, H.; Holmskov, U.; Thiel, S.; Timpl, R.; Reid, K.B.M.
Bur. J. Blochem. 215, 793-799, 1993
Bur. J. Blochem. 215, 793-799, 1993
A; Title: Structural similarity between lung surfactant protein D and conglutinin. Two dis A; Reference number: $35044; MUID: 93358905; PMID: 8354286
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A; Residues: 75-86, xx, 88-89, xx, 91,'I' < LUA>
A; Cross-references: UNIPARC: UD100001741A6
A; Cross-references: UNIPARC: UNIO
B; Young, N.M.; Leon, M.A.
Biochem: Biophys: Res. Commun. 143, 645-651, 1987
A; Title: The carbohydrate specificity of conglutinin and its homology to proteins in the A; Reference number: A29416; MUID:87184551; PMID:3566740
A; Contents: annotation
B; Malhotra, R; Laursen, S.B; Willis, A.C.; Sim, R.B.
Biochem: J. 293, 15-19, 1993
A; Title: Research Communication. Localization of the receptor-binding site in the collect A; Reference number: S34054; MUID:93319501; PMID:8328957
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A;Residues: 1-371 <LIO>
A;Cross-references: UNIPARC:UPI0000127EB3; EMBL:U06860; NID:9507183; PIDN:AAB60624.1; PII
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A;Title: Bovine conglutinin gene exon structure reveals its evolutionary relationship to A;Reference number: 146010; MUID:94267222; PMID:8207234
       Accession: JN0450; JC2396; S33235; A23740; S36879; S35044; I46010; A29416; S34054
                                    Risuzuki, Y.; Yin, Y.P.; Makino, M.; Kurimura, T.; Wakamiya, N.
Biochem. Biophys. Res. Commun. 191, 335-342, 1993
A;Title: Cloning and sequencing of a cDNA coding for bovine conglutinin.
A;Reference number: JNO450; MUID:93213261; PMID:8460993
A;Accession: JNO450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: protein
A;Reddudes: 21-20;S'.211-371 <LEE>
A;Reddudes: 21-20;S'.211-371 <LEE>
A;Cross-references: UNIPARC:UP1000014DF2A
R;Kawasaki, N.; Yokota, Y.; Kawasaki, T.
Arch. Blochem. Blophys. 305, 533-540, 1993
A;Title: Differentiation of conglutination activity and A;Title: Differentiation of conglutination activity and A;Reference number: S36879; MUID:93384312; PMID:8373191
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A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-371 < KA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H84314
R;Ng, V., Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Kenler, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc, Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A; A;Eference number: A84160; MUID:20504483; PMID:11016950
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R;Lim, B.L.; Lu, J.; Reid, K.B.M.
Immunology 78, 159-165; 1993
A;Title: Structural similarity between bovine conglutinin and bovine lung surfactant pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: UNIPROT: Q9HP13; UNIPARC: UPI0000063931; GB: AE004437; NID: g10581096;
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NyAlternate names: C3b-binding protein
NyContains: conglutinin-N
C5Species: Bos primigenius taurus (cattle)
C5Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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C,Date: 02-Deca-1993 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
                                                                            Gaps
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A;Cross-references: UNIPARC:UP10000177932
C;Superfamily: pulmonary surfactant protein D; C-type lectin homology F;248-367/Domain: C-type lectin homology <LCH>
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   DB 2;
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66.7%; Pred. No. 33;
ive 3; Mismatches
   Score 36; DB 2
Pred. No. 7.1;
2; Mismatches
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90.08;
                                       Best Local Similarity 77.8
Matches 7; Conservative
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surfactant protein D - bovine
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97 VLLPLQVIL 105
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LLLPLSVLL 10
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A.Molecule type: DNA
A.Residues: 1-277 <STO>
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C,Genetics:
A,Gene: ccp
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A,Gene: STY0984
C,Superfamily: competence protein ComEC
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 87.5%;
Matches 7; Conservative
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Matches 7; Conservative
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A;Gene: CAC2137
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C;Comment: This protein mediates the agglutination of erythrocytes with antibody and composed comment: This protein is a Ca2+-dependent serum lectin specific for N-acetylglucosamin A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Introns: 67/1; 106/1; 142/1; 178/1; 217/1; 245/1
A;Introns: 67/1; 106/1; 142/1; 178/1; 217/1; 245/1
A;Introns: 67/1; 106/1; 142/1; 178/1; 217/1; 245/1
C;Superfamily: pulmonary surfactant protein D; C-type lectin homology
C;Superfamily: pulmonary surfactant protein D; C-type lectin homology
C;CyVormain: signal sequence #status predicted <SIG->
F;21-371/Product: conglutinin #status predicted <MAZ->
F;21-371/Product: conglutinin-N #status predicted <WAZ->
F;248-369/Domain: C-type lectin homology <LCH->
F;38,387,99,135,141,159,162,198,210/Modified site: 5-hydroxylysine (Lys) #status experime F;83,87,99,135,141,159,162,198,210/Modified site: 5-hydroxylysine (Pto) #status experime F;78,98,108,111,129,122,147,153,171,195/Modified site: 5-hydroxyproline (Pto) #status experime F;337/Binding site: carbohydrate (Asn) (covalent) #status experimental
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Gene 141, 277-281, 1994
A;Title: Bovine conglutinin (BC) mRNA expressed in liver: cloning and characterization char
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable competence-related protein STY0984 [imported] - Salmonella enterica subsp. ente C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 25-Aug-2003 C;Accession: AE0614
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seroy A;Reference number: AB0502; MUID:21534947; PMID:11677608
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Superfamily: pulmonary surfactant protein D; C-type lectin homology
;248-369/Domain: C-type lectin homology <LCH>
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A;Molecule type: DNA
A;Rresidues: 1-754 <PAR>
A;Rresidues: 1-754 <PAR>
C;Genetics:
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C;Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
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Pred. No. 45;
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77.8%;
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LLLPLSVLL 10
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Best Local Similarity
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Best Local Similarity
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C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C; Accession: D97163
C; Accession: D97164
C; Accession: D97165
C; Comelchanko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, C; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J; Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A; Accession: D97163
A; Accession: D97163
A; Accession: D97163
A; Accession: D97163
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Accession: G65039
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col.
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Accession: G65039
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A,Restdues: 1-196 <BLAT>
A,Cross-references: UNIPARC:UPI000016ED74; GB:AE000347; GB:U00096; NID:g2367142; PIDN:AAC
A,Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA'
*Residues: 1-845 - KURD.
A;Cross-references: UNIPROT:097H76; UNIPARC:UPI00000CA412; GB:AE001437; PIDN:AAK80095.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                  cation transport P-type AFPase CAC2137 [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum
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C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
                                                                              Gaps
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Score 34; DB 2; Length 754;
Pred. No. 92;
1; Mismatches 1; Indels
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Pred. No. 37;
1; Mismatches 1; Indels
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Pred. No. 1e+02;
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Length 398,

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Score 33;
Pred. No.
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C, Genetics:
A, Gene: PA4338
                                                                                                      82.5%;
77.8%;
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Best Local Similarity 77.00
7; Conservative
                                                                                                   Query Match 82.5
Best Local Similarity 77.8
Matches 7; Conservative
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Matches 7; Conservative
                        A;Gene: ECB3475
C;Superfamily: yfjD protein
                                                                                                                                                                                                                                                          101 LLAPLÖİLM 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 LLAPLOILM 124
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C; Genetics:
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                Richard, S.T.; Broach, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature. 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Authors: Sqares, R.; Sulston, J.E.; Taylor, R.; Whitehead, S.; Barrell, B.G. A;Accession: E70890

A;Accession: E70890

A;Accession: E70890

A;Accession: Preliminary nucleic acid sequence not shown; translation not shown
A;Residues: 1-282 <COL>
A;Accession: E7080

A;Cross-references: UNIPROT:053979; UNIPARC:UPI00001652BF; GB:AL022073; GB:AL123456; NIC
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(991063)
hypothetical protein ECS3475 [imported] - Escherichia coli (strain O157:H7, substrain RI
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 31-Dec-2004
C;Accession: C91063
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 9, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gency A; Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C91063
A;Residue: preliminary
A;Molecule type: DNA
A;Residues: 1-398 c4AX>
A;Residues: 1-398 c4AX>
A;Residues: 1-398 c4AX>
A;Residues: 1-398 c4AX>
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J. Mazur, M.; Goltsman, E.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Aolecule type: DNA
A;Residues: 1-370 «KUR»
A;Cross-references: UNIPROT:Q8YHY9; UNIPROT:Q8FZX1; UNIPARC:UPI0000057D7A; GB:AE008917;
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             daunorubicin resistance transmembrane protein [imported] - Brucella melitensis (strain C;Species: Brucella melitensis (c;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
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Pred. No. 53;
1; Mismatches 1; Indels
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Pred. No. 70;
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77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
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Matches 6; Conservative
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196 LLLPLHLLL 204
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293 ILLPLQVL 300
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probable membrane protein corB [imported] - Salmonella enterica subsp. enterica serovar 1 probable membrane protein corB [imported] - Salmonella enterica serovar Typhi A;Note: this species has also been called Salmonella typhi G;Species: Salmonella ervelia species has also been called Salmonella typhi G;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 G;Accession: AC0834 R;Daxkhill, J;Dougan, G;James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R; Moule, S; O'Gaora, P. Navine, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S; Moule, S; O'Gaora, P. Naviner 413, 848-852, 2001
A;Authors: Parry (C; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Attle: Complete genome sequence of a multiple drug resistant Salmonella enterica serove A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AC0834
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Brisdann, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 599-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathoc A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Recession: C83103
A;Status: preliminary
A;Molecule type: DNA
A;Residuss: 1-426 <STO>
A;Residuss: 1-426 <STO
A;Residuss: 1-426 <STO>

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C;Genetics:
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                                                                                                             1; Indels
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DB 2;
75;
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Pred. No. 81;
1; Mismatches
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                                                                                                             1; Mismatches
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C,Superfamily: hypothetical protein H10107
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RESULT 15
A90083
hypothetical protein orf470 [imported] - Guillardia theta nucleomorph
C; Species: nucleomorph Guillardia theta
C; Species: nucleomorph Guillardia theta
C; Species: nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C; Date: 10-May-2001 #sequence_revision May-2001 #text_change 09-Jul-2004
A; Title: The highly reduced genome of an enslaved algal nucleus.
A; Reference number: A99082; MUID:11323671; PMID:11323671
A; Residues: A90083
A; Status: preliminary
A; Residues: 1-470 < DOU>
A; Residues: 1-470 < DOU>
A; Residues: 1-470 < DOU>
A; Genetics:
C; Genetics:
A; Genetics:
A; Gene: orf470
A; Map position: 1
A; Genome: nucleomorph
C; Keywords: nucleomorph
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Search completed: March 11, 2006, 00:40:48 Job time : 16.1111 secs

1 LLLPLQILL 9 :|||:||: 253 MLLPLEILI 261

충 음

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TISSUE=Skin;
MEDINE=94308225; PubMed=8034709;
Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A.,
Egelrud T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase."; J. Biol. Chem. 269:19420-19426(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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s
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QEDIY1 HUMAN
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KLK7 HUMAN
ID KLK7 H
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0561m7 mus musculu
0565w trichosurus
07775 trichosurus
09026 pyrococcus
06532 oryza sativ
06133 oryza sativ
06136 rhodopseudo
041b17 gibberella
06ppa4 leishmania
05xfw rattus norv
09140 lumpy skin
091m24 lumpy skin
091m24 lumpy skin
05v730 haloarcula
05v730 haloarcula
05b56 synechococc
09hpi3 halobacteri
0863a1 bos taurus
0863a1 bos taurus
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Q8r5d6 mus musculu
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                                                                                                                                             March 11, 2006, 00:11:15; Search time 95.2222 Seconds (without alignments) 66.684 Million cell updates/sec
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Q58cu7
Q749q7
Q8z802
Q8zqc3
Q7n6c7
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Q5n0s0
                  GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                  2166443 seqs, 705528306 residues
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MLKT, HUMAN
MCASO SYNP6
08VCA9_MOUSE
08REDE MOUSE
06BENE2 MOUSE
FKB11_MOUSE
FKB11_MOUSE
05BENE 9TRYP
INHA_TRIVU
02157_CLEGA
09C5323_OKYSA
06C5323_OKYSA
06C533_OKYSA
06C533_OKYSA
06C533_OKYSA
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Q58CU7_BOVIN
Q749Q7_GEOSL
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Q8ZQC3_SALTY
Q7N6C7_PHOLL
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Maximum Match 100%
Listing first 45 summaries
                                                                                                          protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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Match Length DB
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Maximum DB
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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097h76
06kg65
06kg65
09x620
09x620
09d226
07d7m8
06gnt6
06gnt6
08fxx1
08fxx1
08fxx1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P49862; Q8NSN9; Q8NFV7;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
13-SEP-2005 (Rel. 34, Last annotation update)
Kallikrein 7 precursor (EC 3.4.21.-) (hK7) (Stratum corneum chymotryptic enzyme) (hSCCE).
Home sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
Kishi T., Michael I.P., Diamandis B.P.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY64615; AAT66047.1; -: mRNA.
SEQUENCE 66 AA; 7171 MW; 82EIC392BC822FDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 2;
Pred. No. 5.5;
0; Mismatches 0
                                                                                                                                                                                                                                                                      66 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 AA
                                                           090226 MOUSE
053979 MYCTU
071Z68 MYCBO
0707M8 MYCTU
06GNT6 XENLA
04NVN1 90ELT
                                                                                                              Q6GNT6_XENLA
Q4NVN1_9DELT
Q8FZX1_BRUSU
                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                   Q8YHY9_BRUME
Q57CF5_BRUAB
                                                                                                                                                                                                                                                                                               Created)
                         Q8BJK7
Q7M8B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 100.0%;
Similarity 100.0%;
9; Conservative 0;
                                                                                                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, Kallikrein 7 splice variant Homo Bapiens (Human).
  000000000000
                                                                                                                                                                                                                                                                      QEDTYL HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
 1 LLLPLQILL 9
                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
NCBI_TaxID=9606;
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TISSUE-Skin;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;

A Itschul S.E.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

A Itschul S.E.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hatch F.;

DA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;

Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.;

A Raha S.S.; Loquellano N.A.; Peters G.J.; Abrameon R.D.; Mullahy S.J.;

Bosak S.A.; McZeanan K.J.; Malek J.A.; Gibbs R.A.;

Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.M.;

A Nilalon D.X.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

Pahey J.; Helton E.; Ketteman M.; Madan A.; Rodrigues S.; Sanchez A.;

Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;

Blakesley R.W.; Touchman J.W.; Green E.D., Dickson M.C.;

Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.E.;

Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.E.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                     Diamandis E.P.; "The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic enzyme is a new member of the human kallikrein gene family - genomic characterization, mapping, tissue expression and hormonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chymotryptic enzyme.";
Biochem. Biophye. Res. Commun. 211:586-589(1995).

--- FUNCTION: May catalyze the degradation of intercellular cohesive structures in the cornified layer of the skin in the continuous shedding of cells from the skin surface. Specific for amino acid residues with aromatic side chains in the PI position. SCCE cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-Phe-|-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the activation of precursors to inflammatory cytokines.
[2]
NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                Hansson L., Baeckman A., NY A., Edlund M., Edholm B., Tornell J., Wallbrandt P., Egelrud T.; Edlund m., Edholm B., Tornell J., "Epidermal overagression of Exratum corneum chymotryptic enzyme in mice; a model for chronic ithchy dermatitis."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION AND TISSUE SPECIFICITY.
TISSUE=Ovarian carcinoma;
MEDLINE=22623266; PubMed=12738725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skytt A., Stroemqvist M., Egelrud T.; "Primary substrate specificity of recombinant human stratum corneum
                                                                                                                                                                                                                                                                            Dong Y., Kaushal A., Brattsand M., Nicklin J., Clements J.A., "Differential splicing of KLKS and KLK7 in epithelial ovarian oproduces novel variants with potential as cancer biomarkers.";
                                                            PubMed=10974542; DOI=10.1016/S0378-1119(00)00280-8;
Yousef G.M., Scorilas A., Magklara A., Soosaipillai A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clin. Cancer Res. 9:1710-1720 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION.
MEDLINE=95314630; PubMed=7794273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                            3ene 257:119-130(2000).
                                                                                                                                                                                                                 Gene 254:119-128(2000).
                                          FISSUE=Keratinocyte;
                                                                                                                                                                                                 regulation."
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                         -i- ALTERNATIVE PRODUCTS:

Bvent=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=Long;
IsoId=P49862-1; Sequence=Displayed;
Name=2; Synonyms=Short;
IsoId=P49862-2; Sequence=VSP 013581;
-i- TISSUE SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermis. Also expressed in the brain, mammary gland, cerebellum, spinal cord and kidney. Lower levels in salivary glands, uterus, thymus, thyroid, placenta, trachea and testis. Up-regulated in ovarian carcinoma, cespecially late-stage serous carcinoma, compared with normal ovaries and benign adenomas (at the protein level).
                                                                                                                                                                                                                                                      -!- INDUCTION: By estrogens and glucocorticoids in a breast carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (By similarity).
(By similarity).
(By similarity).
(By similarity).
SUBCELLULAR LOCATION: Secreted. In ovarian carcinoma, secretals observed at the apical membrane and in cytoplasm at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0008246; F:serine-type peptidase activity; TAS.
GO; GO:0008544; P:epidermis development; TAS.
InterPro; IPR001254; Peptidase_S1_S6.
InterPro; IPR001314; Peptidase_S1_S6.
InterPro; IPR001314; Peptidase_S1_A.
PRINTS; PR00022; CHYMOTYSPIN.
SMART; SM00020; Tryp SPC; I.
PROSITE; PS50240; TRYPSIN_DOM; I.
PROSITE; PS50240; TRYPSIN_DOM; I.
PROSITE; PS00134; TRYPSIN_HIS; I.
PROSITE; PS00135; TRYPSIN_HIS; I.
Alternative splicing; Direct protein sequencing; Glycoprotein;
Hydrolase; Protease; Serine protease; Signal; Zymogen.
                                                                                                                                                                                                                                                                                         -1- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> W (in Ref. 6; AAH32005).
2D68B6B15A76A668 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Activation peptide.
Kallikrein 7.
Peptidase S1.
                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 peptidase S1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L33404; AAC37551.1; -; mRNA.
EMBL; AF166330; AAD49718.1; -; Genomic DNA.
EMBL; AF243527; AAG33360.1; -; Genomic_DNA.
EMBL; AF332583; AAK69624.1; -; Genomic_DNA.
EMBL; AF411214; AAN03662.1; -; mRNA.
EMBL; AF411215; AAN03663.1; -; mRNA.
EMBL; BC032005; AAH32005.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ensembl; ENSG0000169035; Homo sapiens.
HGNC; HGNC:6368; KLK7.
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27525 1
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190
226
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72
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253
250
70
1112
205
246
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HSSP; P00760; 1EZX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 ;
253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; SO1.300;
Ensembl; ENSG000
                                                                                                                                                                                                                                                                                                          subfamily.
                                                                                                                                                                                                                                                                            line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 604438;
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PROPEP
CHAIN
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NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fkbp11 protein.
Name=Fkbp11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome structure of the unicellular cyanobacterium Anacystis nidulans 6301 (Synechococcus sp. PCC6301)."; Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AP008231; BAD80100.1; -; Genomic_DNA.
GO, GO:0006550; P:response to stress; TEA.
InterPro; IPR006153; Na_H_porter.
InterPro; IPR006015; Usp.
InterPro; IPR006015; Usp.
Pfam; PP00582; Usp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=FVB/N; TISSUE-Salivary gland; MEDLINE=2288257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                               100.0%; Score 40; DB 1; Length 253; 100.0%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.5%; Score 39; DB 2; Length 545;
88.9%; Pred. No. 64;
iive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OrderedLocusNames=syc1910_c;
Synechococcus sp. (strain_PCC 6301) (Anacystis nidulans).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=269084;
                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58143 MW; 2DB84E920CD7DEDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 29, Last sequence update)
(TrEMBLrel. 29, Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probable Na+/H+-exchanging protein.
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Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                             QSNOSO SYNP6 PRELIMINARY;
QSNOSO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8VCA9_MOUSE PRELIMINARY;
Q8VCA9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.2
8; Conservative
                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 LLLPLOVLL 201
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                                                                                                                                                                                                              LLLPLOILL 13
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Query Match
Best Local Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
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                                                                                                                                                        LLLPLOILL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=PCC6301;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-2005
01-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugita M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                     RESULT 3
CONOSO SY
IO 01-F
DT 
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QBVCA9 MO
QBVCA9 MO
DD 01-M
DT 01-M
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TISSUE-Mammary tumor metaetatized to lung. Tumor arose spontaneously;

X. TISSUE-Mammary tumor metaetatized to lung. Tumor arose spontaneously;

X. Tataubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X. Staubberg R.L., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X. Altschul S.P., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

X. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

X. Altschul S.P., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

X. Altschul S.P., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

X. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

X. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

X. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

X. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X. Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raba S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X. Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

X. Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

X. Butterfield Y.S. N., Krzywinski M.I., Skalaka U., Smailus D.E.,

X. Generation and initial analysis of more than 15,000 full-length human
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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.B., Schein J.E., Jones S.J.M., Marza M.A., Schein J.E., Jones S.J.M., Marza M.A.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021345; AAH21345.1; -; mRNA.
MGI; MGI:191370; Fkbpl1.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
SEQUENCE 73 AA; 7819 MW; 93E8F53399BF3C11 CRC64;
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
STRAIN=FVB/N; TISSUE=Salivary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QBRSD6 MOUSE PRELIMINARY;
Q8RSD6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||||||:||
6 LLLPLQLLL 14
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MOUSE
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                                                                                                                                                                      요
                                                                                                                                                                                                                                                    TISSUE-Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse Taken by biopsy;

KTESUE-Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse Taken by biopsy;

KM Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

By Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Carnhori P., Frange C.,

RA Brownstein M.J., Usdin T.B., Tonallyuki S., Carnhori P., Frange C.,

RA Brownstein M.J., Usdin T.B., Tonallyuki S., Carnhori P., Prange C.,

RA Brownstein M.J., Nederson K.J., Marason R.D., Mullahy S.J.,

RA Brownstein M.J., Nedernan K.J., Matek J.A., Glubbs R.A.,

Robard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Hichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Phila D. K., Muzzy D.M., Sodergren E.J., Lu X., Glbbs R.A.,

Rahes J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Raheseley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                          TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy.;
                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                              Score 38; DB 2; Length 104;
Pred. No. 21;
                                               Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022900; AAH22900.1; -; mRNA.
HSSP; B18203; 1FKL.
HSSP; B18203; 1FKL.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR001179; FKBP PPIase.
PFam; PF00254; FKBP C; 1.
PROSITE; PS0059; FKBP C; 1.
SEQUENCE 104 AA; 11085 MW; 0534D57467566914 CRC64;
                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002311; AAH02311.1; -; mRNA.
MGI; MGI:1913370; Fkbp11.
                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                 138 AA
                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                  95.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                 QEPKE2_MOUSE PRELIMINARY;
                                                                                                                                                                                                               Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.
                                                                                                                                                                                                                                                                        LLLPLOLLL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                          musculus (Mouse).
                                                                                                                                                                                                                                                      1 LLLPLQILL 9
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                    Fkbp11 protein.
                                        Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Fkbp11;
                                                                                                                                                                                                   Query Match
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RY NUCLECOTIDE SEQUENCE [LARGE SCALE MENA].

RY NUCLECOTIDE SEQUENCE [LARGE SCALE MENA].

RY MEDINE-25346483; PubMed-21466851; DOI-10.1038/nature01266;

RY MEDINE-25346483; PubMed-21466851; DOI-10.1038/nature01266;

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Hadarelli R., Hill D.P., Bult C., Hume D.A., Ghorbach C., Gojobori T.,

RA Balke J.A., Bradt D., Brusic V., Chothia C., Corbania E.,

RA Casaterland T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Godzik A., Gough J.,

RA Casaterland T., Gariboidi M., Gissi C., Godzik A., Gough J.,

RA Canagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Kanai A., Kawaji H., Kawasawa Y., Karzer K.B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Sultana R., Takenaka T., Taylor M.S., Teasdale R.D., Tomita M.,

RA Sultana R., Takenaka T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Mining L.G., Wynnahav-Boris A., Yanagisawa M., Yang I.,

RA Mining L.G., Wynnahav-Boris A., Yanagisawa M., Yang I.,

RA Mina Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Hara A., Hashikawa T., Konno H., Nakamura M., Sakazume N., Sakoi K.,

RA Hara A., Hashikawa T., Konno H., Nakamura M., Sakazume N.,

RA Hara A., Hashikawa T., Konno H., Nakamura M., Sakazume N.,

RA Hara A., Hashihino M., Imocani K., Ilahii Y., Ilohii Y.,

RA Mayazaki A., Sakai K., Sasaki D., Shibata K., Ilohoka S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
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Q9DIM7; Q9CRE4;
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
to-haiding protein 11 precursor (EC 5.2.1.8) (Peptidyl-prolyl circums isomerase) (PPIsse) (Rotamase) (19 kDa PKS06-binding protein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                  95.0%; Score 38; DB 2; Length 138; 88.9%; Pred. No. 27; ive 1; Mismatches 0; Indels
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR001179; FKBP_PPlase.
Pfam; PF00254; FKBP_PPL C; 1.
PROSTITE; PS0059; FKBP_PPLSE; 1.
SEQUENCE 138 AA; 15105 MW; C138BBB0EFDDF59D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muroidea; Muridae; Murinae; Mus
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Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
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LLLPLOLLL 14
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                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserv
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INHA TRIVU
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INHA TRIVU
          엄
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyui S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length human
and mouse CDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                             protein synthesis.
-!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=GUTat10.1;
Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trypanosoma brucei.
Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
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PPISSE FKBP-LYDE.
S - F (in Ref. 1; BAB31559).
S -> R (in Ref. 1; BAB31559).
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                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SIMILARITY: Belongs to the FKBP-type PPIase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94D955C57264BD82 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK003331; BAB22719.1; -; mRNA.
EMBL; AK019132; BAB31559.1; -; mRNA.
EMBL; BC03756; AAH37596.1; -; mRNA.
HSEP; P20071; ITCO.
Ensembl; ENSMUSG0000003355; Mus musculus.
MGI; MGI:191370; FKDP11.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
HIREFPEO; IFROULT9; FKBP_PPIASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 39;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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PROSTTE; PSS0059; FKBP PPIASE; 1.
Isomerase; Rotamase; Sīgnal.
ercnar.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QS85W6_9TRYP PRELIMINARY;
QS85W6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        (omega=0).
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -I- PTM: Proteolytic processing yields a number of bioactive forms, consisting either solely of the mature alpha chain, of the most N-terminal propeptide linked through a disulfide bond to the mature alpha chain, or of the entire proprotein.
-I- SIMILARITY: Belongs to the TGF-beta family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Mol. Endocrinol. 21:141-152(1998).

-1- FUNCTION: Inhibins and activins inhibit and activate, respectively, the secretion of follitropin by the pituitary gland. Inhibins/activins are involved in regulating a number of diverse functions such as hypothalamic and pituitary hormone secretion, gonadal hormone secretion, germ cell development and maturation, erythroid differentiation, insulin secretion, nerve cell survival,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCLEOTIDE SEQUENCE.
MEDLINE=99027340; PubMed=9801457; DOI=10.1677/jme.0.0210141;
Vanmontfort D., Fidler A.E., Heath D.A., Lawrence S.B., Tisdall D.J.,
Greenwood P.J., MCNatty K.;
"CDNA sequence analysis, gene expression and protein localisation of
the inhibin alpha subunit of Australian brushtail possum (Trichosurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activins.
SUBUNIT: Dimeric, linked by one or more disulfide bonds. Inhibin P
is a dimer of alpha and beta-A. Inhibin B is a dimer of alpha and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      embryonic axial development or bone growth, depending on their subunit composition. Inhibins appear to oppose the functions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metažoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Diprotodontia, Phalangeridae, Trichosurus.
Shallom J., Hou L., Djikeng A., Feldblyum T., Hostetler J., Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J., Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S., Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 38; DB 2; Length 246; 88.9%; Pred. No. 47; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=GUTat10.1;
Haas B., Blandin G., El-Sayed N.;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, AC009259; AAX80785.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                      STRAIN=GUTat10.1;
El-Sayed N.M., Khalak H., Adams M.D.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 246 AA; 27875 MW; 706DDB3BA6BB46AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trichosurus vulpecula (Brush-tailed possum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibin alpha chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:|||||||
163 LMLPLQILL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LLLPLQILL 9
                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vulpecula).";
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us-09-905-083a-33.rup

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sigmodontine rodents.";

Mol. Biol. Evol. 15:35-49(1998).

EMBL; U83808; AAB87168.1; ; Genomic_DNA.

GO; GO:0005739; C:mitochondrion; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0016491; P:oxidoreductase activity; IEA.

GO; GO:0016491; P:oxidoreductase activity; IEA.

GO; GO:0016491; P:Oxidoreductase activity; IEA.

InterPro; IPR001918; NADHub oxred4.

InterPro; IPR001560; Oxidored G5.N.

PERN; PP01059; Oxidored G5.N.

PRINTS; PR01437; NUOXDRDTASE4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=GES / Oreay;

MEDLINE=22511545; PubMed=12622808;

MEDLINE=22511545; PubMed=12622808;

MEDLINE=22511545; PubMed=12622808;

Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O., Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,

Van der Oost J., Weisenbach J., Zivanovic Y., Forterre P.;

"An integrated analysis of two genome of the hyperthermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                 MEDLINE-98152303; PubMed-9491603;
Engel S.R., Hogan K.M., Taylor J.F., Davis S.K.;
"Molecular systematics and paleobiogeography of the South American
                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.5%; Score 37; DB 2; Length 208; 88.9%; Pred. No. 63; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 146;
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EMBL, AJ248283; CAB49063.1; -; Genomic_DNA.

PIR, H75201; H75201.

InterPro; IPR008537; DUF819.

Pfam; PF05684; DUF819; 1.

Complete procecome; Hypothetical protein.

SEQUENCE 146 AA; 16092 MW; 7182941371258CIF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               208 208 23967 MW; 8AF1788697AED6A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
OrderedLocusNames=PYRAB01390; ORFNames=PAB0088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQV2DS PYRAB PRELIMINARY; PRT; Q9V2DS; 01-MAY-2000 (TrEMBLrel. 13, Created)
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QE5323 ORYSA PRELIMINARY;
QE5323;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 88.2
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 LLLPLQIII 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
7; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=29292;
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                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion
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SEQUENCE
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ID 06
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    EMBL, AF03340; AAACS345.1; -: mRNA.

DR GO; GO:0005576; C:extracellular region; ISS.

GO; GO:0001256; F:activin inhibitor activity; ISS.

GO; GO:0001256; F:activin inhibitor activity; ISS.

BG; GO:0001215; F:growth factor activity; ISS.

DR GO; GO:0005179; F:ported binding; ISS.

GO; GO:0005179; F:hormone activity; ISS.

BR GO; GO:0007159; F:ported binding; ISS.

BR GO; GO:0007159; F:ported binding; ISS.

BR GO; GO:0007159; F:cell adifferentiation; ISS.

BR GO; GO:0007159; P:cell adifferentiation; ISS.

BR GO; GO:000726; P:cell adifferentiation; ISS.

BR GO; GO:000726; P:cell adifferentiation; ISS.

BR GO; GO:000726; P:cell adifferentiation of B cell differentiation; ISS.

BR GO; GO:000518; P:megative regulation of B cell differentiation; ISS.

BR GO; GO:0004578; P:megative regulation of interferon-gamma bio. .; ISS.

BR GO; GO:0004578; P:megative regulation of interferon-gamma bio. .; ISS.

BR GO; GO:0004578; P:megative regulation of interferon-gamma bio. .; ISS.

BR GO; GO:0004509; P:megative regulation of macrophage different. .; ISS.

BR GO; GO:0004509; P:megative regulation of phosphorylation; ISS.

BR GO; GO:0004509; P:megative regulation of follicle-stimulating. .; ISS.

BR GO; GO:0004509; P:megative regulation of follicle-stimulating. .; ISS.

BR GO; GO:0004509; P:megative regulation of follicle-stimulating. .; ISS.

BR GO; GO:0004509; P:megative regulation of follicle-stimulating. .; ISS.

BR GO; GO:0004509; P:megative regulation of follicle-stimulating. .; ISS.

BR FRMYTS; PRO0669; IMHIBINA.

BR PROSTTE: PSO0250; TGF BETA 1; 1.

BR PROPER SYMART; SM00204; FORDER 1.

FT STGMAL 1 PROPER 2.

BR PROPER 2.

BR PROPER 2.

BR PROPER 3.

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Mitochondrion.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Arvicolinae; Clethrionomys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cleavage (By similarity).
Cleavage (By similarity).
N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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By similarity.
Inhibin alpha N-terminal region (By similarity).
Inhibin alpha chain.
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Pred. No. 67;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interchain (By similarity).
D661CDF93CDAA87D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 CLEGA

021527 CLEGA PRELIMINARY; PRT; 208 AA.

021527;

01-JAN-1998 (TrEMBLrel. 05, Created)

01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

NADH dehydrogenase subunit 4 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     By similarity.
By similarity.
By similarity.
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nes 8, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 AA;
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65
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
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RESULT 10
021527 CLE
1D 02152
AC 02152

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RATAIN-ENTIL B., Nubbaum C., Abouelleil A., Allen N., Anderson S., Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L., Barchchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L., Bukukgalter B., Butler J., Calvo S.B., Camarata J., Chang J., Dooley K., Dorris L., Elkins T., Engels R., Elickson J., Farco S., Ferreira P., FitzGerald M., Gage D., Galagan J., Radfe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A., Raffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A., Kalls C., Landers T., Lindblad-Toh K., Liu G., Lui A., Mallova T., Margay C., Maclean C., Macdonald P., Major J., Manning J., Matthews C., Maucell E., McCarthy M., Meldrim J., Meneus L., Anicol R., Mielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D., O'Lorn J., Spencer B., Schupback R., Seaman S., Severy P., Sumirnov S., Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P., Ramas J., Tesfaye S., Theodore J., Topham K., Travers M., Talamas J., Tesfaye S., Theodore J., Topham K., Travers M., Vassilev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B., Wallander B., Tander B., Zimmer A., Zimmer A., Zimmer A., Zalmmer R., Zimmer 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tarentolae (Sauroleishmania tarentolae).
Buglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Fusarium graminearum genome sequence.";
Submitted (FRB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                      Gibberella zeae PH-1.
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Hypocreomycetidae, Hypocreales, Nectriaceae, Gibberella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 2; Length 1064;
Pred. No. 7.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AACM01000229; EAA73727.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 1064 AA; 117828 MW; 2174A5BE94DEEBSF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leprohon P.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
P-glycoprotein D.
                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1527 AA
                                                             1064 AA
                                                                                                                     Created)
                                                                                                               13-SEP-2005 (TrEMBLrel. 31, 0
13-SEP-2005 (TrEMBLrel. 31, 1
13-SEP-2005 (TrEMBLrel. 31, 1
Hypothetical protein.
ORFNames=FG05591.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.5%;
88.9%;
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GGPPA4 LEITA

AC GEPPA4.

DT G6-PDA4.

DT 05-JUL-2004 (TrEMBLrel. 27,

DE P-GIVCOPCOCION D.

GN Name-PGPD.

GN Name-PGPD.

CO Leishmania tarentolae (Saurcoc)

CO Eukaryota; Euglenozoa; Kinet

CO Eukaryota; Euglenozoa; Kinet

CO Ilzard Leishmania.

CO NCBI TaxID=5689;

RN NCBI TaxID=5689;

RN Leprohon P.;

RL Leprohon P.;

RL Leprohon P.;

RL Leprohon P.;

RL Submitted (APR-2004) to the
                                                          Q4IB17 GIBZE PRELIMINARY;
Q4IB17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 86..
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 862 LLLPLNILL 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary data.
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                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=PH-1;
     RESULT 14
Q4IB17 GIE
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STRAIN-GGA009 / ATCC BAA-98;

STRAIN-GGA009 / ATCC BAA-98;

STRAIN-GGA009 / ATCC BAA-98;

PubMed=14704707; DOI=10.1038/nbt923;

Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,

Larimer F.W., Ghaon P., Hauser L., Torres Y Torres J.E.,

Gibson J.L., Hanson T.E., Bobst C., Torres Y Torres J.L., Peres C.,

Harrison F.H., Gibson J., Harwood C.S.;

"Complete genome sequence of the metabolically versatile

photosynthetic bacterium Rhodopseudomonas palustris.";

Nat. Blocchonol. 22:55-61(2004).

BNBL; BX572595; CAE26376.1; -; Genomic_DNA.

Complete proteome; Hypothetical protein.

SRQUENCE 181 AA; 19632 MW; CDB44D8210E565D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                         Name=OSJNBD0065C04.45;
Oryza sativa (japonica cultivar-group).
Dukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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Bradyrhizobiaceae, Rhodopseudomonas,
NCBI_TaxID=1076;
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GO; GO:0016787; F:hqdrolase activity; IEA.
GO; GO:0000287; F:nagnesium ion binding; IEA.
GO; GO:0006281; P:DNA repair; IEA.
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Sasaki T., Matsumoto T., Yamamoto K.;
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                                                                                          Endonuclease V protein-like.
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Hypothetical protein.
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DR CG: GO: 0016021; C:integral to membrane; IEA.

GO: GO: 0016021; C:integral to membrane; IEA.

BR GO: GO: 00016021; C:integral to membrane; IEA.

GO: 00160824; F:ATP binding; IEA.

GO: 0016887; F:ATPase activity; IEA.

GO: GO: 00042626; F:ATPase activity; coupled to transmembrane m. .; IEA.

BR GO: GO: 000166; F:nuclectide binding; IEA.

GO: GO: 0000810; P:transport; IEA.

InterPro: IPR001359; AAA ATPase.

InterPro: IPR001359; AAA ATPase.

InterPro: IPR001340; ABC membrane 1.

InterPro: IPR00140; ABC membrane; 2.

InterPro: IPR00343; ABC transport.

INTERPRO: ABC membrane; 2.

BR Fam; PF00066; ABC transporter; 2.

ProDom; PD000006; ABC transporter; 2.

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BR PROSITE; PS0021; ABC TMIE; 2.

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TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 35,
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GenCore version 5.1.7
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		ILT 1 19-502-600- 19-502-600- 10-502-600- 10-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600- 11-502-600-	Matcl Local		LT 2 9-918-243 quence 33 quence 33 quence 33 publicant: ppLICANT: pPLICANT: ITLE OF ILE REPER URRENT APPL URRENT APPL RIOR APPL RIOR PILL UNBER OF IL UNBER OF IL URBER OF IL
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PRIOR APPLICATION DATA:
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Patent No. 5834290
GENERAL INFORMATION:
APPLICANT: Beginner TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic TITLE OF INVENTION: Bazyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER: BLOGGE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: PAPENTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
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                                                                                                   Query Match 100.0%; Score 40; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 9; Conservative 0; Mismatches 0; Indels
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-918-243-33
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NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMINICATION INFORMATION:
TELEFAX: (212) 819-873
TELEFAX: (212) 34-8113
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08824874
Patent No. 5962300
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Novel KALLIKREIN
ITILE OF INVENTION:
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
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US-08-824-874-3
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US-08-557-146-2
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100.0%; Score 40; DB 2; Length 253; ilarity 100.0%; Pred. No. 3.7; Conservative 0; Mismatches 0: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: DISKETTE
COMPUTER: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                         US-09-210-084-3

Sequence 3, Application US/09210084

Sequence 3, Application US/09210084

Sequence 3, Application US/09210084

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Hillman, Jennifer L.

TITLE OF INVENTION: NOVEL KALLIKREIN

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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Patent No. 6472195
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Lal, Preett
TILE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INPORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 anino acids
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Best Local Similarity 100.
Matches 9; Conservative
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IMMEDIATE SOURCE:
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      Query Match
Best Local Similarity
Matches 9; Conserv
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CLONE: 532504
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| Patent No. 6093397
| GENERAL INFORMATION:
| APPLICANT: Dixton, Eric P. APPLICANT: Little, Sheila P. TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: RELATED NUCLEIC ACIDS NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: ADDRESSEE: Bli Lilly Corporate Center CITY: Indianapolis STREET Lilly Corporate Center CITY: Indianapolis STREET: Lidianapolis
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                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 253;
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ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
         FILLING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/ODCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEPHONE: (212) 819-8783
INFORMATION FOR SEQ ID No: 2:
SEGUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
...ino acid
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CLASSIPICATION NUMBER: US/08/330,188
FILING DATE:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERNENCE/OCKET NUMBER: X9239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
ITELEFAX: 317-277-1090
ITELEFAX: 317-277-1090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
    APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indiana
: United States of America
                                                                                                                                                                                                                                                                     LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity 100.
Matches 9; Conservative
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Query Match
Best Local Similarity 100.
Matches 9; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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Best Local Similarity
Matches 9; Conservat
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US-09-949-016-7716
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US-09-949-016-7716
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GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Johnstone, Edward M.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 40; DB 2; Length 253; Best Local Similarity 100.0%; Pred. No. 3.7; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATER:
COMPUTER: IBM COMPATER:
COMPUTER: FISH COMPATER:
COMPATING SYSTEM: DOS
SOFTWARE: FASTESCO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: PCT/US96/04294
ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                              FILING DATE: 16-Jan-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/210,084
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Billing9, Lucy J.
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0252 US
TELEPHONE: 415-845-055
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
STRIE: Indianapolis
STATE: Indiana
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 253 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear IMMEDIATE SOURCE:
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                                                                                      COUNTRY: USA
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CLASSIFICATION:
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Sequence 12075, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
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                                                                                                                                                                                                                                                                                                        0; Mismatches
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          US 08/416,257
PRIOR AFELICATION NUMBER: US 08/416,
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: BLAIOCK, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9235
TELEFONMUNICATION INFORMATION:
TELEFAX: 317-27-1090
TELEFAX: 317-27-1090
TELEFAX: 317-27-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
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Gaps

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RESULT 14
US-09-18-23-35
US-09-18-23-35
; Sequence 35, Application US/09918243
; Patent No. 6627403
; Fatent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: Cannon, Martin J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT PILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR APPLICATION NUMBER: US
; PRIOR PILING DATE: 2001-07-13
; NUMBER OF EQ ID NOS: 136
; SEQ ID NO 35
; LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 36, Application US/09918243

Patent No. 6627403

GENERAL INFORMATION :
GENERAL INFORMATION :
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
FILE REFERENCE: D6223CHZ/C/D/CIP
CURRENT APPLICATION NUMBER: US/09/918,243
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 136

SEQ ID NO 36

LENGTH: 9
           Indels
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NAMEKKEY: CHAIN
STHER INFORMATION: Residues 4-12 of the SCCE protein US-09-918-243-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CHAIN
OTHER INFORMATION: Residues 6-14 of the SCCE protein
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           0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
           8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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1 LLPLQILL 8
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US-09-918-243-36
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Patent No. 6294344

GENERAL INFORMATION:
APPLICANT:
Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT FILING DATE: 2000-02-11

PRIOR PELLING DATE: 2000-02-11

PRIOR PELLING DATE: 09/039,211

PRIOR PELLING DATE: 03-14-1998

SEQ ID NOS: 136

SEQ ID NOS: 136

MANDER NO 36

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LEMBET NO 36
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Patent No. 6294344
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Ovarian Cancer
FILE REFRENCE: D623CIP-C
CURRENT FILING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: US/09/502,600A
PRIOR FILING DATE: 03/09/39,211
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 35
LENGTH. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Residues 4-12 of the SCCE protein US-09-502-600-36
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12075
LENGTH: 812
                                                                                                                  TYPE: PRT; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12075
                                                                                                                                                                                                         Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                            429 LLLPLOLLL 437
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-502-600-36
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US-09-502-600-35
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Best Local Similarity 100.
Matches 9; Conservative
                TYPE: PRT
ORGANISM: Homo sapiens
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RESULT 2
US-09-905-083-33
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96, Appl
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                                                                                                                  March 11, 2006, 01:24:47; Search time 69.444 Seconds (without alignments) 54.151 Million cell updates/sec
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(cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*):

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(cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*):
                GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-905-083-33
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US-10-831-075-33
US-10-450-763-53/37
US-10-262-511-96
US-10-262-511-96
US-10-262-511-96
US-10-071-214-48
US-10-071-214-48
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US-10-173-999-48
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US-10-948-518-95
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US-10-948-518-95
US-10-948-518-95
US-10-344-394-38
US-10-424-599-207950
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Maximum Match 100%
Listing first 45 summaries
                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Result No.

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Patent No. US20020146708A1

GENERAL INFORMATION:

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of

TITLE OF INVENTION: Ovarian Cancer

FILE REFERENCE: D6223CTP/C/Div

CURRENT PILING DATE: 2001-07-13

PRIOR PELICATION NUMBER: US/09/905,000

PRIOR PELICATION NUMBER: US 09/502,600

PRIOR FILING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 136

LENGTH: 9
                                                                                                                         Sequence 57128, A Sequence 19, Appl Sequence 27327, Sequence 64, Appl Sequence 74, Appl Sequence 3, Appli Sequence 24, Appl Sequence 24, Appl Sequence 51875, A Sequence 51875, A Sequence 51875, A Sequence 265948,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33, Application US/09918243

Fatent No. US20020142317A1

GENERAL INFORMATION:

APPLICANT: Cannon, Martin J.

APPLICANT: Cannon, Martin J.

APPLICANT: Cannon, Methods for the early diagnosis of ovarian cancer;

TILLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

FILE REFERENCE: D6223CIP/C/D/CIP

CURRENT APPLICATION NUMBER: US/09/918,243

CURRENT APPLICATION NUMBER: US

PRIOR APPLICATION NUMBER: US

PRIOR FILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 33

LENGTH: 9

MARCH OF SEQ ID NOS: 136
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Sequence
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CTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-918-243-33
                US-10-437-963-110905
US-10-425-115-348070
US-10-425-115-348070
US-10-425-115-218429
US-10-425-115-218429
US-10-425-115-218429
US-10-425-115-227327
US-10-820-155-64
US-10-820-155-64
US-10-820-155-74
US-10-820-155-74
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US-10-424-599-265948
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                                                                                                                                                                                                                                                                                US-10-820-155-4
US-10-820-155-24
US-10-820-155-54
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Best Local Similarity 100,
Matches 9; Conservative
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US-10-262-511-96
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APPLICANT:
APPLICANT:
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APPLICANT:
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Sequence 33, Application US/10831075

Sequence 33, Application US/10831075

Publication No. US20040224891A1

GENERAL INFORMATION:
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
FILE REPRENCE: D6223CIP/C/D/CIP3
CURRENT FILING DATE: 2004-04-23

PRIOR PRILING DATE: 2004-04-23

PRIOR FILING DATE: 2003-02-21

NUMBER OF SEQ ID NOS: 140
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Publication No. US20030223973A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
TITLE OF INVENTION: Martin J.
TITLE OF INVENTION: Marthods for the early diagnosis of ovarian cancer FILE REFERENCE: D6223CIP/C/D/CIP2
CURRENT APPLICATION NUMBER: US/10/372,521
CURRENT FILING DATE: 2003-02-21
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 136
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                                                                                                                  Query Match 100.0%; Score 40; DB 3; Length 9; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 9; Conservative 0; Mismatches 0; Indels
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                  FEATURE:
NAME/KEY: CHAIN
OTHER INFORMATION: Residues 5-13 of the SCCE protein US-09-905-083-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-10-372-521-33
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OTHER INFORMATION: Residues 5-13 of the SCCE protein
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1 LLLPLQILL 9
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEX: DOMAIN
LOCATION: (61)...(78)
OTHER INFORMATION: Serine proteases trypsin family, histidine proteins. domain
OTHER INFORMATION: 20, raw score of 11.96
FEATURE:
NAME/KEX: DOMAIN
LOCATION: (36)...(133)
OTHER INFORMATION: Trypsin domain identified by PPam, accession name trypsin, E-
OTHER INFORMATION: Trypsin domain identified by PPam, accession name trypsin, E-
US-10-450-763-53737
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                                                                                                                                                                                                                                                                                  APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR PLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUBCOM
SEQ ID NO 53737
                         IndelB
100.0%; Pred. No. 1.7e+06; tive 0; Mismatches 0;
                                                                                                                                                                                                                  Sequence 53737, Application US/10450763 Publication No. US20050196754A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 96, Application US/10262511; Publication No. US20040038223A1
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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Malyankar, Uriel M.
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Anderson, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
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Best Local Similarity 100.
Matches 9; Conservative
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Li, Li
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FRIOR APPLICATION NUMBER: 60/326,483
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR FILING DATE: 2002-10-19
PRIOR PELING DATE: 2002-04-19
PRIOR PELING DATE: 2002-05-19
PRIOR PELING DATE: 2002-05-17
PRIOR PELING DATE: 2002-05-17
PRIOR PELING DATE: 2002-05-16
PRIOR PELING DATE: 2002-04-17
PRIOR PELING DATE: 2002-04-17
PRIOR PELING DATE: 2002-04-19
PRIOR PELING DATE: 2002-04-19
PRIOR PELING DATE: 2002-04-19
PRIOR PELING DATE: 2002-04-19
PRIOR PELING DATE: 2001-10-05
                                                                                                                               APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: Shinkets, Richard A.
APPLICANT: Chinkets, Richard A.
APPLICANT: Leach, Markin D.
APPLICANT: Berghe, Constance
APPLICANT: Berghe, Constance
TILLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
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CURRENT FILING DATE: 2001-06-26
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Patent No. USZO020064856A1
GENERAL INFORMATION:
APPLICANT: WHYTE, DAVID
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CANNING GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 036602/1214
Zerhusen, Bryan D.
Anderson, David W.
Zhong, Mei
                                                                                                         Catterton, Elina
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Best Local Similarity 100.
Matches 9; Conservative
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APPLICANT: Rethenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERENCE: 12402-462C
CURRENT APPLICATION NUMBER: 60/326,483
PRIOR PELLING DATE: 2003-05-28
PRIOR PELLING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR PELLING DATE: 2001-10-09
PRIOR PELLING DATE: 2002-06-19
PRIOR PELLING DATE: 2002-06-16
PRIOR PELLING DATE: 2002-04-17
PRIOR PELLING DATE: 2001-10-05
PERUOR PELLING PERUOR PERUOR PELLING DATE: 2001-10-05
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Publication No. US20040038223A1
GENERAL INFORMATION:
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
Ort, Tatiana
                     Miler, Charles B. Rastelli, Luca Stone, David J. Pena, Carol E. A. Shenoy, Suresh G.
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
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   Catterton, Elina
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CORGANISM: Homo sapiens
US-10-262-511-96
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US-10-262-511-92
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPFRARE: FREESED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIPICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/210,084
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ 1D NO: 3:
US-09-764-762-3
; PRIOR APPLICATION NUMBER: 60/214,047; PRIOR FILING DATE: 2000-06-26; NUMBER OF SEQ ID NOS: 150; SEQ ID NO 98; LENGTH: 253; LENGTH: 253; TYPE: PRT; CARANESH: HOMO SADIENSUS ONGANISM: HOMO SADIENSUS ONGANISM: HOMO SADIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09764762; Patent No. US20020068341A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
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Best Local Similarity
Matches 9; Conserv
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US-09-764-762-3
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LLLPLQILL 13

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Sequence 2, Application US/10071214

Publication No. US20030066099A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN FILE REPERENCE: HANSSON=3A
CURRENT APPLICATION NUMBER: US/10/071,214
CURRENT FILING DATE: 2001-02-09
PRIOR PELLOR DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTLY OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 48, Application US/10071214
| Sequence 48, Application US/10071214
| Sequence 48, Application No. US20030066099A1
| Publication No. US20030066099A1
| GENERAL INFORMATION:
| APPLICANT: HANSSON, Lennart
| APPLICANT: GEGLRUD, TOIDJOIN
| TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
| TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
| FILE REFERENCE: HANSSON-3A
| CURRENT PELICATION NUMBER: US 60/267,422
| PRIOR FILING DATE: 2001-02-09
| NUMBER OF SEQ ID NOS: 50
| SOFTWARR: PARCENTION OF SEQ ID NOS: 50
| SOFTWARR: PARCENTION OF SEQ ID NOS: 50
| CONTINUED OF SEQ ID NOS: 50
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Pred. No. 36;
0; Mismatches 0
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US-10-264-283-90
; Sequence 90, Application US/10264283
; Publication No. US20030144494A1
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Best Local Similarity 100.0%;

Matches 9; Conservative 0
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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APPLICANT: Glynne, Richard
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Marked of Diagnosis of Cancer.
ITILE OF INVENTION: Methods of Screening for Modulators of Cancer.
ITILE OF INVENTION: Whomber: US 60/10/295,027

TITLE OF INVENTION: Whomber: US 60/350,027

CURRENT APPLICATION NUMBER: US 60/350,666
FRIOR PILING DATE: 2001-11-13
FRIOR APPLICATION NUMBER: US 60/335,394
FRIOR APPLICATION NUMBER: US 60/335,394
FRIOR APPLICATION NUMBER: US 60/335,394
FRIOR PILING DATE: 2001-11-29
FRIOR PILING DATE: 2001-11-29
FRIOR PILING DATE: 2001-11-29
FRIOR PILING DATE: 2001-12-14
FRIOR APPLICATION NUMBER: US 60/347,211
FRIOR PILING DATE: 2002-01-06
FRIOR PILING DATE: 2002-01-06
FRIOR PILING DATE: 2002-01-10
FRIOR PILING DATE: 2002-01-06
FRIOR PILING DATE: 2002-01-06
FRIOR PILING DATE: 2002-01-06
FRIOR PILING DATE: 2002-01-06
FRIOR FILING DATE: 2002-01-10
FRIOR PILING DATE: 2002-01-10
FRIOR FILING DATE: 2002-01-10
                         APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF OVARIAN CANCER
FITLE REFERENCE: 210121.590
CURRENT PILLING DATE: 2002-10-02
CURRENT FILLING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 111
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 90
LENGTH: 253
TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-283-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 40; DB 4; Length 253; 100.0%; Pred. No. 36; 0; Indels tive 0; Mismatches 0; Indels
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Publication No. US20030232350A1
GRNERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Afar, Daniel
APPLICANT: Giasherg, Wendy M.
APPLICANT: Giasherg, Wendy M.
APPLICANT: Gish, Kurt C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 9; Conservative
APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LLLPLOILL 9
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Query Match 100.0%; Score 40; DB 4; Length 253; Best Local Similarity 100.0%; Pred. No. 36; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 1 LLLPLQILL 9 ||||||||| 5 LLLPLQILL 13 දු දු

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Search completed: March 11, 2006, 01:37:22 Job time : 69.4444 secs

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LLLPLQILL 13
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Matches 9; Conserv
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Sequence 1151, Ap
Sequence 1355, Ap
Sequence 2, Appli
Sequence 1350, Ap
Sequence 1351, Ap
Sequence 7, Appli
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Sequence 14, Appl
Sequence 17, Appl
Sequence 98, Appl
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Sequence 9, Appli
Sequence 1151, Ap
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                                                                                                                                                     Description
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1: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
                      GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-096-568A-27351
US-11-096-568A-27351
US-11-096-568A-27351
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US-10-973-115B-136
US-10-973-115B-136
US-10-973-115B-360
US-10-973-115B-360
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-11-051-720-1351
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB
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                                                                                                                                                            Run on:
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Sequence 1352, Ap Sequence 1356, Ap Sequence 1356, Ap Sequence 1354, Ap Sequence 1354, Ap Sequence 1439, Ap Sequence 16, Appl Sequence 26, Appl Sequence 26, Appl Sequence 2450, Ap li Sequence 2854, Appli
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Sequence 14, Application US/10412748

Sequence 14, Application US/10412748

Publication No. US20060035219A1

GENERAL INPORMATION:
APPLICANT: Queensland University of Technology
APPLICANT: Clements, Judith A

TITLE OF INVENTION: Aberrant Kallikrein Expression
FILE REPERENCE: DAVI172.0034US

CURRENT APPLICATION NUMBER: US/10/412,748

CURRENT FILING DATE: 2003-04-09

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin version 3.2

SEQ ID NO 14

LENGTH: 233

TYPE: PRI
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US-10-412-748-11
Sequence 11, Application US/10412748
Sequence 11, Application US/10412748
Publication No. US20060035219A1
GENERAL INFORMATION:
APPLICANT: Clements, Judith A
TITLE OF INVENTION: Aberrant Kallikrein Expression
FILE REFERENCE: DAVI172.003AUS
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US/10/412,748
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: AU PS1616/02
PRIOR APPLICATION NUMBER: AU PS1616/02
SEQ ID NO. 11
SOFTWARE: PatentIn version 3.2
LENGTH: 253
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
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US-11-051-720-1353
US-11-051-720-1439
US-11-051-720-1439
US-11-102-240-16
US-11-102-240-16
US-11-133-136-26
US-11-072-512-3255
US-11-072-512-3255
US-11-131-234-5
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Query Match
Best Local Similarity 87.5
Trans 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
                       S LLLPLQILL 13
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US-11-096-568A-27353
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                                      Query Match 100.0%; Score 40; DB 6; Length 253; Best Local Similarity 100.0%; Pred. No. 1.6; Matches 9; Conservative 0; Mismarches 7. 7.1.
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                                                                                                                                                                                                                                                                           Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REPERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR PILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin version 3.2
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US-11-037-243-98

Sequence 98, Application US/11037243

Sequence 98, Application US/11037243

Publication No. US20050287546A1

GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: GENEREEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: GENEREEL, SEAN
APPLICANT: GENEREEL, SEAN
APPLICANT: GURNENCY DERRY
APPLICANT: GURNENCY DERRY
APPLICANT: SUDARSANAM, SUCHA
FILE REFERENCE: 036602/1214
CURRENT APPLICATION NUMBER: US/09/889,615
PRIOR APPLICATION NUMBER: US/09/889,615
PRIOR FILING DATE: 2000-06-26
PRIOR PRILOR DATE: 2000-06-26

NUMBER OF SEQ ID NOS: 150

SEQ ID NO 98

LENGTHARE: PATENTIN VEY. 2.1

SEQ ID NO 98

LINGTON DATE: SUDARSANAM
SEQ ID NO 98
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LLLPLQILL 13
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ORGANISM: Homo sapiens
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                                                                                                                                         1 LLLPLOILL 9
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ORGANISM: Human
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US-10-412-748-17
  ; ORGANISM: Hur
US-10-412-748-14
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Sequence 27354, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INFORMATION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I
TITLE OF INVENTION: Therby
FILE REPERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 27354
LENGTH: 71
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Publication No. US20060048240A1

GENERAL INFORMATION:
APPLICANT: Alexandrow, Nickolai et al.
APPLICANT: Alexandrow, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides FILE REFERENCE: 2750-1592PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 27391
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LOCATION: (1). (71)
OTHER INFORMATION: Ceres Seq. ID no. 13500184
                                                                                                                                                                                                                                                                                                                                                                                | FEATURE:
| NAME/KEY: misc feature
| LOCATION: (1). (71)
| OTHER INFORMATION: Ceres Seq. ID no. 5677704
| US-11-096-568A-27354
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GENERAL INFORMATION: APPLICANT: Alexandrov, Nickolai et al.
                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Arabidopsis thaliana
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ORGANISM: Arabidopsis thaliana
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Sequence 10163, Application US/11098686

Sequence 10163, Application US/11098686

GENERAL INFORMATION:

APPLICANT: Kapur, Vivek and Gebhart, Connie J.

TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES

TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING FILE REFERENCE: 09531-128001

CURRENT APPLICATION NUMBER: US/11/098,686

CURRENT FILING DATE: 2005-04-04
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                                                                                                         Score 33; DB 7; Length 125;
Pred. No. 16;
0; Mismatches 1; Indels
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Pred. No. 19;
1; Mismatches 1; Indels
    ; NAME/KEY: misc_feature
; LOCATION: (1)..(125)
; OTHER INFORMATION: Ceres Seq. ID no. 12415965
US-11.096-568A-23862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REPERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR PILING DATE: 2002-01-25
PRIOR PILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-11-05
                                                                                                                                                                                                                                                                                                                       US-11-072-512-2266; Application US/11072512; Sequence 2266, Application US/11072512; Publication No. US20060029945A1; GENERAL INFORMATION: APPLICANT: ISOGAI, TAKAO
                                                                                                                                                                                                                                                                                                                                                                                                                            SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YUKI
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SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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88.9%;
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NAGAI, KEIICHI
IRIE, RYOTARO
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SEQ ID NO 2266
                                                                                                            Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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US-11-072-512-2266
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APPLICANT:
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APPLICANT:
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Sequence 27390, Application US/11096568A

Sequence 27390, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

TITLE OF INVENTION: 2105-04-01

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 27390
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| Sequence 23862, Application US/11096568A
| Sequence 23862, Application US/11096568A
| Publication No. US20060048240A1
| GENERAL INFORMATION:
| APPLICANT: Alexandrow, Nickolai et al.
| TITLE OF INVENTION: Therby
| TITLE OF INVENTION: Therby
| TITLE OF INVENTION: Therby
| FILE REFERENCE: 2750-1522PUS2
| CURRENT APPLICATION UNDER: US/11/096,568A
| CURRENT FILING DATE: 2005-04-01
| NUMBER OF SEQ ID NOS: 34471
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REPERENCE: 2.75-0-1592PUSC
CURRENT APPLICATION NUMBER: US.11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 27353
LENGTH: 85
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                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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Pred. No. 6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
; LOCATION: (1)...(85)
; OTHER INFORMATION: Ceres Seq. ID no. 13500183
US-11-096-568A-27390
                                                                                                                                                                                                                                     NAME/KEY: misc_feature
| LOCATION: (1)..(85)
| JOHEN INDEMATION: Ceres Seq. ID no. 5677703
| US-11-096-568A-27353
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ORGANISM: Zea mays subsp. mays
FEATURE:
                                                                                                                                                                                                ORGANISM: Arabidopsis thaliana
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87.5%;
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Best Local Similarity 87.5
Herban 7; Conservative
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MLLPLQIL 22
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APPLICANT: Wood, William I.
APPLICANT: Dang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SAME
FILE REPRENCE: 39870-3330R102300C1
CURRENT APPLICATION NUMBER: US/10/973,115B
CURRENT FILING DATE: 2004-10-22
            FILE REFERENCE: P3330RIC128
CURRENT APPLICATION: ACLIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 12002-04-24
FRIOR APPLICATION NUMBER: 60/056974
FRIOR APPLICATION NUMBER: 60/05911
FRIOR APPLICATION NUMBER: 60/059113
FRIOR APPLICATION NUMBER: 60/059113
FRIOR APPLICATION NUMBER: 60/059115
FRIOR APPLICATION NUMBER: 60/059117
FRIOR PILING DATE: 1997-09-17
FRIOR PELING DATE: 1997-09-17
FRIOR PILING DATE: 1997-09-17
FRIOR FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31; DB 6; Length 278;
Pred. No. 85;
1; Mismatches 1; Indela
          TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 10/145,747
PRIOR FILING DATE: 2002-05-14
PRIOR PELICATION NUMBER: US 10/028,072
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: PCT/US00/32678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 136, Application US/10973115B Publication No. US20060040351A1 GENERAL INPORMATION: APPLICANT: Baker, Kevin P. APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maureen APPLICANT: DeForge, Laura
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Tumas, Daniel
Watanabe, Colin K.
Wood, William I.
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Best Local Similarity 77.8%;
Matches 7; Conservative 1
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Gerritsen, Mary E.
Goddard, Audrey
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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; ORGANISM: Homo Sapien
US-10-131-826A-136
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Fublication No. US20050272054A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHIEMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DETECTION AND USES THEREOF

TILLE REPERENCE: CLO01559

CURRENT PILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SEQ ID NO 1024

SEQ ID NO 1024
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 40;
1; Mismatches 1; Indels
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PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: PASLESQ for Windows Version 4.0
SEQ ID NO 10163
LENGTH: 202
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                                                                                                                                                                                                                                                                                                             80.0%;
77.8%;
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77.8%;
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Watanabe, Colin K
Wood, William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Filvaroff, Ellen
Gao, Wei-Qiang
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Gurney, Austin L.
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Best Local Similarity 77.6
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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146 LLLPLTILI 154
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; ORGANISM: Homo sapiens
US-10-995-561-1024
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                                                                                                                                                                                                                                                                                                                                                                  Query Match 77.5%; Score 31; DB 6; Length 278; Best Local Similarity 77.8%; Pred. No. 85; Matches 7; Conservative 1; Mismatches 1; Indels
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US-10-878-5564-162
is advance 162, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
    TITLE OP INVENTION:
    TITLE OP INVENTION:
    FILE REFERENCE: 21762
; CURRENT FILION NUMBER: US/10/878,556A
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: ParentIn version 3.1
; SEQ ID NO 162
; LENGTH: 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CRGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: sw_hum/ncbl_human
BATABASE BRITEY DATE: 1993-07-01
US-10-878-556A-162
| PRIOR FILING DATE: 2000-12-01
| PRIOR APPLICATION NUMBER: US 09/581,742
| PRIOR FILING DATE: 2000-06-16
| PRIOR PILING DATE: 2000-03-02
| PRIOR FILING DATE: 2000-03-02
| PRIOR APPLICATION NUMBER: US 60/135,736
| PRIOR APPLICATION NUMBER: US 60/135,736
| PRIOR FILING DATE: 1999-05-25
| PRIOR FILING DATE: 1999-05-05
| NUMBER OF SEQ ID NOS: 550
| SEQ ID NO 136
| LENGTH: 278
                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
US-10-973-1158-136
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13 LELPELLEL 21
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Search completed: March 11, 2006, 01:38:40 Job time : 9 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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protein search, using sw model OM protein

March 11, 2006, 00:10:50; Search time 86.6667 Seconds (without alignments) 45.628 Million cell updates/sec Run on:

US-09-905-083A-34 score: Title: Perfect :

1 VLVNERWVL 9 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2443163 segs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp2005s:\* A Geneseq\_21:\*

1: geneseqp1990s:\*
2: geneseqp1990s:\*
3: geneseqp2000s:\*
5: geneseqp2001s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	• .	Description	Aae08239 Human str	Human	Ada05740 Human NOV	Human	Novel	Ada05738 Human NOV	Human	Ada05736 Human NOV	0 Human	Human	Adn62908 Human NOV	Adv21100 Human str	2 Human	Human	Adn62906 Human NOV	Human	Adn62896 Human NOV	Human	Adn62898 Human NOV	Aar67888 Human str	Aaw05383 Human amy	Human	Abb84406 Human SCC	Aau82740 Amino aci
SUMMARIES		ΩI	AAE08239	ADR68795	ADA05740	ADN62904	ABG23378	ADA05738	ADN62902	ADA05736	ADN62900	ADA05744	ADN62908	ADV21100	AAB98502	ADA05742	ADN62906	ADA05732	ADN62896	ADA05734	ADN62898	AAR67888	AAW05383	ABB84421	ABB84406	AAU82740
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		Length DB	σ	σ	97	97	136	181	181	198	198	224	224	224	225	247	247	250	250	252	252	253	253	253	253	253
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		Score	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47
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Abu07440 Protein d Abu07471 Protein d Abr58471 Human etr			Human Human	Aab21326 Human HSC Aae08245 Human str		Adr68811 Human str Abb84419 Bovine SC	Abb84420 Porcine S Aay28590 Human Fac	Aae39994 Human adi Adn04134 Antipsori
ABU07440 ABU07471 ABR58471	ADB80484 ADJ68833 ADN39180	ADL06515 ADN04182 ADR72880	ADY67588 AEC00353	AAB21326 AAE08245	AAE08255 ADR68801	ADR68811 ABB84419	ABB84420 AAY28590	AAE39994 ADN04134
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25 26 27	3 6 8 3 7 8	1000	19 19 19 19 19 19 19 19 19 19 19 19 19 1	36 37	38 39	40 41	42 43	4.4 5.

## ALIGNMENTS

Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia. Human stratum corneum chymotrypsin enzyme peptide #3 (residues 58-66). AAE08239 standard; peptide; 9 AA. (first entry) 01-NOV-2001 AAE08239; RESULT 1 AAE08239 

Homo sapiens.

WO200159158-A1.

16-AUG-2001.

07-FEB-2001; 2001WO-US003977.

11-FEB-2000; 2000US-00502600.

(UYAR-) UNIV ARKANSAS.

O'brien TJ;

WPI; 2001-514676/56.

Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.

Claim 25; Page 103; 127pp; English.

The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide

Sequence 9 AA;

antidiabetic; anorectic; antibacterial; virucide;

Ä.

(first entry)

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immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoletic disorder; dyslipidaemia.
                                                                            Human NOV18e protein SEQ ID NO:100
  ADA05740 standard; protein; 97
                                                                                                                                                                                                                                                                     02-OCT-2002; 2002WO-US031373
                                                                                                                                                                                                                     WO2003029424-A2.
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12-0CT-2001;
15-0CT-2001;
17-0CT-2001;
18-0CT-2001;
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09-OCT-2001;
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24-OCT-2001;
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16-MAY-2002;
                                                                                                     human; NOVX;
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19-APR-2002;
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                                                  06-NOV-2003
                                                                                                                                                                                                                                              10-APR-2003
                          ADA05740;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel method for vaccinating an individual against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating an individual with a SCCE peptide, which elicits an immune response in the individual with a SCCE peptide, which elicits an immune response in chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or at risk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligonucleotide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or pancreatic cancer, and other cancers in which SCCE is overexpressed. The peptides are also useful in the monitoring and development of immunotherapies for ovarian and other malignancies. The present sequence represents a peptide fragment of serine protease SCCE (stratum corneum corneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
                                                                                                                                                                                                                     Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:34.
                             Gaps
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                                                                                                                                                                                                                                            serine protease; stratum corneum chymotrytic enzyme; SCCE; immune response; ovarian cancer; lung cancer; prostate cancer; pancreatic cancer; colon cancer.
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 100.0%; Score 47; DB 4; Length 9; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; SEQ ID NO 34; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Santin A;
                                                                                                                                          ADR68795 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                         20-FEB-2004; 2004WO-US005134.
                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2003; 2003US-00372521
                                                                                                                                                                                            02-DEC-2004 (first entry)
Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     O'brien TJ, Cannon MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                            (UYAR-) UNIV ARKANSAS
                                                    1 VLVNERWVL 9
                                                                  VLVNERWVL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chymotrytic enzyme)
                                                                                                                                                                                                                                                                                                                         WO2004075723-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9 AA;
                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                    ADR68795;
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                                                                                                                  RESULT 2
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2001US-0327435P. 2001US-0327449P. 2001US-0327917P. 2001US-0328029P. 2001US-0328044P.

2001US-0329414P. 2001US-0330142P. 2001US-0330309P. 2001US-0341058P.

2001US-0339266P

2001US-0328056P. 2001US-0328849P.

2001US-0343629P. 2001US-0349575P. 2001US-0346357P. 2002US-0373260P.

2002US-0373815P. 2002US-0373817P. 2002US-0373826P.

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New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                          Dipippo VA;
                                                                                                                                                                                                                                                                                Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 171; 586pp; English.
2002US-0381642P.
2002US-0383656P.
                                                                           2002US-0383831P.
                                                                                                                                               2002US-00262511
                                                                                                                                                                                                                       (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2003-381626/36.
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                                                                               29-MAY-2002;
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Best Local Similarity 100. Matches 9; Conservative

1 VLVNERWVL 9 ||||||||||||||| vl.vnerwvl 9

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2002US-0373884P. 2002US-0374977P. 2002US-0381037P.

2002US-0381038P. 2002US-0381042P.

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(RIEG/)
(SPAD/)
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(PEYM/)
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(LEAC/)
(AGEE/)
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(GANG/)
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                The present invention describes NOVX proteins, where X can be 1 to 55 cd eac. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) at the composition described above; (3) an isolated nucleic acid described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cellally comprising the nucleic acid molecule described above; (5) a cellally brinds to the polypeptide described above; (5) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a disease associated with altered levels of expression of the above; (10) a method for identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for a pathology associated with the polypeptide; (11) a method of careening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (11) a method for modulation or preventing a pathology associated with the above polypeptide; (12) a method for mammal; and (14) a method for producing the above polypeptide in a correspondent and (14) a method for producing the above polypeptide in a manulation and (14) a method for producing the above polypeptide or preventing a pathology associated with the above polypeptide or the nucleic syndrome associated with a human disease. The polypeptide or the nucleic avid molecule may be used to diagnose, treat or prevent metabolic activities, and can be used in gene therapy. The card molecule may be used to diagnose, treat or prevent metabolic dyshipidaemias. The nucleic acids can also be used as hybridisation and present sequence a pathore and substances and as diabetes or obesity, infections, cancer, or prevention.
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05-0CT-2001; 2001US-0327435P.
05-0CT-2001; 2001US-0327449P.
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Matches 9; Conservative
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Dipippo VA;
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                                      2001US-0328849P.
2001US-032944P.
2001US-03303042P.
2001US-0330309P.
2001US-033226F.
2001US-0343629P.
2001US-0343629P.
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2002US-0373860P.
2002US-0373815P.
2002US-0373817P.
2002US-0373826P.
2002US-0373844P.
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2002US-0381038P.
2002US-0381042P.
2002US-0381642P.
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2002US-0383831P.
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GANGOLLI E A.
RIEGER D K.
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SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
LEACH M D.
AGER M L.
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MALYANKAR U M.
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PATTURAJAN M.
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EDINGER S R.
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ANDERSON D W.
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CATTERTON E.
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PEYMAN J A
KEKUDA R.
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09-OCT-2001; 2
12-OCT-2001; 2
15-OCT-2001; 2
17-OCT-2001; 2
                                                                                                                                                                                           22-OCT-2001; 24-OCT-2001; 24-OCT-2001; 29-OCT-2001; 20-OCT-2001; 20-OC
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NoVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the abberrant expression and activity of NoVX polypeptides. For example, NoVX polypeptides and condition in human related to the abberrant expression and activity of NoVX polypeptides and conversely, antisense NA molecules may be administered to down regulate expression of NoVX polypeptides by binding with the cells own genes and preventing their expression. NoVX bolymeticotides and complementary sequences may also be used as DNA probbe in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NoVX polypeptides may also be used as untigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NoVX. The trie production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NoVX.

Toplypeptides. The anti-NoVX polypeptide antibodies may also be used as anti-NoVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NoVX in samples. NoVX polypeptides antibodies may be used in this way to prevent, diagnose and treat: metabolic disorders, immune disorders, disorders, anorexia, cancer, cancer-associated cachexia, neurodegenerative disorders, and the various dyslipidaemias, metabolic and substances associated with obesity, the metabolic syndrome X and the various dyslipidaemias, metabolic man and the various dyslipidaemia, metabolic man and the various dyslipidaemias, metabolic man and the various dyslipidaemias, metabolic man and the various dys
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diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represents the amino acid sequence of a human NOVX protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 47; DB 8; Length 97; 100.0%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  may also be used as antibacterial agents. T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                            Claim 1; SEQ ID NO 100; 395pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #23369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG23378 standard; protein; 136 AA.
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Best Local Similarity luv.
9, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 97 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200175067-A2.
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromesome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food polypeptide in tissue, as molecular weight markers and as a food polypeptide in tissue, as molecular weight markers and as a food polypeptide and polymucleotide sequences have applications in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The colypeptide and polymucleotide sequences have applications of mutations diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and produce other types of data and produce of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 53737; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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2001US-0327449P.
2001US-0327917P.
2001US-0328029P.
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Best Local Similarity 10v.v.

Best Accal Similarity 10v.v.
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N-PSDB; AAS87565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003029424-A2.
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09-OCT-2001;
09-OCT-2001;
                                                                                                                                                                                      biodiversity.
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05-OCT-2001;
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disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tisuse typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the

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Gaps

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0; Indels

0; Mismatches

9; Conservative

Query Match Best Local Similarity Matches 9; Conserv

present invention.

8888888

Sequence 181 AA;

100.0%; Score 47; DB 6; Length 181; 100.0%; Pred. No. 2.6;

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09-OCT-2001; 2001US-0328056P.
12-OCT-2001; 2001US-0328849P.
15-OCT-2001; 2001US-0329844P.
17-OCT-2001; 2001US-0330142P.
18-OCT-2001; 2001US-0330309P.
24-OCT-2001; 2001US-0343629P.
24-OCT-2001; 2001US-0343629P.
29-OCT-2001; 2001US-0343629P.
10-NOV-2001; 2001US-0343629P.
17-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373817P.
19-APR-2002; 2002US-0373817P.
19-APR-2002; 2002US-0373817P.
                                                                                                   16-MAY-2002; 2002US-0381037P.

16-MAY-2002; 2002US-0381038P.

17-MAY-2002; 2002US-0381642P.

28-MAY-2002; 2002US-0381642P.

29-MAY-2002; 2002US-0383666P.
                                                                                                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                    WPI; 2003-381626/36.
N-PSDB; ADA05737.
                                                                                                                                                                                                                                                           pharmacogenomics
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Dipippo VA; New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or M, Catterton B; Shenoy SG; Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM, Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipig Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

Guo. X;

Claim 1; Page 171; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOV1). Also described: (1) a composition comprising a polypeptide

coestibled above and a carrier; (2) a kit comprising in one or more

containers, the composition described above; (3) an isolated nucleic acid

containers the muclic acid molecule described above; (5) a cell

comprising the nucleic acid molecule described above; (5) a cell

comprising the above vector; (6) an antibody that immunospecifically

binds to the polypeptide described above; (7) methods for determining the

comprising the above vector; (6) an antibody that immunospecifically

comprising the above vector; (6) an antibody that immunospecifically

comprising the above vector; (6) an antibody that immunospecifically

comprising the above vector; (6) an antibody that immunospecifically

comprising the above vector; (6) an antibody that immunospecifically

comprising the above polypeptide or nucleic acid molecule in a

disease associated with altered lavels of expression of the above

comprising to a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for a bearrant physiological interactions of the polypeptide; (11) a method of

compression of activity or of latency or predisposition to a pathology associated with the above polypeptide. Novx

commanal; and (14) a method for producing the above polypeptide. Novx

commanal; and (14) a method for producing the above polypeptide. Novx

commanal; and (14) a method for producing the above polypeptide or the nucleic and antilipaemic activities, and crapic antiparterial, viruciae, and converse or immunomodulator, cycostatic, and crapic and properties and antilipaemic activities, and crapic and properties or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic

control molecule may be used to observe treater prevent metabolic. neurodegenerative disorders such as Alzheimer's disease or Parkinson's

(MIELL/)

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human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dislipidaemia; metabolic syndrome X;
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2002US-0373817P.
2002US-0373826P.
2002US-0373884P.
2002US-0374977P.
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2002US-0383656P
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25-JUN-2002; 2002US-0391335P
                                                                                                                                                                                                                                                                                    01-JUL-2004 (first entry)
                                                39 VLVNERWYL 47
1 VLVNERWVL 9
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MILLET I.
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15-OCT-2001; 2
17-OCT-2001; 2
18-OCT-2001; 2
22-OCT-2001; 2
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09-OCT-2001;
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01-NOV-2001;
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MILLER C E.
RASTELLI L.
STONE D J.
PRIN C E A.
SHENOY S G.
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SHENOY S G.
CHENERER R A.
LEACH M D.
                        SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
                                                                                                                   EISEN A.
GANGOLLI E A.
                                                                                                      AGEE M L.
BERGHS C.
DIPIPPO V A.
                    PATTURAJAN M.
                                                                                                                              SPADERNA S K.
                                                 ZERHUSEN B D.
ANDERSON D W.
                                                         ZHONG M.
CATTERTON E.
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The invention relates to isolated NOVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and continuous control or activity of NOVX by supplementing the patient our control or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX polypeptide and complementary sequences may also be used as DNA probabe in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists may also be used as anti-NOVX polypeptide antibodies, agonists and antagonists may also be used as diagnose and treat: metabolic disorders, diaberes, obesity, infectious disorders, anorexia, cancer, cancer-associated cancexia, neurodegenerative disorders, and the various dyslipidaemias, metabolic disorders, haematopoletic disorders, parkinson's bisorder, immune disorders, and the various dyslipidaemias, metabolic distracts, the metabolic syndrome X and Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Raetelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen A, Gangolli EA, Rieger DK, Spaderna SK; Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease. Claim 1; SEQ ID NO 98; 395pp; English.

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                                                                                                                                                                                                                                                                                                    immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obseity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoletic disorder; dyslipidaemia.
                                                                                           Gaps
            present sequence
wasting disorders associated with chronic diseases and various They may also be used as antibacterial agents. The present sequrepesents the amino acid sequence of a human NOVX protein.
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                                                                                                                                                                                                                                                                                           human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                                   100.0%; Score 47; DB 8; Length 181;
100.0%; Pred. No. 2.6;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                 ADA05736 standard; protein; 198 AA.
                                                                                                                                                                                                                                                                  Human NOV18c protein SEQ ID NO:96.
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2001US-0328849P.
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2001US-0330142P.
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2001US-0349575P.
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2002US-0373815P.
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                                                                                                                                                                                                                                             06-NOV-2003 (first entry)
                                                         Query Match
Best Local Similarity luv.
                                                                                                                                         39 VLVNERWUL 47
                                                                                                                  1 VLVNERWVL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CURA-) CURAGEN CORP
                                              Sequence 181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                WO2003029424-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-OCT-2001; 2
09-OCT-2001; 2
12-OCT-2001; 2
15-OCT-2001; 2
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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24-OCT-2001;
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19-APR-2002;
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anorexia; cancer, cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;

wasting disorder

US2004038223-A1.

26-FEB-2004

Homo sapiens.

01-OCT-2002; 2002US-00262511

02-OCT-2001; 05-OCT-2001; 09-OCT-2001;

05-OCT-2001;

09-OCT-2001; 2 09-OCT-2001; 2 12-OCT-2001; 2 15-OCT-2001; 2

09-OCT-2001;

human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;

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The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comportising; in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a forest method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for method of identifying a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of serening for a modulator of activity or of latency or presipposition to a pathology associated with the polypeptide; (12) a method of mammal; and (14) a method for producing the above polypeptide in a pathology associated with the above polypeptide; (10) a method of producing the above polypeptide in a method of producing the above polypeptide or the aniquator, cytostatic, anotropic, anitheresing and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a method or provent metabolic and antilipaemic activities, and can be used in gene therapy. The collegenerative disorders such as Aliabeimer's disease or Parkinson's disease such as diabetes or obesity, infections, cancering and collegenerative disorders such as Aliabeimer's and vale arious and disperse or obesity in farmance and an inventive metabolic acide can also be used as hybridisation and probes, in chromosome mapping, issue typing, preventive metabolic and probes, in chromosome 
Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenborg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                            New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 170; 586pp; English.
                                                                                                                                                                                               WPI; 2003-381626/36.
N-PSDB; ADA05735.
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                                                                                                                                                                                                                                                                                                                                                                pharmacogenomics.
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2001US-0326483P.
2001US-0327435P.
2001US-0327435P.
2001US-0328024P.
2001US-0328044P.
2001US-0328044P.
2001US-0328044P.
2001US-0338049P.
2001US-0338049P.
2001US-0338049P.
2001US-034805P.
2001US-034905P.
2001US-034905P.
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2001US-034905P.
2001US-034905P.
2001US-034905P.
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2002US-0381042P.
2002US-0381642P.
2002US-0383656P.
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2002US-0373817P.
2002US-0373826P.
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2002US-0374977P.
2002US-0381037P.
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25-JUN-2002; 2002US-0391335P
                                                                                                                                                                                                                                                                                                                                                                                 EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MILLER C B.
RASTELLI I.
STONE D J.
PENA C B A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
                                                                                                                                                                                                                                                                                                                                                                                                             GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                             GUO X.
PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                          MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                    ZHONG M.
CATTERTON E.
                                                                                                                                                                                                                                                                                                                   SMITHSON G.
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AGEE M L.
BERGHS C.
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22-OCT-2001;
24-OCT-2001;
24-OCT-2001;
29-OCT-2001;
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(AGEE/)
(BERG/)
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(STON/)
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(SHEN/)
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(ROTH/)
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(LILL)
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ZHON/
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ADN62900 standard; protein; 198 AA.

9; Conservative

Matches

Query Match Best Local Similarity

[[[[]]]] VLVNERWVL 66

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RESULT 9 ADN62900

VLVNERWVL 9

01-JUL-2004 (first entry)

2XXXXXXXX

ADN62900;

Human NOV18c

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human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective;
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                                                                                                                             Claim 1; SEQ ID NO 96; 395pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human NOV18g protein SEQ ID NO:104.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADA05744 standard; protein; 224 AA
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                        SPADERNA S K.
                                                                                                                                                                                                                                                                                                                                                                                   1 VLVNERWVL 9
                                                                                      WPI; 2004-213931/20.
N-PSDB; ADN62899.
                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                           Sequence 198 AA;
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antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabbetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; Immune disorder; heemacopoietic disorder; dyslipidaemia.
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                                                                                                                                               WO2003029424-A2.
                                                                                                                                                                                                                                                                                                                                   09-OCT-2001;
09-OCT-2001;
09-OCT-2001;
                                                                                                          Homo sapiens
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22-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAY-2002
    The invention relates to isolated NOVX polypeptides and polynucleotides. NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and polynucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polynucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (agonists and antagonists) of the expression and activity of NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polymcleotide expression and activity of NOVX polypeptides. The anti-NOVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX diagnose and treat: metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer, associated cachexia, neurodegenerative diagnosers. Alzhaimer's Disease, Parkinson's Disorder, immune disorders, haematopoietic disorders and the various dyslipidaemias, metabolic disorders, the metabolic syndrome X and disturbances associated with obesity, the metabolic syndrome X and
                                                                                                                                                                                                              Dipippo VA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
                                                                                                                         Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                     Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                     EISEN A.
GANGOLLI E A.
RIEGER D K.
  DIPIPPO V A.
                 (EISE/)
(GANG/)
(RIEG/)
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2002US-0373815P. 2002US-0373817P.

2002US-0373884P. 2002US-0374977P.

2002US-0373826P

2002US-0381037P. 2002US-0381038P.

002US-0381042P

2002US-0383831P 2002US-00262511

2001US-0327435P. 2001US-0327449P. 2001US-0327917P. 2001US-0328029P. 2001US-0328044P.

2001US-0328849P.

2001US-0328056P 2001US-0329414P 2001US-0330142P

2001US-0330309P. 2001US-0341058P. 2001US-0339266P. 2001US-0343629P. 2001US-0349575P. 2001US-0346357P. 2002US-0373260P.

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ng M, Catterton E;
A, Shenoy SG;
Berghs C, Dipippo VA;
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                                        Malyankar UM;
                                                                                                                                                                                                                                                                                                                          New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing
Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li Patturajan M, Spytek KA, Edinger SR, Ellerman K, Mal Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Bergh Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 172; 586pp; English.
                                                                                                                                                                                                                                       WPI; 2003-381626/36.
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Gaps

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The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOVI). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule above; (8) methods for determining the parample; (8) methods for determining the presence of or predisposition to

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c a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of acreving for a medulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide above; (13) methods of treating or preventing a pathology associated with the above polypeptide. Now sequences have antidiabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a pathology associated with a buman disease. The polypeptide or the nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyelipidaemia; mecabolic syndrome X;
                                                                                                                                                                                                                                                                                                                  acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, hacmatopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 47; DB 6; Length 224; 100.0%; Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADN62908 standard; protein; 224 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-2001; 2001US-0326483P.
05-OCT-2001; 2001US-0327435P.
09-OCT-2001; 2001US-0327449P.
09-OCT-2001; 2001US-0328029P.
09-OCT-2001; 2001US-0328044P.
09-OCT-2001; 2001US-0328044P.
12-OCT-2001; 2001US-0328414P.
15-OCT-2001; 2001US-0329414P.
17-OCT-2001; 2001US-0329414P.
18-OCT-2001; 2001US-03391042P.
22-OCT-2001; 2001US-0339309P.
24-OCT-2001; 2001US-0341058P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100 es 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VLVNERWVL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wasting disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 224 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human NOV18g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADN62908;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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ADN62908
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated NOVX polypeptides and polynucleotides. NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and polynucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 104; 395pp; English.
               2001US-034637P.
2002US-0373260P.
2002US-0373817P.
2002US-0373817P.
2002US-0373864P.
2002US-0374977P.
2002US-0381037P.
2002US-0381038P.
2002US-0381038P.
2002US-0381038P.
2002US-0381042P.
2002US-0381042P.
2002US-0381656P.
                                                                                                                                                         2002US-0391335P
                                                                                                                                                                                                                                                                                                                                                                                                                  PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
LEACH M D.
                                                                                                                                                                                                                                                                                                 MALYANKAR U M.
                                                                                                                                                                                                                                                                  SPYTEK K A.
EDINGER S R.
ELLERMAN K.
                                                                                                                                                                                                                                              GUO X.
PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EISEN A.
GANGOLLI E A.
                                                                                                                                                                                                                                                                                                                                ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                    ZHONG M.
CATTERTON E.
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                                                                                                                                                                              SMITHSON G.
MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                           JI W.
MILLER C E.
RASTELLI L.
STONE D J.
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BERGHS C.
                                                                                                                                                                                                                                                                                                                       GORMAN L.
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                                                19-APR-2002; 2
19-APR-2002; 2
19-APR-2002; 2
22-APR-2002; 2
16-MAY-2002; 2
16-MAY-2002; 2
                                                                                                                           17-MAY-2002;
                                                                                                                                     28-MAY-2002;
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                                                                                                                                                          25-JUN-2002;
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(GANG/)
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                                                                                                                                                                                                                                                                                                                                                                                     (MILL/)
(RAST/)
                                                                                                                                                                                                                                                                                                                                                                                                                   (PENA/)
(SHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ROTH/)
(LEAC/)
(AGEE/)
                                                                                                                                                                                         (MILL/)
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                                                                                                                                                                                                                                                                                        ELLE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SHIM/)
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production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOWX polypeptides by binding with the cells own genes and preventing their expression. NOVX polynuclectides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and anteaponists) of the expression and activity of NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polypeptide antibodies and antibodies and activity of NOVX polypeptides. The anti-NOVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polynucleotides may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and the various dyslipidamias, metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein purification; PS133 protein; serine protease; prostate disease; andrology; genitourinary disease; prostatic cancer; cytostatic; protein therapy; chymotrypsin; enzyme.
                                                                                                                                                                                                                                                                                                                      disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 47; DB 8; Length 224; 100.0%; Pred. No. 3.3; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                          represents the amino acid sequence of a human NOVX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26. .42
/note = Catalytically functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83. .87
/note = Catalytically functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note = Catalytically functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human stratum corneum chymotrypsin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADV21100 standard; protein; 224 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-FEB-2001; 2001US-00789210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-00944483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COLPITTS T L. FRIEDMAN P N. GRANADOS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLASS M R.
RUSSELL J C.
STEWART K D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VLVNERWVL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 224 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COHEN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2004241646-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KLAS/)
(RUSS/)
(STEW/)
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(FRIE/)
(GRAN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                           New isolated polypeptides, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining predisposition to diseases or conditions of the prostate such as prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to human tumour antigen-derived gene 15 (TADG-15) protein and coding sequence (see AAH23601 and AAB98500). TADG-15 is an extracellular serine protease. It was found that TADG-15 is over
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene 15
                                                                                                                                                                                                                                     The invention relates to PS133 protein, a member of the human serine protease family and its corresponding nucleic acid sequence. PS133 polypeptide is useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to diseases or conditions of the prostate such as prostatic cancer. The present sequence is the human stratum corneum chymotrypsin protein. This sequence is used to align with PS133 consensus protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel extracellular serine protease, termed tumor antigen-derived gene protein overexpressed in carcinomas and DNA encoding it, for diagnosis, treatment, prevention of cancer, particularly breast, ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; TADG-15; cytostatic; vaccine; ovarian tumour; cancer; tumour antigen-derived gene 15; serine protease; Stratum Corneum Chymotryptic Enzyme; SCCE.
                                Granados E, Klass MR;
                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 47; DB 9; Length 224; 100.0%; Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                          Example 1; SEQ ID NO 33; 96pp; English.
                              Friedman PN,
Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB98502 standard; protein; 225 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                              lpitts TL, E
Stewart KD,
                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYAR-) UNIV ARKANSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 VLVNERWYL 37
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(STRO/) STROUPE S D.
                                                                               WPI; 2005-011614/01
                                Colpitts
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VLVNERWVL
                                                                                                GENBANK; L33404.
                                                                                                                                                                                                                                                                                                                                                                          Seguence 224 AA;
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                              Cohen M, Co
Russell JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O'brien TJ,
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 $X444X444444X8X955555X8
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(CURA-) CURAGEN CORP.

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-expressed in ovarian tumours. TADG-15 protein or its fragments of 9-20 residues that lack TADG-15 protease activity are useful for vaccinating an individual against TADG-15, having, suspected of having or at risk of getting cancer. Furthermore, the TADG-15 gene can be used as a diagnostic or therapeutic target in cancer. The present sequence was used in a sequence homology alignment with the catalytic domain of TADG-15
                                                                                                                                                                                                                                                                                                                                                                                                                                               human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antipaemic; gene therapy; human disease; metabolic disorder; diabetes; obsety; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
                                                                                                                                                                            Gaps
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                                                                                                                                           100.0%; Score 47; DB 4; Length 225; 100.0%; Pred. No. 3.3;
                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immune disorder; haematopoietic disorder; dyslipidaemia
                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                   Human NOV18f protein SEQ ID NO:102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-2001; 2001US-0326483P.

05-OCT-2001; 2001US-0327435P.

05-OCT-2001; 2001US-0327449P.

09-OCT-2001; 2001US-0327917P.

09-OCT-2001; 2001US-0328029P.

09-OCT-2001; 2001US-0328044P.

12-OCT-2001; 2001US-0328044P.

15-OCT-2001; 2001US-0328044P.

15-OCT-2001; 2001US-0339144P.

17-OCT-2001; 2001US-034942P.

18-OCT-2001; 2001US-0341058P.

24-OCT-2001; 2001US-0341058P.

24-OCT-2001; 2001US-0341058P.

24-OCT-2001; 2001US-0341058P.

24-OCT-2001; 2001US-0341058P.

24-OCT-2001; 2001US-034552P.

25-OCT-2001; 2001US-034557P.

01-NOV-2001; 2001US-034557P.
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19-APR-2002; 2002US-0373817P.
19-APR-2002; 2002US-0373826P.
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22-APR-2002; 2002US-0374977P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-OCT-2002; 2002WO-US031373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAY-2002; 2002US-0381038P
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01-OCT-2002; 2002US-00262511
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                          Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                            30 VLVNERWVL 38
                                                                                                                                                                                                        1 VLVNERWVL 9
                                                                                                              Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003029424-A2.
                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                      ADA05742;
                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                      RESULT 14
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The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOV1). Also described: (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit comprising, in one or more
containers, the composition described above; (3) an isolated nucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
comprising the nucleic acid molecule described above; (5) a cell
comprising the nucleic acid molecule described above; (6) a cell
comprising the above vector; (6) an antibody that immunospecifically
binds to the polypeptide described above; (7) methods for determining the
presence or amount of the above polypeptide or nucleic acid molecule in a
sample; (8) methods for determining the presence of or predisposition to
a disease associated with alered levels of expression of the above
CC adisease associated with alered levels of expression of the above
CC above; (10) a method for identifying a potential therapeutic agent for
custod identifying an agent that binds to the polypeptide described
cc above; (10) a method for identifying a potential therapeutic agent for
custod identifying a pathology that is related to an aberrant expression or
aberrant physiological interactions of the polypeptide; (11) a method of
cor presenting for a modulator of activity or of latency or predisposition to
a pathology associated with the polypeptide; (12) a method for modulating
cc a pathology associated with the above polypeptide. NOVX
sequences have antidiabetic, anorectic, antibacterial, virucide,
cor preventing a pathology associated with the above polypeptide. NOVX
sequences have antidiabetic, nocropic, neuroprotective, antiparkinsonian
and antilipaemic activities, and can be used in gene therapy. The
colypeptide is useful in manufacturing a medicament for treating a
colypeptide is useful in manufacturing a medicament for treating a
colypeptide and as diabetes or obesity, infections, caechexia, cancer,
colypeptide andisorders, haematopolected disorders and various
colypeptide and s
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                                                              n G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
jan M, Spyrek KA, Edinger SR, Ellerman K, Malyankar UM;
Gorman Li, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
B RA, Rothenberg MB, Leach MD, Agee ML, Berghs C, Dipippo VA;
J, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 172; 586pp; English
                                                                                                                   Gorman -, Miller CE, Rastelli w,
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Matches 9; Conservative
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                                                                                           Patturajan M,
                                                                                                                                                              Shimkets RA,
                                                                   Smithson G,
                                                                                                                                                                                    Eisen AJ,
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01-JUL-2004 (first entry)

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02-OCT-2001; 2001US-0326483P.
05-OCT-2001; 2001US-0327435P.
09-OCT-2001; 2001US-0327435P.
09-OCT-2001; 2001US-0327449P.
09-OCT-2001; 2001US-0328044P.
09-OCT-2001; 2001US-0328044P.
12-OCT-2001; 2001US-0328044P.
17-OCT-2001; 2001US-0328044P.
17-OCT-2001; 2001US-0328044P.
17-OCT-2001; 2001US-0339405P.
18-OCT-2001; 2001US-034058P.
24-OCT-2001; 2001US-034058P.
24-OCT-2001; 2001US-034058P.
24-OCT-2001; 2001US-034362P.
19-APR-2002; 2002US-0373804P.
16-MAY-2002; 2002US-0381033P.
16-MAY-2002; 2002US-0381034P.
17-MAY-2002; 2002US-0381642P.
17-MAY-2002; 2002US-0381642P.
                                                                                                                                                                                                                                                                                                                                                                                  29-MAY-2002; 2002US-0383831P.
25-JUN-2002; 2002US-0391335P.
                                                                                                                              01-OCT-2002; 2002US-00262511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E.
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EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GUO X.
PATTURAJAN M.
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                                                                                                                                                                                                                                                                                                                                                                                                                   MILLET I.
PEYMAN J A.
KEKUDA R.
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                                                                                                                                                                                                                                                                                                                                                                                                             SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GORMAN L.
                                                           wasting disorder
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                                                                                              US2004038223-A1
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                                                                             Homo sapiens.
         Human NOV18f
                                                                                                               26-FEB-2004.
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(MILL/)
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(MILL/)
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(EDIN/)
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The invention relates to isolated NOVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or activity of NoVX polypeptides. For example, NoVX polypeptides and activity of NoVX polypeptides are associated with decreased activity of NoVX polypeptides. For example, NoVX polypeptides and polymucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our crecify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX polypeptides may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators the production of antibodies, agonists and activity of NOVX. The cused to modulate NOVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX colypeptides and polymolecities may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, hatheimer's bisease, parkinson's bisorder, immune disorders, hatmatopoietic disorders, and the various dyslipidaemias, metabolic mand and the particular matabolic syndrome X and the wasting disorders associated with obesity, the metabolic syndrome x and wasting disorders associated with obesity the metabolic syndrome sancers.
                                                                                                                                                                                                                                    Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhueen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shency SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 47; DB 8; Length 247; 100.0%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            They may also be used as antibacterial agents. The present represents the amino acid sequence of a human NOVX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 102; 395pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                  (DIPI/) DIPIPPO V A.
(RISE/) EISEN A.
(GANG) GANGOLLI E A.
(RIEG/) RIEGER D K.
(SPAD/) SPADERNA S K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 VLVNERWVL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VLVNERWVL 9
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-213931/20.
                         AGEE M L.
BERGHS C.
LEACH M D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADN62905
LEAC/)
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                                                                           human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
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Gaps

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present sequence

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds (without alignments) 61.367 Million cell updates/sec Run on:

US-09-905-083A-34

1 VLVNERWVL 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pir 80:\*
1: pir1:\*
2: pir2:\*
1: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	aseniatore animas		~	neuropsin - mouse	hypothetical prote	ന	trypsin (EC 3.4.21		chymotrypsin (EC 3		hypothetical prote		A20R protein - vac	probable 49.1K pro	١	hypothetical prote		hypothetical prote		trypsin (EC 3.4.21	_	_	trypsin (EC 3.4.21	trypsin (EC 3.4.21	뜨	haptoglobin - rhes			coagulation factor
ID	253968	DBHU	KOPG	156559	T25594	T01779	S31384	S44184	849129	T05892	F82825	A45161	D42519	T37408	C72166	T28563	C36850	T47075	T25570	S31778	831776	831775	S49489	A25852	JC2479	G02959	I36945	9	147078
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Length	253	246	232	260	417	250	250	258	259	1421	72	258	426	426	426	426	426	216	178	231	242	242	242	247	257	258	258	258	274
% Query Match	0 001	83.0	80.9	80.9	80.9	78.7	78.7	78.7	78.7	78.7	9.9/	9.9/	9.9/	9.9/	9.9/	9.92	9.9/	9.9/	74.5	74.5	•	74.5	74.5	•	74.5	٠	74.5	٠	74.5
Score	47	3.9	38	38	38	37	37	37	37				36			36	36	36	35	32	35	35	35	35	35	35	35	35	35
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ribosomal protein	hypothetical prote	haptoglobin precur	haptoglobin - chim	haptoglobin - chim	haptoglobin precur	haptoglobin - blac	haptoglobin-relate	haptoglobin - chim	haptoglobin precur	branched-chain-ami	coagulation factor	acrosin (EC 3.4.21	hypothetical prote	unknown protein [i	probable membrane
E70472	A83757	HPDG	I36941	I36942	HPHU1	900009	HPHUR	I36944	HPHU2	T46034	KFBO	S11674	G96695	C86443	S54045
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35 74.	35 74	35 74	35 74	35 74	35 74	35 74	35 74	35 74	35 74	35 74	35 74	35 74	35 74	35 74	35 74

## ALIGNMENTS

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serine proteinase SCCE precursor - human
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N;Alternate names: stratum corneum chymotryptic enzyme C;Species: Homo sapiens (man) C;Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 09-Jul-2004

Ciracession: A13968
Ritansson, L.; Stroemqvist, M.; Backman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A; Fittle: Cloning, expression, and characterization of stratum corneum chymotryptic enzym. A; Reference number: A53968; MUD:94308225; PMID:8034709
A; Accession. A53968
A; Access

A,Gene: GDB:PRSS6; SCCE
A,Cross-references: GDB:377730
A,Cross-references: GDB:377730
C,Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology

Gaps ö Query Match 100.0%; Score 47; DB 2; Length 253; Best Local Similarity 100.0%; Pred. No. 0.25; Matches 9; Conservative 0; Mismatches 0; Indels

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||||||||||||| 58 VLVNERWVL 66 1 VLVNERWVL 9 В ò

### RESULT 2

Complement factor D (EC 3.4.21.46) precursor [validated] - human (fragment)

NyAlternate names: adipsin; C3 convertase activator
C5pecides: Homo sapiens (man)
C5pecides: Homo sapiens (man)
C5pecides: Homo sapiens (man)
C5pecides: Aug-1985 #sequence revision 31-Dec-1992 #text\_change 09-Jul-2004
C5Accession: A40197; A00936; A60571; S6645
R7 White, R.T.; Damm, D.; Hancock, N.; Rosen, B.S.; Lowell, B.B.; Usher, P.; Flier, J.S.; J. Biol. Chem. 267, 9210-9213, 1992
A; Fitle: Human adipsin is identical to complement factor D and is expressed at high level A; Reference number: A40197; MUID:92250520; PMID:1374388
A; Accession: A40197
A; Molecule Cype: mRNA
A; Residues: 1-246 < WHI>
A; Cross-references: UNIPROT: P00746; UNIPARC: UD10000172AE4; GB: M84526
R; Niemann, M.A.; Bhown, A.S.; Bennett, J.C.; Volanakis, J.E.
B; Diochemistry 23, 2482-2486, 1984
A; Title: Amino acid sequence of human D of the alternative complement pathway.
A; Reference number: A00936; MUID:85000441; PMID:6383466
A; Accession: A00936

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F;1-224/Domain: trypsin homology <TRY>
F;1-80/Product: tissue kallikrein chain A #status experimental <MPTA>
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61 VLVGDRWVL 69
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nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                  A Molecule type: protein

A, Molecule type: protein

A, Residues: 19-20, 'XX', 23-27, 'XX', 30-31,'XX', 34,'X', 36-40 <MIY>

A, Residues: 19-20, 'XX', 100000172AB6

B, Balke, N.; Holtkamp, U.; Hoerl, W.H.; Tacheache, H.

B, Balke, N.; Holtkamp, U.; Hoerl, W.H.; Tacheache, H.

A, Title: Inhibition of degranulation of human polymorphonuclear leukocytes by complement A, Reference number: S66645; MUID: 96013156; PMID: 7556615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: protein
A;Residues: 19-44,'C',46-48 <BAL>
A;Cross-references: UNIPARC:UPI0000172AE7
C;Comment: Factor D cleaves factor B when the latter is complexed with factor C3b, activ C;Genetics:
A;Molecule type: protein
A;Residues: 19-44,'G',46-51,'Q',53-75,'TH',78,'P',80-83,'XXXITIE',90-172,86-91,185-235,'
A;Cross-references: UNIPARC:UP10000172AE5
A;Cross-references: UNIPARC:UP10000172AE5
A;Note: a few residues were assigned from the previously published sequence of Reid et a
R;Miyata, T.; Oda, O.; Inagi, R.; Sugiyama, S.; Miyama, A.; Maeda, K.; Nakashima, I.; Ya
Mol. Immunol. 27, 637-644, 1990
A;Title: Molecular and functional identification and purification of complement componen
A;Reference number: A60571; MUID:90370044; PMID:2395435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Molecule type: protein
A;Residues: 1-224, 'B'.226-232 <BOD>
CCOMMENT: The protein consists of two chains, A and B, held together by disulfide bonds C;Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release 1 C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; pancreas; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Molecule type: Molecule type: Molecule type: Molecule the residue identified as 225-Asx is bound to carbohydrate; therefore, we have R; Modes W; Chen, Z.; Bartels, K.; Kutzbach, C.; Schmidt-Kastner, G.; Bartunik, H. J. Mol. Biol. 164, 237-282, 1983
A; Mol. Biol. 164, 237-282, 1983
A; Mol. Biol. 164, 237-282, The transport of porcine pancreatic kallikrein A, R; Reference number: A92895; MUID: 81389107; PMID: 6551452
A; Contents: X-ray crystallography, 2 angstroms
A; Accession: A92895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue kallikrein (EC 3.4.21.35), pancreatic - pig (tentative sequence)
N;Alternate names: glandular kallikrein; kininogenin
C;Species: Sus seriad domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 31-Mar-2000
C;Accession: A00938; A92895
R;Tschesche, H: Nair, G:; Godec, G:; Fiedler, F:; Ehret, W.; Hirschauer, C.; Lemon, Avr. Exp. Med. Biol. 120, 245-260, 1979
Adv. Exp. Med. Biol. 120, 245-260, 1979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase P;1-18/Domain: signal sequence #status predicted <$15> P;1-246/Product: complement factor D (fragment) #status experimental <MAT> P;19-241/Domain: trypsin homology  Fixty
P;4-60,141-207,172-188,197-222/Disulfide bonds: #status predicted
P;59,105,201/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: GDB:132645; OMIM:134350
A,Map position: Xpter-Xqter
C,Superfamily: trypsin; trypsin homology
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Best Local Similarity 88.9
Matches 8; Conservative
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A;Accession: A00938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 VLVAERWVL 55
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Nichen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nishind J. Neurosci. 15, 5088-5097, 1995
A; Title: Expression and activity-dependent changes of a novel limbic-serine protease gene A; Reference number: 156559; MUID:95348817; PMID:7623137
A; Accession: 156559
A; Retautus preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-260 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:061955; UNIPARC:UPI00000292C5; GB:D30785; NID:g1648847; PIDN:
C;Superfamily: trypsin; trypsin homology
F;33-252/Domain: trypsin homology <TRY>
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C,Species: Caenorhabditis elegans
C,Accession: T25594
R,Gattung, S.
submitted to the EMBL Data Library, February 1997
A,Description: The sequence of C. elegans cosmid C32E8.
A,Recession: T25594
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: 11417 - CGAT>
A,Residues: 11417 - CGAT>
A,Ross-references: UNIPROT:P91123; UNIPARC:UDIO00017B7F4; EMBL:UB8308; FIDN:AAB42324.1;
A,Experimental source: strain Bristol N2; clone C32E8
F;79-82/Region: autolysis loop
F;81-232/Product: tissue kallikrein chain B #status experimental <MPTB>
F;81-232/Product: tissue kallikrein chain B #status experimental
F;7-144,26-42,121-190,155-169,180-205/Disulfide bonds: #status experimental
F;41,89,184/Active site: His, Asp, Ser #status experimental
F;78/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;225/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
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C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                            80.9%; Score 38; DB 1; Length 232; 77.8%; Pred. No. 11; ive 1; Mismatches 1; Indels
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12;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 1
A;Introns: 22/3; 51/2; 92/1; 297/1; 354/1
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A;Description: Cloning of blood meal induced serine protease genes of the mosquito Anophe
A;Reference number: 835412
A;Accession: 849130
                                                                                                A; Molecule type: DNA
A; Residues: 1-165, 'R', 167-193, 'FPD', 197-258 < MU2>
A; Residues: 1-165, 'R', 167-193, 'FPD', 197-258 < MU2>
A; Residues: 1-165, 'R', 167-193, 'FPD', 197-258 < MU2>
A; Cross-references: UNIPARC: UP1000016B7D4; EMBL: 218888; NID:g509416; PIDN: CRA79326.1; PII
C; Genetics:
A; Introns: 78/2; 209/3
C; Superfamily: trypsin; trypsin; homology
C; Keywords: hydrolase; protein digestion; serine proteinase
F; 1-17/Domain: signal sequence #status predicted < SIG>
F; 18-32 Chomain: serivation peptide #status predicted < PRO>
F; 33-258/Domain: crypsin; homology < TRY>
F; 33-258/Domain: trypsin; homology < TRY>
F; 33-258/Domain: trypsin; homology < TRY>
F; 35-75,182-198,208-232/Disulfide bonds: #status predicted
F; 74,119,212/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Riwueller, H. submitted to the EMBL Data Library, November 1992
A; Description: Cloning of blood meal induced serine protease genes of the mosquito Anophs
A; Reference number: 835412
A; Accession: 849129
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A; Residues: 1-259 «MUS>
A; Cross-references: UNIPROT: Q27289; UNIPARC: UPI0000128651; EMBL: Z18887; NID: G509414; PIDP
A; Experimental source: strain Suakoko
R; Experimental source: strain Suakoko
R; Mueller, H.M.; Catteruccia, F.; Crisanti, A.
submitted to the RMBL Data Library, April 1994
A; Description: An Anopheles gambiae locus containing the sequences of two closely related
A; Reference number: S44184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Rosaidues: 1-259 - MU2>
A;Crosa-references: UNIPARC:UPI0000128651; EMBL:232645; NID:9474026; PIDN:CAA83568.1; PII
A;Experimental source: strain Suakoko
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Pred. No. 19;
2; Mismatches 0; Indels
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C.Keywords: hydrolaes; protein digestion, serine proteinase
P;1-17/Domain: signal sequence #status predicted <SIG>
F;18-32/Domain: sectivation peptide #status predicted <PRO>
F;18-325/Product: chymotrypsin 1 #status predicted <MAT>
F;33-259/Product: chymotrypsin 1 #status predicted <MAT>
F;59-75,182-198,208-232/Joisulfide bonds: #status experimental
F;74,119,212/Active site: His, Asp, Ser #status predicted
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Similarity 75.0%;
6; Conservative
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Best Local Similarity 75.0.
Then 6; Conservative
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63 LLNDRWVL 70
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63 LLNDRWVL 70
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Best Local Similarity
Matches 6; Conserv
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T05892
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N;Alternate names: chymotrypsin-like proteinase ANCHYM2
S;Species Anopheles gambiae (African malaria mosquito)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: S44184; S49130
S;Mueller, H.M.; Catternccia, F.; Crisanti, A.
Submitted the EMBL Data Library, April 1994
A;Bescription: An Anopheles gambiae locus containing the sequences of two closely relate
A;Reference number: S44184
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R;Mueller, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPARC:UPI000017144C; EMBL:X56744; NID:g1213630; PID:g64240 C;Superfamily: trypsin; trypsin homology C;Keywords: hydrolase; protein digestion; serine proteinase F;23-242/Domain: trypsin homology <TRY>
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                                                                                                                            trypsin (EC 3.4.21.4) - plaice
C;Species: Pleuronectes platessa (plaice)
C;Date: 19-Peb-1999 #sequence_revision 19-Feb-1999 #text_change 16-Jul-1999
C;Accession: T01779
R;Leaver, M.J.; George, S.G.
submitted to the EMBL Data Library, March 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          trypsin (EC 3.4.21.4) - plaice
C;Species: Pleuronactes platessa (plaice)
C;Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S31384
R;Leaver, M.J.; George, S.G.
submitted to the EMBL Data Library, November 1990
A;Reference number: S30567
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A;Status: preliminary
A;Molecule type: mRMA
A;Molecule 1-250 <LEA>
A;Cross_references: UNIPROT:P35034; UNIPARC:UP10000137711; EMBL:X56744
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A;Molecule type: mRNA
A;Residues: 1-250 <LEA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine
F;23-242/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37; DB
Pred. No. 18;
2; Mismatches
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Best Local Similarity 66.7-
6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                   A;Reference number: Z14422
A;Accession: T01779
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50 VLINNQWVL 58
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A; Residues: 1-258 <MUE>
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26-May-1994 #Bequence_revision 26-May-1994 #text_change 09-Jul-2004
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Matches 6; Conserv
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R/Simpson, A.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Bimpson, A.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Cararo, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H as-Neto, E.; Docora, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A,Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm A,Authors: Ferreira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, B.E.; Laigr chado, M.A.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B.A.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, B.C.; Niyaki, C.Y.; F.G.; Numes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J., de M.A.; da Silva, A.C.; da Si
A;Map position: 5
A;Introns: 72/3; 142/3; 227/2; 344/3; 372/3; 941/2; 1016/3; 1038/3; 1055/1; 1095/2; 1155
A;Note: F6H11.110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein XP0279 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2100 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: F82825
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: F82825
A;Status: preliminary
A;Molecule type: DMS
A;Reaidus: 1-72 <SIM>
A;Cross-references: UNIPROT:Q9PGL9; UNIPARC:UPI00000C2364; GB:AE003881; GB:AE003849; NID
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Pred. No. 7.5;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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C,Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 2; I
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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62.5%;
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Local Similarity 66.7%;
les 6; Conservative
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C;Accession: A45161
R;Smyth, M.J.; Wiltrout, T.; Trapani, J.A.; Ottaway, K.S.; Sowder, R.; Henderson, L.E.; F. J. Biol. Chem. 267, 24418-24425, 1992
A;Title: Purification and cloning of a novel serine protease, RNK-Met-1, from the granule A;Title: Purification and cloning of a novel serine protease, RNK-Met-1, from the granule A;Recession: A45161
A;Accession: A45161
A;Status: preliminary
A;Nolecule type: mRNA
A;Residues: 1-258 <SMY>
A;Cross-references: UNIFROT: 003238; UNIPARC: UPI000012BA73; GB:L05175; NID:g206691; PIDN:}C;Supwards: hydrolase; serine proteinase
C;Supwards: hydrolase; serine proteinase
F;21-245/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CiSpecies: vaccinia virus (strain Ankara)
CiSpecies: vaccinia virus
CiSpecies: vaccinia virus
AyVariety: strain Ankara
CiSpecies: 1-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
CiDate: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
CiAccession: T37408
RiAntoine, G.; Scheiflinger, F.; Falkner, F.G.; Dorner, F.
submitted to the EMBL Data Library, March 1997
A;Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strair
A;Description: T37408
A;Scession: T37408
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-426 ANNTA
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A,Experimental source: strain Ankara
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A;Note: host Homo sapiens (man)
C;Date: 90-Nov-1990 #text_change 09-Jul-2004
C;Accession: D42519
R;Johnson, G.P.
Submitted to GenBank, June 1990
A;Reference number: A33172
A;Accession: D42519
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Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Length 258,
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-426 - 4.0Hs
A;Cross-references: UNIPROT: P20995; UNIPARC: UPI0000138054
C;Superfamily: vaccinia virus probable 49.1K protein
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C;Superfamily: vaccinia virus probable 49.1K protein
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29;
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76.6%; Score 36; DB
Best Local Similarity 55.6%; Pred. No. 49;
Matches 5; Conservative 3; Mismatches
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Pred. No.
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RESULT 15
C72166
A22R protein - variola minor virus (strain Garcia-1966)
C;Species: variola minor virus
C;Species: variola minor virus
C;Species: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004
C;Accession: C72166
R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar submitted to GenBank, March 1998
A;Pescription: Analysis of the complete coding sequence of DNA of alastrim variola minor A;Reference number: A72150
A;Accession: C72166
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-426 cSHC>
A;Cross-references: UNIPROT:089166; UNIPARC:UPI0000061D50; GB:Y16780; NID:G5830555; PIDN
A;Experimental source: strain Garcia-1966
C;Genetics:
A;Gene: A22R
C;Superfamily: vaccinia virus probable 49.1K protein
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  0; Gaps
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  1; Indels
3; Mismatches
5; Conservative
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130 VLLNNRWIM 138
                                                 1 VLVNERWVL 9
Matches
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Search completed: March 11, 2006, 00:40:49 Job time : 15.1111 secs

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1 VLVNERWVL 9

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OM protein - protein search, using sw model	Run on:

Title:		US-09-905-083A-34
Perfect score	score:	47
		* ***

1 VLVNERWVL 9 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STHAMMITES

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SUMMARIES		KLK7 HUMAN	Q9FFR7 ARATH	MYV8 BOVIN	K9V0 PSEF5	JFQ7_GADMO	MBG2_XENTR	Q5F3N3_CHICK	XYS8_CTEFE	Q7SZE2_AGKCA	Q66PG8_FUGRU	KLK_PIG	Q5M908_XENTR	NRPN MOUSE	PN RAT	Q7Z0GS_9DIPT	T3B8_CAEEL	SNY8 SOLTU	SNY9_SOLTU	P91123_CAEEL	NUH8 CHRVO	RC62_TEING	Q67PW1_SYMTH	QX46_IDILO	Q9PT51 AGKHA	Q8UUJ1_AGKCA	Q9VEM7 DROME	D9W6K0 9PERC	Q92046_DISMA	2788V0 DISMA	TRYP PLEPL	093265_PSEAM
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	Score	47	40	39	39	39	39	39	38	38	38	38	38	38	38	38	38	38	38	38	38	37	37	37	37	37	37	37	37	37	37	37
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37 78.7 28.3 34 78.7 78.7 78.7 78.7 78.7 78.7 78.7 78.	7.8.7
<b>шшшшшшшш 4 4 4 4</b> Иш 4 № 0 С Ф 0 С 1 С К	1 4 4 1 4 7

## ALIGNMENTS

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Q9FFR7 AR
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                                                                                                                                                                    MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
MICHINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
MICHINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
MICHINE R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Bromstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Arapa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Malkealey R.W., Touchman J.W., Green B.D., Dickson M.C., Malkealey R.W., Touchman J.W., Schwutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., M. Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
M. Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
M. Galeneration and initial malysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=1; Synonyms=Long;
Isold=P49862-1; Sequence=Displayed;
Name=2; Synonyms=Long;
Isold=P49862-1; Sequence=VSP_013581;
Isold=P49862-1; Sequence=VSP_013581;
TISSUE SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermia. Also expressed in the brain, mammary gland, crebellum, spinal cord and kidney. Lower levels in salivary gland, crebellum, spinal cord and kidney. Lower levels in salivary gland, crebellum, cpinal cord and kidney. Lower levels and testis. Up-regulated in ovarian carcinoma, especially late-stage serous carcinoma, compared with normal ovaries and benign adenomas (at the protein level).
INDUCTION: By estrogens and glucocorticoids in a breast carcinoma
                     Dong Y., Kaushal A., Brattsand M., Nicklin J., Clements J.A.;
"Differential splicing of KLKS and KLK7 in epithelial ovarian cancer
produces novel variants with potential as cancer biomarkers.";
Clin. Cancer Res. 9:1710-1720(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95314630; PubMed=7794273;
Skytt A., Stroemgvist M., Egelrud T.;
"Primary substrate specificity of recombinant human stratum corneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 1 peptidase S1 domain.
MEDLINE=22623266; PubMed=12738725;
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<u>:</u>

EMBL; L33404; AAC37551.1; -; mRNA. EMBL; AF166330; AAD49718.1; -; Genomic\_DNA.

removed.

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I. Sequence
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MEDLINE=97471969; PubMed=9330910;
Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
Miyajima N., Tabata S.;
Miyajima N., Tabata S.;
Structural analysis of Arabidopsis thaliana chromosome S. I. Sequenc features of the 1.6 Mb regions covered by twenty physically assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryoča, Viridiplantae, Straptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (By similarity).
(By similarity).
(By similarity).
(Py similarity).
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MBK23.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                       Pfam; PF00089; Trypsin; 1.

PRINTS; PR0722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPS. 1.

PROSITE; PS50240; TryPESIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN SRR; 1.

Alternative splicing; Direct protein sequencing; Glycoprotein; Hydrolase; Protease; Signal; Zymogen.

SIGNAL
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Charge relay system (By similar Charge relay system (By similar Charge relay system (By similar Charge relay system (By similar N-linked (GlcNAc...) (Potenti By similarity. C -> W (in Ref. 6; AAH32005).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                GO; GO:0008236; F:serine-type peptidase activity; TAS. GO; GO:0008544; P:epidermis development; TAS. InterPro; IPR001254; Peptidase_S1_S6. InterPro; IPR001314; Peptidase_S1Ā.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Activation peptide.
Kallikrein 7.
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Genomic_DNA.
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                                     mRNA.
                                                     mRNA.
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                                  AF411214; AAN03662.1; -; AF411215; AAN03663.1; -; BC032005; AAH32005.1; -;
                                                                                                                         MEROPS; S01.300; -.
Ensembl; ENSG00000169035; Homo
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Q9FFR7 ARATH PRELIMINARY;
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Matches 9; Conservative
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                                                                                                                                                             HGNC; HGNC: 6368; KLK7.
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2553
2553
70
1112
205
246
1137
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58 VLVNERWVL 66
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                                                                                       PIR; A53968; A53968.
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253 AA;
                                                                                                          P00760; 1EZX.
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Gaps

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PubMed=15980861; DOI=10.1038/nbt1110;
Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
Mavrodi D., DeBoy R.T., Seehadri R., Ren Q., Madupu R., Dodson R.J.,
Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,
Khouri H.M., Pierson B., Pierson L. III, Thomashow L., Loper J.;
"Complete genome sequence of the plant commensal Pseudomonas Flucrescens Pf-5.";
Nat. Biotechnol. 23:873-878(2005).
EMBL, CP000076; AAY93147.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygit; Neopterygit; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus. NCBI_TaxID=8049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; S01.124; ...
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:peptidase activity; IEA.
GO; GO:0004295; F:rpptidase activity; IEA.
GO; GO:0004295; P:negative regulation of blood coagulation; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IRR001314; Peptidase SIA.
InterPro; IRR01254; Peptidase SIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spilliaert R.; "Atlantic Cod Trypsin Y - Member of a Novel Trypsin Group."; Mar. Biotechnol. 1:598-607(1999).
                                                                                                                                                                                                                                                       83.0%; Score 39; DB 2; Length 235; 66.7%; Pred. No. 46; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 66.7%; Pred. No. 49; 6; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Pyloric caecum;
Gudmundsdottir A.;
Submittad (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ459311; CAD30563.1; -; mRNA.
HSSP; P00746; 1FDP.
                                                                                                                                                                                                                    235 AA; 27624 MW; 75C5203A8254CCAF CRC64;
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249 AA; 27400 MW; 8FB98462CEDBEFC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09JFQ7;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Trypsinogen Y precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 AA
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MARRY, SMO0020; TRYP SPC; 1.
PROSITE; PSS0240; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gadus morhua (Atlantic cod)
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
QBJFQ7 GADMO
ID QBJFQ7_GADMO PRELIMINARY;
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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225 LLVNQRWVI 233
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PubMed=10612685;
                                                                                                                                                                                                                                                                                                                                         1 VLVNERWVL 9
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Best Local Similarity
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SEQUENCE
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SIGNAL
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                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Bovinae, Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0030195; P:negative regulation of blood coagulation; IEA.
GO; GO:0006599; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001254; Peptidase_S1_S6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas. NCBI_TaxID=220664;
                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                     Query Match 85.1%; Score 40; DB 2; Length 455; Best Local Similarity 75.0%; Pred. No. 61; Matches 6; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.0%; Score 39; DB 2; Length 100; 75.0%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lavery K.S., Gabler C., Killian G.J.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ271155; CAC00531.1; -; mRNA.
HSSP: P00751; 1DLE.
MEROPS; S01.972; -.
DNA Res. 4:215-230(1997).

EMBL; AB005233; BAB11469.1; -; Genomic_DNA.

GO; GO:0006512; P:ubiquitin cycle; IEA.

InterPro; IPR001810; F-box.

Pfam; PP00646; F-box; 1.

SEQUENCE 455 AA; 52305 MW; 763F5D5278D22F13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 AA; 11239 MW; FFFEGAESAB43CED9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Arginine-tRNA-protein transferase-related protein.
ORFNames-PFL 3883;
Pseudomonas Fluorescens (strain Pf-5).
                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Haptoglobin (Fregment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00089; Trypsin; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
                                                                                                                                                                                                                                                                                                                           78_BOVIN
Q9MYV8_BOVIN PRELIMINARY;
Q9MYV8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q4K9V0_PSEFS PRELIMINARY;
Q4K9V0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100
                                                                                                                                                                                                                                           ::||||||
104 IINERWUL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:||||:|
22 LINERWLL 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                    2 LUNERWUL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LUNERWUL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Oviduct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Pf-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches

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Gaps

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10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein.
ORFNames=RCJMB04 11h6;
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Caldwell R. B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J., Fielder P., Kutter S., Blagodatski A., Kostovska D., Koer M., A Plachy J., Cardinci P., Hayashizaki Y., Buerstedde J.M.; All told. T. Kull-length cDMAs from chicken bursal lymphocytes to facilitate genefunction analysis "; Genome Biol. e.Re-RG (2005).

R mterpro; IPR000859; GUB.

R interpro; IPR00152; Asx hydroxyl S. Interpro; IPR00152; Asx hydroxyl S. Interpro; IPR00159; EGF_like.

R interpro; IPR00159; EGF_like.

R interpro; IPR001514; Peptidase_S1A.

R interpro; IPR001515; Sushi_SCR_CCF.

R pfam; PF00041; CUB; 2.

R Pfam; PF00041; CUB; 2.

R Pfam; PF00049; EGF_like.

R Pfam; PF00049; Trypashin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ctenocephalides felis (Cat flea).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neopiera; Endopterygota; Siphonaptera; Pulicidae; Pulicinae;
Ctenocephalides.
NCBI_TaxID=7515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.0%; Score 39; DB 2; Length 690; 66.7%; Pred. No. 1.5e+02; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             690 AA; 77326 MW; E85A9C65A1D97E7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Chymotrypsin-like serine protease (Fragment).
Name-SP-4;
                                                        690 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0722; CHYMOTRYPEIN.
SMART; SM00032; CCP; 2.
SWART; SM00042; CUB; 2.
SWART; SM00179; EGF CA; 1.
SWART; SM00179; EGF CA; 1.
SWART; SM00179; Tryp SPC; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS02023; SUSHI; 2.
PROSITE; PS02043; TRYPSIN DOM; 1.
PROSITE; PS01187; TRYPSIN DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.70,
Best Local 6; Conservative
                                                    QSF3N3_CHICK PRELIMINARY;
QSF3N3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9XYS8 CTEFE PRELIMINARY;
Q9XYS8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Bursa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    465 VLISERWVM 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VLVNERWVL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTEFE
                                                                                                                                                                                                                                                                                                                                                                                     Gallus
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                                 Q5F3N3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09XY58
                                                                  HID DE RESERVANTE DE LA PRESENTA DEL PRESENTA DE LA PRESENTA DEL PRESENTA DE LA P
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WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Liscubles R.L., Zeeberg B., Barder L., Shenmen C.M., Schuler G.D.,

A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Capleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

B Roberstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahe J., Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Butterfield Y.S. M., Krzywinski M.I., Skalska U., Smailus D.E.,

B Cherestion and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus tropicalis (Western clawed frog) (Silurana tropicalis). Usukaryota; Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Whole body;
Klein S., Gerhard D.S.;
Klein S., Gerhard S., F.
Klein S., AAH80318.1, -; mRNA.
GO; GO:0004233; F:Deptidase activity; IEA.
GO; GO:0004295; F:Lrypsin activity; IEA.
GO; GO:0004295; F:Lrypsin activity; IEA.
GO; GO:0004296; F:Lrypsin activity; IEA.
GO; GO:000508 P:proteolysis and peptidolysis; IEA.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001254; Peptidase_S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER 1 1 5 SEQUENCE 254 AA; 27526 MW; 64A2AFC41A467C38 CRC64;
                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                      254 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYBSIN.
SMART; SM00020; Tryp_SPC; 1.
PR0SITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                           01-FEB-2005 (TrEMBLrel. 29, Cr
01-FEB-2005 (TrEMBLrel. 29, La
01-FEB-2005 (TrEMBLrel. 29, La
10C446767 protein (Fragment).
                                                                                                                                                                                                      Q5M8G2_XENTR PRELIMINARY;
Q5M8G2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVNERWVL 9
|:||:|||
LINEKWVL 60
                                 ||:|::|||
50 VLINDQWVL 58
1 VLVNERWVL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8364;
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87.5%;

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7; Conservative
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                                                                              2 LVNERWVL 9
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=31033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feugita A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLK PIG
P00752;
                                                                                                                                                                                                RESULT 10
Q66PG8_FUGRU
                                                                                                                                                                                                                                                                         Q66PG8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLK_PIG
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A SUN D.-J. Yang T.-S.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY204242; AAP20637.1; -; mRNA.
RSSP; Q91516; 1BQY.
R HSSP; Q91516; 1BQY.
R SMR; Q752E2; 1-234.
R MEROPS; SO1.347; -.
R GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:rypeldase activity; IEA.
R GO; GO:0004295; F:rypeliase activity; IEA.
R GO; GO:000509; F:rypeliase activity; IEA.
R GO; GO:0006509; P:negative regulation of blood coagulation; IEA.
R GO; GO:0006509; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR001314; Peptidase_S1A.
R InterPro; PR001254; Peptidase_S1A.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2004 (TrEMBLrel. 26, Last amnotation update)
01-MAR-2004 (TrEMBLrel. 26, Last amnotation update)
Thrombin-like enzyme defibrase (Fragment).
Agkistrodon caliginosus (Korean viper) (Gloydius ussuriensis).
Rukaryotas, Metazota, Chordata; Craniata; Vertebrata, Eueleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Gloydius
                                                                                             Insect Mol. Biol. 81:11-22(1999).

EMBL, AF053916, AAD21836.1; -; mRNA.

HSSP; P00761; IEPT.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0008233; F:chymotrypsin activity; IEA.

GO; GO:000195; F:regative regulation of blood coagulation; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
                         Gaines P.J., Sampson C.M., Rushlow K.E., Stiegler G.L.; "Cloning of a family of serine protease genes from the cat flea Ctenocephalides felis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                  InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001254; Peptidase_S1_S6.
Pfam, PR00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PR0SITE; PS0240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
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SMART; SMO020; Tryp. SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_HS; UNKNOWN_1.
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Best Local Similarity 75.vv,
6; Conservative
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Q7SZE2;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Trypsinogen (Fragment).

Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha, Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Glandular kallikrein precursor (EC 3.4.21.35) (Tissue kallikrein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Generation of alpha- and beta-kallikreins from porcine pancreatic prokallikrein by the action of trypsin."; Chem. Pharm. Bull. 36:4891-4899(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roach J.C.; Submitted (JUN-2004) to the EWBL/GenBank/DDBJ databases. Submitted (JUN-2004) to the EWBL/GenBank/DDBJ databases. EMBL; Ax0661446; Ax006121.1; -; Genomic_DNA. GO; GO:0004223; F:chymotrypsin activity; IEA. GO; GO:0004295; F:trypsin activity; IEA. GO; GO:0030195; P:negative regulation of blood coagulation; IEA. GO; GO:0006508; P:proteolysis and peptidolysis; IEA. InterPro; IPR001254; Peptidase_S1A. InterPro; IPR001254; Peptidase_S1A.
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MEDLINE-89230643; PubMed-3246048;
Kamada M., Aoki K., Ikekita M., Kizuki K., Moriya H., Kamo M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.9%; Score 38; DB 2; Length 235; 66.7%; Pred. No. 72; cive 3; Mismatches 0; Indels
  Indels
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0; Mismatches
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SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
NON_TER
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 X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF COMPLEX WITH BOVINE PANCREATIC TRYPSIN INHIBITOR.

MEDLINE=8318919108; PubMed=6188842;

Chen Z., Bode W.;

Chen Z., Bode W.;

Refined 2.5 A X-ray crystal structure of the complex formed by porcine kallikrein A and the bovine pancreatic trypsin inhibitor.

Crystallization, Patterson search, structure determination, refinement, structure and comparison with its components and with the bovine trypsin-pancreatic trypsin inhibitor complex.";

J. Mol. Biol. 164:283-311(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIJNE-97184690; PubMed-9032072; DOI=10.1016/S0969-2126(97)00183-4; Mittl P.R.E., di Marco S., Fendrich G., Pohlig G., Heim J., Sommerhoff C., Fritz H., Priestle J.P., Gruetter M.G.; An new structural class of serine protesse inhibitors revealed by the structure of the hirustasin-kallikrein complex.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Refined 2-A X-ray crystal structure of porcine pancreatic kallikrein
                      Tschesche H., Mair G., Godec G., Fiedler F., Ehret W., Hirschauer C., Lemon M., Fritz H., Schmidt-Kastener G., Kutzbach C.; Tritz H., Schmidt-Kastener G., Kutzbach C.; "The primary structure of porcine glandular kallikreins."; Adv. Exp. Med. Biol. 120:245-260(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, a specific trypsin-like serine proteinase. Crystallization, structure determination, crystallographic refinement, structure and its comparison with bovine trypsin."; Its comparison with bovine trypsin."; Mol. Biol. 164:237-282(1983).
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                                                                                                                                                                            MEDLINE=99336040; PubMed=2379280;
Kamada M., Ikekita M., Kurahashi T., Aoki K., Kizuki K., Moriya H., Sweeley C.C., Kamo M., Taugita A.;
Generation of a different type of beta-kallikrein from porcine pancreatic alpha-kallikrein by the action of chymotrypsin --
observation of proteolytic processing occurring around 'kallikrein autolysis loop' region.";
                                                                                                                          "The primary structure of the kallikrein from porcine pancreas."; Thesis (1976), University of Munich, Germany.
                                                                                                                                                                                                                                                                                                                                    "Investigation of the sequence of amino acid residues 127 to 174 the kallikrein from porcine pancreas."; Thesis (1978), University of Munich, Germany.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH HIRUSTASIN
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MEDLINE=89062455; Pubmed=3196708;
Tomiya N., Yamaguchi T., Awaya J., Kurono M., Endo S., Arata Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-83189107; PubMed-6551452;
Bode W., Chen Z., Bartels K., Kutzbach C., Schmidt-Kastner G.,
Bartunik H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mittl P.R.E., di Marco S., Fendrich G., Pohlig G., Heim J., Sommerhoff C., Fritz H., Priestle J.P., Gruetter M.G.; Structure 5:585-585(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K-RAY CRYSTALLOGRAPHY (2 ANGSTROMS), AND SEQUENCE REVISION
                                                                           [3]
PROTEIN SEQUENCE OF 8-87; 95-127 AND 176-246.
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-82194877; PubMed-7043199;
Fiedler F., Fink E., Tschesche H., Fritz H.;
"Porcine glandular kallikreins.";
                                                                                                                                                                                                                                                             autolysis loop, region.";
Chem. Pharm. Bull. 38:1053-1057(1990)
PROTEIN SEQUENCE OF 8-87 AND 95-246
                                                                                                                                                                                                                                                                                                                                                                                                                                           Meth. Enzymol. 80:493-532(1981).
                                                                                                                                                                                                                                                                                     [5]
PROTEIN SEQUENCE OF 128-175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Structure 5:253-264(1997).
                                                                                                                                                                    PROTEIN SEQUENCE OF 84-98.
                                                                                                  TISSUE=Pancreas;
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                                                                                                                 Ehret W.;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
Takahashi N., Ishihara H., Mori M., Tejima S.;
"Structural analyses of asparagine-linked oligosaccharides of porcine
pancreatic kallikrain.";
Biochemistry 27:7146-7154(1988)
-!- FUNCTION: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds
in kininogen to release Lys-bradykinin.
-!- CATIVITY: Preferential Cleavage of Arg-|-Xaa bonds in
small molecule substrates. Highly selective action to release
kallidin (1ysyl-bradykinin) from kininogen involves hydrolysis of
Met-|-Xaa.
                                                                                                                                                                                                                            SIMILARITY: Contains 1 peptidase S1 domain.
CAUTION: Native porcine kallikrein is a monomer. Chains of the pancreatic beta-kallikrein are heterogeneous artifacts of proteolytic degradation during isolation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001254; Peptidase_S1_S6.
InterPro; IPR001314; Peptidase_S1Ā.
InterPro; IPR001314; Peptidase_S1Ā.
PREM; PR00089; Trypain; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
BROSITE; PS00135; TRYPSIN HIS; 1.
3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Potential)
                                                                                                                                                                                           SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glandular kallikrein.
Peptidase Sl.
Kallikrein (autolysis) loop.
Charge relay system.
Charge relay system.
Charge relay system.
N-linked (GlCNAC. . .) (Potent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pancreas; Protease; Srine protease; Zymogen.
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PDB; 2KAI; X-ray; A=8-87, B=95-246.
PDB; 2PKA; X-ray; A/X=8-87, B/Y=95-246.
SMR; P00752; 8-245.
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                                                                                                                                                                                                                                                                                                                   SEQUENCE
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X Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

REDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIJaugner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Bucrow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Haisch F.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahesley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rotherteield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Manneron A., Schein J.E., Jones E. Dickson M.A.;

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                             27172 MW; 5991CEDE406A19A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
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Pred. No.
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Name=LOC496635;
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QSM908;
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Matches 7; Conservative
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                              246 AA;
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X MEDLINE-22861 II; TISGUE-Mamary gland;

X MEDLINE-2288557; Pubméd=12477932; DOI=10.1073/pnas.242603899;

A Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Prange C.,

A Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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"Cloning and assignment of mouse neuropsin gene, Prss19 to chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T., Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.; "Expression and activity-dependent changes of a novel limbic-serine procease gene in the hippocampus."; J. Neurosci. 15:5088-5097(1995).
                                                                                                                                                                                                                                                                                                                                                                           coagulation; IEA.
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Klein S., Gerhard D.S.; submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases. BMBL, BC087753; AAH87753.1; -; mRNA.

EMBL, BC087753; AAH87753.1; -; mRNA.

GO; GO:0004233; F:peptidase activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0004295; P:pregative regulation of blood coagulation of colonomial of princeptive regulation of blood coagulation of proposition of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 AA; 27288 MW; DD68633914557564 CRC64;
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 34, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Neuropsin precursor (EC 3.4.21..) (NP) (Kallikrein 8).
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PRINTS; PR00722; CHYMOTRYPSIN.
PMART; SM00020; Tryp.SPS; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN 1.
PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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STRAIN=BALB/c; TISSUE=Hippocampus;
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Matches 7; Conservative
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STANDARD;
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61 VLVGDRWVL 69
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260 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use as long as its content is in no way modified and this statement is not
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerto A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.

TISSUB-Hippocampus;

MEDLINE-99134351; PubMed=9933620; DOI=10.1074/jbc.274.7.4220;

Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,

Shiosaka S., Hakoshima T.;

"Crystal structure of neuropsin, a hippocampal protease involved in kindling epileptogenesis.";

J. Blod. Chem. 274:4220-4224(1999).

-I- FUNCTION: Suggested to be involved in kindling epileptogenesis and hippocampal plasticity. Has a strong proteolytic activity against
                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Secreted.

TISSUE SPECIFICTTY: Expressed specifically in the limbic system of mouse brain and is localized at highest concentration in pyramidal neurons of the hippocampal Call subfields.

MASS SPECTROMETRY: WW=26613; METHOD=MALDI; RANGE=29-260;
                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
ENZYME REGULATION: Strongly inhibited by disopropyl
fluorophosphate, leupeptin and (4-amidinophenyl)methanesulfonyl 1-
                                                                                                            STRAIN=BALB/C; TISSUE=Brain; MBDIINE=9825502; PubMed=9556608; DOI=10.1074/jbc.273.18.11189; Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K., Shiosaka T., Madorikawa R., Kamachi T., Kawabe A., Shiosaka S.; "Characterization of recombinant and brain neuropsin, a plasticity-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; S01.244; ...

MEROPS; S01.244; ...

Ensembl; RNSMUSGO000064023; Mus musculus.

MG1; MG1: BQ2018; Klk8.

InterPro; IPR001254; Peptidase_S1_K.

InterPro; IPR001314; Peptidase_S1_K.

InterPro; IPR001314; Peptidase_S1_K.

PR00175; PR00792; CHYMOTYPSIN.

PROSITE; PS00134; TRYPSIN_BOM; 1.

PROSITE; PS00134; TRYPSIN_BIK; 1.

3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;

Protease; Serine protease; Signal, Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                              NOTE-Ref.4.
SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                            NOTE=Ref.4.
-!- MASS SPECTROMETRY: MW=26229; METHOD=MALDI; RANGE=33-260;
                                                                                            PROTEIN SEQUENCE OF N-TERMINUS, CHARACTERIZATION, AND MASS
                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 1 peptidase S1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D30785; BAA06451.1; -; mRNA.
EMBL; AB032202; BAA92435.1; -; Genomic_DNA.
EMBL; BC055895; AA455895.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuropsin.
Peptidase S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential
                                                                                                                                                            related serine protease.";
J. Biol. Chem. 273:11189-11196(1998).
[5]
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PDB; 1NPM; X-ray; A/B=33-257.
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                                                                                     Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
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(By similarity).
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HSSP; Q61955; 1NPM.
SMR; O98790; 33-256.
MEROES; S01.244; -.
Ensembl; ENSRNOG0000018580; Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                           subfamily.
-!- SIMILARITY: Contains 1 peptidase S1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001254; Peptidase_S1_S6 InterPro; IPR001314; Peptidase_S1A. Pfan; PP00089; Trypsin; I. PR1NTS; PR00722; CHYMOTRYPEIN. SMART; SM00020; Tryp_SPC; I. PR0SITE; PS0040; TryPSIN_DOM; I. PROSITE; PS00134; TRYPSIN_HIS; I. PROSITE; PS00135; TRYPSIN_SER; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28510 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OGS 9DIPT
OTSOSS 9DIPT PRELIMINARY;
OTZOGS;
01-OCT-2003 (TrEMBLrel. 25, C.
01-OCT-2003 (TrEMBLrel. 25, Li
01-OCT-2003 (TrEMBLrel. 25, Li
CHymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 77.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||| :||||
61 VLVGDRWVL 69
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                                                           [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 AA;
                                     NCBI_TaxID=10116;
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ACT SITE
ACT SITE
ACT SITE
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Matches
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Q720G5 9DII
ID Q720G1
AC Q720G1
DT 01-0C
DT 01-MAD
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Ramalho-Ortigao M., Kamhawi S., Rowton E., Sacks D.L., Ribeiro J.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
Name=chyml;
Phlebotomus papatasi.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Psychodoidea;
Psychodidae; Phlebotomus; Phlebotomus.
NCBI_TaxID=29031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                           Valenzuela J.G.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX128106; AAM96938.1; -; mRNA.
HSSP; P18291; IFI8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00089; Trypsin; 1.

SMART; SM00020; Trypsin; 1.

ROSITE; PR00722; CHYMOTRYPSIN.

ROSITE; PS00134; Trypsin DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.

PROSITE; PS00135; TRYPSIN HIS; UNKNOWN 1.

Hydrolase; Protease; Serine protease.

SEQUENCE 262 AA; 28863 MW; 31F11012206A65D4 CRC64;
                                                                                                                                                                                                                                                                                                                                  GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:000233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0005608; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001254; Peptidase SI S6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 2;
Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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75.0%;
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Best Local Similarity 75.0
دری 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ::||||||
57 ILNERWVL 64
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Seguence Seguence Seguence

Sequence Sequence Sequence

75, 75, 75, 75, 75, 75, 715, 117, 117,

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence

Sequence

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database :

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Sequence 34, Application US/09502600A
Patent No. 6294344
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Openion Cancer
TITLE OF INVENTION: Openion Cancer
FILE REFERENCE: D6223CIP-C
CURRENT FILING DATE: 2000-02-11
CURRENT PAPLICATION NUMBER: 08/09/502,600A
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 34
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 34, Application US/09918243

Sequence 34, Application US/09918243

Batent No. 6627403

GENERAL INFORMATION:
APPLICANT: Cannon, Martin J.
CURRENT PLING PILING DATE: 2001-07-30

PRIOR PILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 34

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 47; DB 2; Length 9; 100.0%; Pred. No. 4.6e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE: OTHER INFORMATION: Residues 58-66 of the SCCE protein
US-08-906-769-75
US-08-906-16-75
US-08-817-795-75
US-08-817-795-75
US-09-012-431-75
US-09-012-431-75
US-09-012-431-75
US-08-906-613-75
US-08-906-613-75
US-08-482-130C-17
US-08-482-130C-17
US-08-817-795-17
US-08-817-795-17
US-08-817-795-17
US-08-906-769-17
US-08-906-769-17
US-08-906-769-17
US-08-906-769-17
US-08-906-769-17
US-08-906-769-17
US-08-906-769-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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   US-09-502-600-34
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US-09-918-243-34
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Sequence 12, Appl
Sequence 12, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 7716, Appli
Sequence 7716, Appli
Sequence 7716, Appli
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Sequence 40, Appl
Sequence 50, Appl
Sequence 44, Appl
Sequence 6, Appli
Patent No. 5223425
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Sequence 34, Appl
Sequence 7, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 75, Appl
Sequence 75, Appl
Sequence 75, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                            March 11, 2006, 00:41:16 ; Search time 21.222 Seconds (without alignments) 35.061 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued Patents AA:*

(cgn2_6/ptodata/1/iaa/5_COMB.pep:*
(cgn2_6/ptodata/1/iaa/f_COMB.pep:*
(cgn2_6/ptodata/1/iaa/H_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-918-243-34
US-09-918-243-34
US-08-944-4483-34
US-09-027-1346-12
US-09-027-1346-12
US-09-027-1346-12
US-09-644-6004-4
US-09-644-6004-4
US-09-154-12
US-09-154-12
US-08-913-146-2
US-08-913-146-2
US-08-913-146-2
US-08-910-144-2
US-09-154-146-2
US-09-154-16-2
US-09-16-1716
US-09-16-2716
US-09-918-243-50
US-09-918-243-50
US-09-918-243-50
US-09-918-243-50
US-09-918-243-60
US-09-918-243-60
US-09-918-243-60
                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-485-455D-75
US-08-482-130C-75
US-08-484-211C-75
                                                                                                                                                                                                                                                                                         572060 segs, 82675679 residues
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                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                               protein search, using sw model
                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 200000000
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Match Length DB
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US-08-944-483-33
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Sequence 33. Application US/08944483

Patent No. 623456

GENERAL INFORMATION:

APPLICANT: COLPITYS, TRACEY L.

APPLICANT: GRADMADOS, EDWARD N.

APPLICANT: RUSSELL, JOHN C.

APPLICANT: STRONES, MICHAEL R.

APPLICANT: STRONES, STEVEN D.

TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS

TITLE OF INVENTION: OF THE PROSTATE

NUMBER OF SEQUENCES: 76

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:

NUMBER OF SEQUENCES: 76

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Sequence 7. Application US/09261416A
Sequence 7. Application US/09261416A
GENERAL INFORMATION:
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease;
FILLE REFERENCE: Dels 2
CURRENT APPLICATION NUMBER: US/09/261,416A
CURRENT PILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Serine protease catalytic domain of stratum corneum OTHER INFORMATION: chymotryptic enzyme (Scce) homologous to similar OTHER INFORMATION: domain in TADG-12
                                                                                                                                                                                      Gaps
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                                                                                                                  Query Match 100.0%; Score 47; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 9; Conservative 0; Mismatches 0; Indels
NAME/KEY: CHAIN
COTHER INFORMATION: Residues 58-66 of the SCCE protein
US-09-918-243-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 9; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 VLVNERWYL 12
                                                                                                                                                                                                                                             1 VLVNERWVL 9
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-08-944-483-33
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US-09-261-416-7
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Gaps
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Retent No. 5834290

GENERAL INFORMATION:
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Rezombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Bnzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
STREET: 10155 Avenue of the Americas
COUNTRY: U.S.A.
ZIP: 101036-2787

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U.84

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OPERATING SYSTEM: DOS
SOFTWARE: FaetSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 424
FILING DATE:
FILING DATE:
APPLICATION NUMBER: 35,441
REGISTRATION NUMBER: 35,441
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELEPHONE: 847/935-1729
TELEPHONE: 847/938-2623
TELEFAX: 847/938-2623
TELEFAX: POP CECT TO NO. 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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NAME: Sterner Richard J.
REGISTRATION UNDRER: 35,372
REFERENCE/DOCKET UNDRER: 1103:
TELECOMMUNICATION INFORMATION:
TELEFRAM: (212) 354-8113
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                33:
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MOLECULE TYPE: No. 6232456e
                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 VLVNERWVL 37
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US-09-654-600A-4
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US-09-644-600-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
US-09-154-344-12
; Sequence 12, Application US/09154344
; Patent No. 5981256
; GENERAL INFORMATION:
    APPLICANT: Egelrud, Torbjorn
    APPLICANT: Bellrud, Torbjorn
    APPLICANT: Brown Combinant Stratum Corneum Chymotryptic
    TITLE OF INVENTION: Enzyme (SCCE)
    TITLE OF INVENTION: Enzyme (SCCE)
    TITLE OF SEQUENCES: 17
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: White & Case, Patent Department
    STREET: 1155 Avenue of the Americas
    CITY: New York
    COUNTRY: U.S.A.
    ZIP: 10036-2787
    COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBH PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
    CUBRENTION UNBER: US/09/154,344
    FILING DATE: 16-SEP-1998
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                                                                        100.0%; Score 47; DB 1; Length 225; 100.0%; Pred. No. 0.62; tive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 47; DB 1; Length 225; Best Local Similarity 100.0%; Pred. No. 0.62; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-08-557-146-12
                                                                        Ouery Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                      30 VLVNERWVL 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                          RESULT 6
US-09-027-337-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-027-337-4
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RESULT 12
US-09-154-344-2
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US-08-557-146-2
i Sequence 2, Application US/08557146
j Patent No. 5834200
j GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
TITLE OF INVENTION:
TITLE OF INVENTION: Brayme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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COUNTRY: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PLOPPY disk
COMPU
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 47; DB 2; Length 225; Best Local Similarity 100.0%; Pred. No. 0.62; Matches 9; Conservative 0; Mismatches 0; Indels
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100.0%; Score 47; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 9; Conservative 0; Mismatches 0; Indels
; 09/027,337
; PRIOR FILING DATE: 1999-10-20
1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                     THER INFORMATION: SCCE
                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 VLVNERWVL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VLVNERWVL 9
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                                                                                                                                                                                                                                                                                                  FEATURE:
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RESULT 11 US-08-824-874-3

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| Sequence 1, Application US/08824874
| Sequence 1, Application US/08824874
| Patent No. 5962300
| GENERAL INFORMATION:
| APPLICANT: Hillman, Jennifer I. APPLICANT: July Porter Drive Paramecuticals, Inc.
| STREET: July Porter Drive Paramecuticals, Inc. STREET: July Porter Drive Paramecuticals, Inc. COMPUTES: Ind Computation Street: July Porter Drive Paramecuticals (Trice Paramecuticals) (
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Gaps

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Query Match
100.0%; Score 47; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09210084
; Sequence 3, Application US/09210084
; Patent No. 6197511
; GENERAL INFORMATION:
    APPLICANT: Hallman, Jennifer L.
    APPLICANT: Lal, Preeti
    TITLE OF INVENTION: NOVEL KALLIKREIN
    TITLE OF INVENTION: NOVEL KALLIKREIN
    NUMBER OF SEQUENCES: 5
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Incyte Pharmaceuticals, Inc.
    STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICALL...
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: B111ings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCY DOCKNUMICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
  , LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-930-188-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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58 VLVNERWVL 66
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TOPOLOGY: linear
IMMEDIATE SOURCE:
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Best Local Similarity
Matches 9; Conserv
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US-09-764-762-3
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Matches
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| Patent No. 6093397
| GENERAL INPORMATION:
| APPLICANT: Dixon, Eric P.
| APPLICANT: Dixon, Eric P.
| APPLICANT: Dixtle, Sheila P.
| TILE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: AMYLOID PRECURSOR ACIDS
| NUMBER OF SEQUENCES: 3
| CORRESPONDENCE ADDRESS: ADDRESSE: Bli Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 47; DB 1; Length 253; Best Local Similarity 100.0%; Pred. No. 0.7; Matches 9; Conservative 0; Mismatches 0; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
ATTONNEY/AGENT INFORMATION:
ATTONEY/AGENT INFORMATION:
TELEPHONE: Sterney, Richard J.
REGISTRATION NUMBER: 35,372
REGISTRATION NUMBER: 35,372
TELEPHONE: (212) 819-8783
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
ZIP: 46285
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTAATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 253 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-09-154-344-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 VLVNERWYL 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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Query Match

100.0%; Score 47; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 9; Conservative 0; Mismatches 0; Indels
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ZIP: 94304

COMPUTER READABLE FORM:
MEDLIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILING DATE: I-Jan-2001
CLASSIFICATION: CURROWN>
PRIOR APPLICATION NUMBER: US/09/764,762
FILING DATE: CALCOWNOWN>
APPLICATION NUMBER: US/09/10,084
FILING DATE: CURROWN>
APPLICATION NUMBER: US/149
REPERRNCE/DOCKET NUMBER: 36,749
REFERRNCE/DOCKET NUMBER: 36,749
REPERRNCE/DOCKET NUMBER: BF-0252 US
TELEPHONE: 415-855-0555
TELEPHAN: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TYPE: US/09/07/07/10-20-04
Sequence 3, Application US/09764762

Patent No. 6472195

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

Lal, Preeti

TITLE OF INVENTION: NOVEL KALLIKREIN

NUMBER OF SEQUENCES: 5

CORRESPONDENCE S.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRAKY: Genbank
CLONRE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3
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1 VLVNERWVL 9

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Gaps

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Search completed: March 11, 2006, 01:24:25 Job time : 22.222 secs

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TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 34, Appl
Sequence 34, Appl
Sequence 100, App
Sequence 53737, A
Sequence 98, Appl
Sequence 96, Appl
Sequence 104, Appl
Sequence 102, Appl
Sequence 94, Appl
Sequence 94, Appl
Sequence 94, Appl
Sequence 94, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 48, Appl
Sequence 48, Appl
Sequence 48, Appl
Sequence 48, Appl
Sequence 69, Appl
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                                                                                                                                                                      March 11, 2006, 01:24:47; Search time 69.444 Seconds (without alignments) 54.151 Million cell updates/sec
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
                     GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications AA Main:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1867569 seqs, 417829326 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Best Local Similarity 100.0%; Fred. No. 1.7e+06; Matches 9; Conservative 0; Mismatches 0;
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Publication No. US20040038223A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       Guo, Xiaojia (Sasha)
Patturajan, Meera
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Ort, Tatiana
Gorman, Linda
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Miller, Charles E.
Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
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Edinger, Shlomit R.
Ellerman, Karen
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Anderson, David W.
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
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Catterton, Elina
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Li, Li
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ORGANISM: Homo sapiens
                                                             1 VLVNERWVL 9
                                                                                        1 VLVNERWVL
                                                                                                                                                                RESULT 5
US-10-262-511-100
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Sequence 34, Application US/2030223973A1

Sequence 34, Application No: US20030223973A1

Sequence 34, Application No: US20030223973A1

Septicant: Cannon, Martin J.

APPLICANT: Cannon, Martin J.

APPLICANT: Santin, Alessandro

TITLE OF INVENTION METHORS (US/10/372,521)

CURRENT APPLICATION NUMBER: US/10/372,521

CURRENT FILING DATE: 2003-02-21

PRIOR FILING DATE: 2001-07-30

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 34

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-831-075-34

Sequence 34, Application US/10831075

Publication No. US20040224891A1

GENERAL INFORMATION

APPLICANT: Cannon, Martin J.

APPLICANT: Cannon, Martin J.

APPLICANT: Santin, Alesandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

FILE REPERENCE: D6223CIP/C/D/CIP3

CURRENT PAPLICATION NUMBER: US/10/831,075

CURRENT PILING DATE: 2004-04-23

PRIOR APPLICATION NUMBER: US 10/372,521

PRIOR FILING DATE: 2003-02-21

NUMBER OF SEQ ID NOS: 140

LENGTH: 9
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                                                                                                                        100.0%; Score 47; DB 3; Length 9; 100.0%; Pred. No. 1.7e+06; Live 0; Mismatches 0; Indels
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                           NAME/KEY: CHAIN
NAME/KEY: CHAIN
OTHER INFORMATION: Residues 58-66 of the SCCE protein US-09-905-083-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 58-66 of the SCCE protein
US-10-372-521-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CHAIN
CHER INFORMATION: Residues 58-66 of the SCCE protein US-10-831-075-34
                                                                                                                    Query Match
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
FEATURE:
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                                                                        1 VLVNERWVL 9
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FILE REPERENCE: 2.1402-462C

CURRENT APPLICATION NUMBER: 60/326,483
FRICA APPLICATION NUMBER: 60/326,483
FRICA APPLICATION NUMBER: 60/326,483
FRICA FILING DATE: 2001-10-02
FRICA FILING DATE: 2002-04-19
FRICA FILING DATE: 2002-04-19
FRICA FILING DATE: 2002-05-17
FRICA FILING DATE: 2002-05-16
FRICA FILING DATE: 2002-05-16
FRICA FILING DATE: 2002-06-17
FRICA FILING DATE: 2002-04-17
FRICA FILING DATE: 2001-10-05
FRICA FILING DATE: 2002-04-17
FRICA FILING D
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APPLICANT: Shimkete, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Age, Michele L.
APPLICANT: Bergel, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-465C
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FRIOR PELING DATE: 2003-05-28

FRIOR PILING DATE: 2001-10-02

FRIOR FILING DATE: 2001-10-03

FRIOR FILING DATE: 2002-04-19

FRIOR FILING DATE: 2002-04-19

FRIOR FILING DATE: 2002-04-19

FRIOR FILING DATE: 2002-05-17

FRIOR FILING DATE: 2002-05-16

FRIOR FILING DATE: 2002-05-16

FRIOR FILING DATE: 2002-05-16

FRIOR FILING DATE: 2002-04-17

FRIOR FILING DATE: 2001-10-05

FRIOR FILING DATE: 2001-10-05

FRIOR FILING DATE: 2002-04-17

FRIOR FILING DATE: 2001-10-05

FRIOR FILING DATE: 2001-10-05

FRIOR PRIOR PRIOR APPLICATION NUMBER: 60/373,435

FRIOR FILING DATE: 2001-10-05

FREMAINING PRIOR APPLICATION NUMBER: 60/373,435

FRIOR FILING DATE: 2001-10-05

FREMAINING PRIOR APPLICATION NUMBER: 60/373,435

FRIOR FILING DATE: 2001-10-05

FREMAINING PRIOR APPLICATION NUMBER: 60/373,435

FRIOR FILING DATE: 2002-04-17

FREMAINING PRIOR APPLICATION NUMBER: 60/373,435

FRIOR FILING DATE: 2002-04-17

FREMAINING PRIOR APPLICATION NUMBER: 60/373,435

FRIOR FILING DATE: 2002-04-17

FREMAINING PRIOR APPLICATION NUMBER: 60/373,435

FRIOR FILING DATE: 2002-04-17

FREMAINING PRIOR APPLICATION NUMBER: 60/373,435

FRIENCE FILING DATE: 2002-04-17

FREMAINING PRIOR APPLICATION NUMBER: 60/373,435

                                                                                                                                 APPLICANT: Ji, Weizlen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: Pena, Carol E. A.
APPLICANT: Shinkets, Richard A.
APPLICANT: Lacach, Mark E.
APPLICANT: Lacach, Mark E.
APPLICANT: Berghe, Constance
APPLICANT: Berghe, Constance
TILLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
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; APPLICANT: Smithson, Glennda; APPLICANT: Millet, Isabelle
; APPLICANT: Rekuda, Ramesh; APPLICANT: Kekuda, Ramesh; APPLICANT: Li, Li,
; APPLICANT: Li, Li,
; APPLICANT: Li, Li,
; APPLICANT: Guo, Xiaojia (Sasha)
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Li, Li
Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
                             Zerhusen, Bryan D.
Anderson, David W.
Zhong, Mei
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Best Local Similarity 100.
Matches 9, Conservative
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LOCATION: (61)..(78)
OTHER INFORMATION: Serine proteases trypsin family, histidine proteins. domain
OTHER INFORMATION: identified by eMATRIX, accession number BL00134A, p-value=6.143e-
OTHER INFORMATION: 20, raw score of 11.96
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OTHER INFORMATION: Trypsin domain identified by PFam, accession name trypsin, E-

OTHER INFORMATION: value=3.2e-31, PFam score of 101.0
US-10-450-763-53737
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REFERENCE: 790CIP3/US

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR FILING DATE: 2000-03-30

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: Custom

SEQ ID NO 53737
                                                       100.0%; Score 47; DB 4; Length 97; 100.0%; Pred. No. 3;
                                                                                                                 0; Indels
                                                                                                                 0; Mismatches
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Publication No. US20040038223A1
GENERAL INFORMATION:
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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Malyankar, Uriel M.
Ort, Tatiana
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
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9; Conservative
                                                 Query Match
Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                     1 VLVNERWVL 9
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US-10-262-511-100
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APPLICANT:
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APPLICANT:
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STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
OF THE PROSTATE
                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 600643500
COMPUTER READMABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1EM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/789,210
FILING DATE: 20 Feb-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/944,483
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear;
MOLECULE TYPE: None
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-789-210-33
                                                                                             NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 104, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
; APPLICANT: Willet, Isabelle
; APPLICANT: Reyman, John A.
; APPLICANT: Reyman, John A.
; APPLICANT: Li, Jingfang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 224 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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TELEX: <UNANUMANION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
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Zerhusen, Bryan D.
Anderson, David W.
Zhong, Mei
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Malyankar, Uriel M.
Ort, Tatiana
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Best Local Similarity 100.
Matches 9; Conservative
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APPLICANT:
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APPLICANT:
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APPLICANT: Ages, Michaele L.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERENCE: 21402-462C
CURRENT APPLICATION NUMBER: 60/326,483
PRIOR PLILING DATE: 2001-10-02
PRIOR PLILING DATE: 2001-10-03
PRIOR PLILING DATE: 2001-10-09
PRIOR PLILING DATE: 2002-04-19
PRIOR PLILING DATE: 2002-04-19
PRIOR PLILING DATE: 2002-05-07
PRIOR PLILING DATE: 2002-05-16
PRIOR PLILING DATE: 2002-05-16
PRIOR PLILING DATE: 2002-05-16
PRIOR PLILING DATE: 2002-05-16
PRIOR PLILING DATE: 2001-10-09
PRIOR PLILING DATE: 2001-10-09
PRIOR PLILING DATE: 2001-10-09
PRIOR PLILING DATE: 2002-05-16
PRIOR PLILING DATE: 2002-04-17
PRIOR PLILING DATE: 2001-10-05
PRIOR PLING DATE: 2001-10-05
PRIOR PLILING DATE: 2001-10-05
PRIOR PLILING DATE: 2001-10-05
PRIOR PLILING DATE: 2001-10-05
PRIOR PLING DATE: 2001-10-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-09-789-210-33
; Sequence 33, Application US/09789210
; Publication No. UB20040241646A1
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; FRIEDMAN, FALL N. FRIEDMAN, PAULA N. GRANADOS, EDWARD N. KLASS, MICHARL R. RUSSELL, JOHN C. STEMART, KENT D.
                                                                                                                                                                Cattorion, Elina
Ji, Weizhen
Miller, Charles E.
Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
Shimkets, Richard A.
Ellerman, Karen
Malyankar, Uriel M.
Ort, Tatiana
                                                                                                                                                                                                                                                                                                                                                                       Rothenberg, Mark E.
Leach, Martin D.
Agee, Michele L.
                                                                        Gorman, Linda
Zerhusen, Bryan D.
Anderson, David W.
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
US-10-262-511-96
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58 VLVNERWVL 66
                                                                                                                                                   Zhong, Mei
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APPLICANT:
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APPLICANT:
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                                     Gaps
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100.0%; Score 47; DB 3; Length 224; 100.0%; Pred. No. 6.5; cive 0; Mismatches 0; Indel8
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Gorman, Linda
                                                                                                       FEATURE:
CTHER INFORMATION: SCCE
US-10-600-187-4
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Li, Li
SEQ ID NO 4
LENGTH: 225
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                     30 VLVNERWYL 38
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US-10-262-511-102
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APPLICANT:
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APPLICANT: Rothenborg, Martin D.

APPLICANT: Age, Michele L.

APPLICANT: Age, Michele L.

APPLICANT: Age, Michele L.

APPLICANT: Berghs, Constance

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

CURRENT FILING DATE: 2003-05-28

PRIOR APPLICATION NUMBER: 60/337,917

PRIOR PILING DATE: 2002-06-10-09

PRIOR FILING DATE: 2002-05-17

PRIOR PILING DATE: 2002-05-17

PRIOR PILING DATE: 2002-05-16

PRIOR PILING DATE: 2002-05-17

PRIOR APPLICATION NUMBER: 60/381,038

PRIOR APPLICATION NUMBER: 60/381,666

PRIOR PILING DATE: 2002-05-17

PRIOR APPLICATION NUMBER: 60/373,260

PRIOR PILING DATE: 2002-04-17

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NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 104
LENGTH: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/10600187

Publication No. US20040086910A1

GENERAL INFORMATION

APPLICANT: O'Brien, Timothy J.

APPLICANT: Tanimoto, Hirotoshi

TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease

FILE REFERENCE: D6064CIP/D

CURRENT APPLICATION NUMBER: US/10/600,187

CURRENT FILING DATE: 2003-06-20

PRIOR PILING DATE: 2000-09-01

PRIOR PLICATION NUMBER: 09/421,213

09/027,337

PRIOR FILING DATE: 1999-10-20

1998-02-20

NUMBER OF SEQ ID NOS: 98
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                                                                         Stone, David J. Stone, Carol E. A. Shenoy, Suresh G. Shimkets, Richard A. Shimkets, Richard A.
                                                      , Charles E.
     Catterton, Elina
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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100.0%;
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Anderson, David W.
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Ji, Weizhen
Miller, Charles E.
Rastelli, Luca
Stone, David J.
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
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Li, Li
                                                                                                                                                                                           TYPE: PRT
CORGANISM: Homo sapiens
US-10-262-511-92
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Best Local Similarity
Matches 9; Conserv
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APPLICANT: Miller. Charles E.
APPLICANT: Maller. Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shanker, Richard A.
APPLICANT: Shanker, Richard A.
APPLICANT: Shanker, Richard A.
APPLICANT: Beach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 2140-2462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
                                                                                                                                                                                                                                                         Gaps
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR FILING DATE: 2001-10-05
Remaining Prior Application data removed - See File Wrapper or PALM.
WUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                           Query Match 100.0%; Score 47; DB 4; Length 247; Best Local Similarity 100.0%; Pred. No. 7.1; Matches 9; Conservative 0; Mismatches 0; Indels
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PRIOR FILING DATE: 2001-10-02
PRIOR PELING DATE: 2001-10-02
PRIOR PELING DATE: 2001-10-02
PRIOR PELING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327, 917
PRIOR APPLICATION NUMBER: 60/327, 917
PRIOR PELING DATE: 2001-10-09
PRIOR FILING DATE: 2002-05-17
PRIOR PELING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 60/328, 029
PRIOR APPLICATION NUMBER: 60/328, 039
PRIOR PELING DATE: 2002-05-16
PRIOR PELING DATE: 2002-06-16
PRIOR FILING DATE: 2001-00-09
PRIOR FILING DATE: 2001-00-09
PRIOR FILING DATE: 2001-00-09
PRIOR PELING DATE: 2001-00-09
                                                                                                                                                                                                                                                                                                                                                                                        Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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Malyankar, Uriel M.
Ort, Tatiana
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Zerhusen, Bryan D.
Anderson, David W.
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0; Gaps
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR PILING DATE: 2003-04-19
PRIOR FILING DATE: 2001-10-05
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 92
LENGTH: 250
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APPLICANT: Rothenberg, Mark B.
APPLICANT: Leach, Marthin D.
APPLICANT: Age, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: ONDEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERENCE: 21402-462C
                                                                                                                                                                                                                                                                                                                                                               ; Score 47; DB 4; Length 250;
; Pred. No. 7.2;
0; Mismatches 0; Indels
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CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR PLILNG DATE: 2001-10-02
PRIOR FILING DATE: 2001-10-03
PRIOR PLILNG DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/37,917
PRIOR APPLICATION NUMBER: 60/31,642
PRIOR FILING DATE: 2001-10-09
PRIOR PLILNG DATE: 2002-05-17
PRIOR PLILNG DATE: 2002-05-17
PRIOR FILING DATE: 2002-10-09
PRIOR FILING DATE: 2002-10-09
PRIOR FILING DATE: 2002-05-17
PRIOR FILING DATE: 2002-05-16
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
Ort, Tatiana
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Search completed: March 11, 2006, 01:37:23 Job time : 70.4444 secs

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Sequence 1533, Ap Sequence 149, App Sequence 210, App Sequence 23071, A Sequence 86, Appl Sequence 47, Appl Sequence 47, Appl Sequence 32, Appl Sequence 31, Appl Sequence 61, Appl Sequence 62, Appl Sequence 62, Appl Sequence 63, Appl Sequence 1043, Ap

260,

Sequence 10, Sequence 2, A Sequence Sequence 8

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Query Match
100.0%; Score 47; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels
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US-10-412-748-11
; Sequence 11, Application US/10412748
; Publication No. US20060035219A1
; Publication No. US20060035219A1
; GENERAL INFORMATION:
    APPLICANT: Queensland University of Technology
    APPLICANT: Clements, Judith A
    TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERBING: DAVIATO:003404
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
    NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin version 3.2
; LENGTH: 253
; TYPE: PRT
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Publication No US20060035219A1
GENERAL INPORMATION:
APPLICANT: Queensland University of Technology
TITLE OF INVENTION: Aberrant Kallikrein Expression
FILE REFRENCE: DAVI172.003AUS
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US/10/412,748
CURRENT FILING DATE: 2003-04-09
PRIOR FILING DATE: 2003-04-09
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
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US-10-821-234-1043
US-11-096-568A-23070
US-11-166-028-1
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US-11-080-991-86
US-11-019-711-130
US-11-174-816-47
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US-11-074-176-260
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US-11-174-819-81
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TYPE: PRT
ORGANISM: Human
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US-10-412-748-21
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Sequence 11, Appl
Sequence 14, Appl
Sequence 19, Appl
Sequence 39, Appl
Sequence 114, Appl
Sequence 114, Appl
Sequence 59, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 17, Appl
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Sequence 140, App
Sequence 141, App
Sequence 133, App
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40, Appl
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Sequence 39, Appl
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                                                                                                                                                                                                                                              March 11, 2006, 01:27:17 ; Search time 8 Seconds
    (without alignments)
    31.314 Million cell updates/sec
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Sequence 40,
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1: /cgn2_6/ptodata/2/pubpaa/US06_NEW_FUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_FUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_FUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_FUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/US10_NEW_FUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US11_NEW_FUB.pep:*
                                     GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-151-601-39

US-11-151-601-39

US-11-174-816-44

US-11-174-816-44

US-11-174-816-44

US-11-174-819-18

US-11-174-819-18

US-11-174-819-18

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US-11-043-788-141

US-11-043-788-141

US-11-043-788-137

US-11-043-788-137

US-11-043-788-137

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                                                         Query Match 100.0%; Score 47; DB 6; Length 253; Best Local Similarity 100.0%; Pred. No. 0.12; Matches 9; Conservative 0; Mismatches 0; Indels
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Fublication No. US20060035219A1
GENERAL INFORMATION:
APPLICANT: Queensland University of Technology
APPLICANT: Clements, Judith A
TITHE OF INVENTION: Aberrant Kallikrein Expression
FILE REFERENCE DAVITY.003AUS
CURRENT APPLICATION NUMBER: US/10/412,748
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: W PS1616/02
PRIOR FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 41
SOFFWARE: Patentin version 3.2
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; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
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SOFTWARE: Patentin version 3.2
SEQ ID NO 17
LENGTH: 253
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Human
; ORGANISM: Human
US-10-412-748-11
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RESULT 5

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Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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COTHER INFORMATION: mTAAR6

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192 VVVNQNWVL 200
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  ; TYPE: PRT
; ORGANISM: Mus musculus
US-11-174-816-44
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US-11-174-816-44

Sequence 44, Application US/11174816

Publication No. US2006009441A1

GENERAL INFORMATION:
APPLICANT: BEBLING, MARTIN

APPLICANT: HOENER, MARINS

APPLICANT: LINDEMANN, LOTHAR

ITLE OF INVENTION: HUMAN TRACE AMINE ASSOCIATED RECEPTORS

FILE REPERENCE: 22645

CURRENT APPLICATION NUMBER: US/11/174,816

CURRENT FILING DATE: 2005-07-05

PRIOR APPLICATION NUMBER: EP 04103261.6

PRIOR APPLICATION NUMBER: EP 04103261.6

NUMBER OF SEQ ID NOS: 115

SOFTWARE: PatentIn version 3.3

SEQ ID NO 44

LENGTH: 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 78.7%; Score 37; DB 7; Length 359; Best Local Similarity 87.5%; Pred. No. 12; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                           Score 38; DB 7; Length 81;
Pred. No. 1.8;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                         RESULT 7

US-11-037-243-114

Sequence 114, Application US/11037243

Publication No. US20050287546A1

GENERAL INFORMATION:
APPLICANT: CARREPELL, SEAN
APPLICANT: CARREPELL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: GLENARM, SUCHA
TITLE OF INVERTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT FILNG DATE: 2005-05-26
PRIOR APPLICATION NUMBER: US/09/888,615
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SEQ ID NO 114
SEQ ID NO 114
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 39
LENGTH: 81
                                                                                                                             ; FEATURE:
; OTHER INFORMATION: consensus sequence
US-11-151-601-39
                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                           Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CORGANISM: Homo sapiens
US-11-037-243-114
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122 LVRERWVL 129
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5 LINEOWVL 12
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                                                     Gaps
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US-11-174-819-13

Sequence 13. Application US/11174819

Publication No. US2006008880A1

GENERAL INFORMATION:

APPLICANT: BERLING, MARTIN

APPLICANT: HORBER, MARTUS

APPLICANT: LINDEMANN, LOTHAR

TITLE OF INVENTION: MOUSE TRACE AMINE ASSOCIATED RECEPTORS AND

TITLE OF INVENTION: DOLYPEPTIDES

FILE REPERENCE: 22646

CURRENT FILING NATE: 2005-07-08

FILE REPERENCE: 2064-07-08

PRIOR APPLICATION NUMBER: EP 04101262.4

PRIOR PELLING DATE: 2004-07-08

NUMBER OF SEQ ID NOS: 136

SOFTWARE: PATENTIN VERBION 3.3

SEQ ID NO 13

LENGTH: 345

TYPE: PRT

CORMANISM: MUSECULUS

CORMANISM: MUSECULUS
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                                                                                                                                                                                                                                                    Sequence 59, Application US/11174816

Publication No. US20060003441A1

GENERAL INFORMATION:

APPLICANT: EBELING, MARTIN

APPLICANT: LINDEMANN, LOTHAR

TITLE OF INVENTION: HUMAN TRACE AMINE ASSOCIATED RECEPTORS

FILE REFERENCE: 22645

CURRENT FILING DATE: 2005-07-05

FRICK APPLICATION NUMBER: EP 04103261.6

PRIOR FILING DATE: 2004-07-08

NUMBER OF SEQ ID NOS: 115

SOFTWARE: PATENTING DATE: 2004-07-08

NUMBER OF SEQ ID NOS: 115

SOFTWARE: PATENTING DATE: 3004-07-08

LENGTH: 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.6%; Score 36; DB 7; Length 345; 66.7%; Pred. No. 18; tive 2; Mismatches 1; Indels
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7; Length 345;
                                                  1; Indels
Score 36; DB
Pred. No. 18;
2; Mismatches
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RESULT 13
US-10-821-234-1274
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US-11-043-788-141
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Sequence 78, Application US/11174819

Publication No. US2006008880A1

Publication No. US2006008880A1

GENERAL INFORMATION:

APPLICANT: BEBLING, MARTIN

APPLICANT: HOBIER, MARIUS

TITLE OF INVENTION: MOUSE TRACE AMINE ASSOCIATED RECEPTORS AND

TITLE OF INVENTION: POLYPEPTIDES

TITLE OF INVENTION: POLYPEPTIDES

CURRENT APPLICATION NUMBER: US/11/174,819

CURRENT APPLICATION NUMBER: EP 04103262.4

PRIOR FILING DATE: 2004-07-08

NUMBER OF SEQ ID NOS: 136

SEQ ID NO S: 136

SEQ ID NO S: 136

SEQ ID NO S: 136
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Pred. No. 18;
2; Mismatches 1; Indels
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US-11-037-243-97

Sequence 97, Application US/11037243

Sequence 97, Application US/11037243

PADLICATION. US2005028'546A1

GENERAL INFORMATION:

APPLICANT: HINTE, DAVID

APPLICANT: CHENEPEEL, SEAN

APPLICANT: CHENEPEEL, SEAN

APPLICANT: CHENEPEEL, SEAN

APPLICANT: CHENEPEEL, SEAN

TITLE OF INVENTION: NOVEL PROTEASES

TITLE OF INVENTION: NOVEL PROTEASES

FILE REFERENCE: 036602/1214

CURRENT PELING DATE: 2005-05-26

PRIOR APPLICATION NUMBER: US/09/888,615

PRIOR APPLICATION NUMBER: 60/214,047

PRIOR APPLICATION NUMBER: 60/214,047

PRIOR APPLICATION NUMBER: 60/214,047

PRIOR APPLICATION NUMBER: 60/214,047

PRIOR APPLICATION NUMBER: 500-06-26

NUMBER: OF SEQ ID NOS: 150

SEQ ID NO 97

LENGTH: 1128

LENGTH: 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.6%;
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Best Local Similarity 66.,
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Best Local Similarity 77.8
Matches 7; Conservative
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192 VVVNQNWVL 200
                      |:||: |||
192 VVVNQNWVL 200
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925 VLVAERWLL 933
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ORGANISM: Homo sapiens
US-11-037-243-97
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Sequence 141, Application US/11043788

Publication No. US20060014166A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Compuged Ltd
TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF ENDOMETRIOSIS
TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF ENDOMETRIOSIS
GURRENT APPLICATION NUMBER: US/11/043,788
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 506
SEQ ID NO 141
LENGTH: 307
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Fublication No. US20060014166A1

GENUERAL INFORMATION:
APPLICANT: Compugen Ltd
APPLICANT: Compugen Ltd
TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF ENDOMETRIOSIS
TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF ENDOMETRIOSIS
TITLE OF INVENTION: US/11/043,788
CURRENT APPLICATION NUMBER: US/11/043,788
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 506
LENGTH: 299
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Sequence 1274, Application US/10821234

Sequence 1274, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

APPLICANT: Tang, Y. Tom

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REFERENCE: 821

CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT FILING DATE: 2003-04-07

PRIOR APPLICATION NUMBER: US 60/462,047

PRIOR PILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704-07

SEQ ID NO 1274

LENGTH: 236
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Best Local Similarity 62...
5, Conservative
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VLVNERWVL 9
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84 LINEQWLL 91
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-788-141
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Query Match 74.5%; Score 35; DB 7; Length 307; Best Local Similarity 62.5%; Pred. No. 24; Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps

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2 LUNERWUL 9 |:||:||:| 92 LINEQWLL 99

ò g Search completed: March 11, 2006, 01:38:41 Job time : 9 secs

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OM protein - protein search, using sw model

March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds (without alignments) 45.628 Million cell updates/sec Run on:

US-09-905-083A-35

Perfect score:

1 LLPLQILLL 9 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2443163 Total number of hits satisfying chosen parameters: 2443163 segs, 439378781 residues Searched:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

A\_Geneseq\_21:\*
1: geneseqp1980s:\*
2: geneseqp190s:\*
4: geneseqp2000s:\*
5: geneseqp2001s:\*
6: geneseqp2003as:\*
7: geneseqp2003as:\*
8: geneseqp2003bs:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STAMMIN

		di			SUMMAKIES	
Result No.	Score	Query Match	Query Match Length DB	DB	ID	
1	40	100.0	9	4	AAE08240	Aae08240 Human str
7	40	100.0	σ	ω	ADR68796	Adr68796 Human str
٣	40	100.0	136	4	ABG23378	Abg23378 Novel hum
4	40	100.0	198	ø	ADA05736	Ada05736 Human NOV
ß	40	100.0	198	œ	ADN62900	Adn62900 Human NOV
9	40	100.0	250	9	ADA05732	Ada05732 Human NOV
7	40	100.0	250	80	ADN62896	Adn62896 Human NOV
80	40	100.0	253	~	AAR67888	Aar67888 Human str
σ	40	100.0	253	N	AAW05383	Aaw05383 Human amy
10	40	100.0	253	Ŋ	ABB84421	Abb84421 Human SCC
11	40	100.0	253	'n	ABB84406	Abb84406 Human SCC
12	40	100.0	253	'n	AAU82740	Aau82740 Amino aci
13	40	100.0	253	ø	ABU07440	Abu07440 Protein d
14	40	100.0	253	9	ABU07471	Abu07471 Protein d
15	40	100.0	253	9	ABR58471	Abr58471 Human str
16	40	100.0	253	7	ADB80484	Adb80484 Ovarian c
17	40	100.0	253	7	ADJ68833	Adj68833 Human hea
18	40	100.0	253	7	ADN39180	Adn39180 Cancer/an
19	40	100.0	253	œ	ADL06515	Adl06515 Human tum
20	40	100.0	253	œ	ADN04182	Adn04182 Antipsori
21	40	100.0	253	œ	ADR72880	Adr72880 Human ova
22	40	100.0	253	σ	ADY67588	Ady67588 Human kal
23	40	100.0	253	σ	AEC00353	Aec00353 Human kal
24	40	100.0	257	٣	AAB21326	Aab21326 Human HSC

Aab63580 Human gas Aab63582 Human gas Aab63582 Human gas Aac08238 Human str Adr68794 Human str Adr68794 Human str Adr68794 Human str Adr68794 Human str Ads21222 Bacterial Ab43858 Peptide # Aam37771 Peptide # Aam64837 Human bre Apg59233 Human liv Abg59233 Human liv Abg59231 Human pep Aaw98431 H. pylori Ady22422 Plant ful Ady32291 Human sec Ada11692 Human nov Aaw89030 Polypepti Abb51130 Human sec Abb51130 Human sec Abb51130 Human sec Abb51130 Human sec	
4 AAB63580 4 AAB63582 4 AAB63582 4 AAB08238 8 ADR68794 6 AB021322 4 AB843858 4 AAM64837 4 AAM64837 4 ABG59233 5 ABG46617 2 AAW98431 2 AAW98030 6 AD81130 6 ABB51130 7 ABB51130	4 AAO08397
4421 88 46 46 46 46 46 46 46 46 46 46 46 46 46	98
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	85.0
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24444444444444444444444444444444444444	45

## ALIGNMENTS

AAE08240 standard; peptide; 9 AA. RESULT 1 AAE08240

AAE08240;

(first entry) 01-NOV-2001 Human stratum corneum chymotrypsin enzyme peptide #5 (residues 6-14).

Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia. 

Homo sapiens

WO200159158-A1.

16-AUG-2001.

07-FEB-2001; 2001WO-US003977.

11-FEB-2000; 2000US-00502600.

(UYAR-) UNIV ARKANSAS

O'brien TJ;

WPI; 2001-514676/56.

Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme

Claim 25; Page 103; 127pp; English.

The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCB). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide

Sequence 9 AA;

(first entry)

```
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                       Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                             Novel human diagnostic protein #23369.
               ABG23378 standard; protein; 136 AA.
                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-639362/73.
N-PSDB; AAS87565.
                                                                                                                                                                                                                                                                                                                                           Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC
                                                                                                                                                                                         WO200175067-A2
                                                                                                                                                                 Homo sapiens.
                                                                    18-FEB-2002
                                                                                                                                                                                                                   11-OCT-2001
                                         ABG23378;
               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          against stratum corneum chymotrytic coryme (SCCE), comprising incentating an individual with a SCCE peptide, which elicits an immune response in the individual with a SCCE peptide, which elicits an immune response in the individual A peptide of the invention acts as a stratum corneum chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or at risk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligonucleotide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or peptides are also useful in the monitoring and development of immunotherapies for ovarian and other malignancies. The present sequence represents a peptide fragment of serine protease SCCE (stratum corneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
                                                                                                                                                                                                                                               Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel method for vaccinating an individual
                                          Gaps
                                          ;
0
                                                                                                                                                                                                                                                                         protease; stratum corneum chymotrytic enzyme; SCCE; response; ovarian cancer; lung cancer; prostate cancer;
            100.0%; Score 40; DB 4; Length 9; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 40; DB 8; Length 9; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; SEQ ID NO 35; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Santin A;
                                                                                                                                                              ADR68796 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                    pancreatic cancer; colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-2004; 2004WO-US005134.
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                                                                                                                                                                                                                    (first entry)
Query Match
Best Local Similarity luv...
3, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'brien TJ, Cannon MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYAR-) UNIV ARKANSAS
                                                                    1 LLPLQILLL 9
                                                                                     WPI; 2004-653294/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chymotrytic enzyme)
                                                                                                                                                                                                                                                                                                                                                         WO2004075723-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9 AA;
                                                                                                                                                                                                                   02-DEC-2004
                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                    10-SEP-2004.
                                                                                                                                                                                           ADR68796;
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                                                                                                                                                                                                                                                                          serine
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Tang YT;

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed can disconstitute of (II) as useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful in somethodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating cupplement. (II) and (II) and (II) are useful for treating disorders in volving aberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in dispinance of sequences. Abg00010-Abg30377 represent novel human diagnostic amino acid sequences. Abg00010-Abg30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in account of parts of the invention are appeared in the printed specification, but was obtained in a constant of the constant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                       Claim 20; SEQ ID NO 53737; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published pct sequences
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biodiversity.
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ID ADAC
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Best Local Similarity 100. Matches 9; Conservative

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RESULT 3 ABG23378

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Zerhusen BD, Anderson DW, Zhong M, Catterton B; Rastelli L, Stone DJ, Pena CEA, Shenoy SG; enberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; I EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
                                                                                  human; NOVX; antidiabetic; anorectic; antibacterial; virucide, immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obsity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
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SR, Ellerman K,
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1, Edinger
                                                         Human NOV18c protein SEQ ID NO:96
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                                                                                                                                                                                                                                                                                                            02-OCT-2001; 2001US-0326483P.
05-OCT-2001; 2001US-0327435P.
05-OCT-2001; 2001US-0327449P.
09-OCT-2001; 2001US-0329174P.
09-OCT-2001; 2001US-0328029P.
09-OCT-2001; 2001US-0328044P.
12-OCT-2001; 2001US-0328044P.
12-OCT-2001; 2001US-0338049P.
12-OCT-2001; 2001US-0339142P.
13-OCT-2001; 2001US-0339109P.
24-OCT-2001; 2001US-0339266P.
24-OCT-2001; 2001US-0349575P.
01-NOV-2001; 2001US-0349575P.
01-NOV-2001; 2001US-0346357P.
01-NOV-2001; 2001US-034635P.
01-NOV-2001; 2001US-034635P.
01-NOV-2001; 2001US-034635P.
01-NOV-2001; 2001US-034635P.
01-NOV-2001; 2001US-034635P.
01-NOV-2001; 2001US-034635P.
01-NOV-2002; 2002US-0373812P.
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ts RA, Rothenberg ME, I
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22-APR-2002; 2002US-0374977P.
16-MAY-2002; 2002US-0381037P.
16-MAY-2002; 2002US-0381042P.
17-MAY-2002; 2002US-0381642P.
28-MAY-2002; 2002US-0381642P.
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Ort T, Gorman L, Zerhuse
                           06-NOV-2003 (first entry)
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N-PSDB; ADA05735.
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22-APR-2002;
16-MAY-2002;
16-MAY-2002;
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Shimkets RA,
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described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a Novx protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically comprising the above vector; (6) an antibody that immunospecifically comprising the above vector; (6) an antibody that immunospecifically compressed associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for a modulator different in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for a babove; (10) a method for identifying a potential therapeutic agent for a battant physical interactions of the polypeptide described above; (13) a method of activity or of activity or of altency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating or a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating or pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide; Novyx sequences have antidabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, nocropic, neuroprotective, antiparkinsonian antilipaemic activities, and can be used in gene therapy. The collapores such as diabetes or obesity, infections, cachexia, and cancer, and antilipaemic activities, and can be used in gene therapy. The syndrome associated with a human disease. The polypeptide or the nucleic addisorders such as diabetes or obesity, infections, cachexia, and cancer collaporates and as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoletic disorders such as Alzheimer's disease or Parkins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia, cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
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05-OCT-2001; 2001US-0327435P.
05-OCT-2001; 2001US-0327449P.
09-OCT-2001; 2001US-0328029P.
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 198 AA;
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09-0CT-2001; 2001US-0328044P.
12-0CT-2001; 2001US-0328056P.
15-0CT-2001; 2001US-0328449P.
17-0CT-2001; 2001US-0329414P.
17-0CT-2001; 2001US-0330142P.
18-0CT-2001; 2001US-0339266P.
24-0CT-2001; 2001US-0349578P.
24-0CT-2001; 2001US-0346357P.
01-NOV-2001; 2001US-0346357P.

2002US-0374977P. 2002US-0381037P. 2002US-0381088P. 2002US-0381642P. 2002US-0381642P.

16-MAY-2002; 28-MAY-2002; 39-MAY-2002;

2002US-0383831P 2002US-0391335P

25-JUN-2002;

MILLET I. PEYMAN J A. KEKUDA R.

(PEYM/

SMITHSON G.

(/IIWS

PATTURAJAN M. SPYTEK K A. EDINGER S R. ELLERMAN K. MALYANKAR U M.

SPYT/)

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ZERHUSEN B D. ANDERSON D W.

ZERH/) ZHON/

ANDE/

GORMAN L.

CATTERTON E.

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ZHONG M.

2002US-0373815P. 2002US-0373817P. 2002US-0373826P. 2002US-0373884P.

19-APR-2002; 22-APR-2002; 16-MAY-2002; 16-MAY-2002; 17-MAY-2002;

19-APR-2002; 19-APR-2002;

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The invention relates to isolated NOVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the abberrant expression and activity of NOVX by supplementing the patient our polypeptides and carivity of NOVX by supplementing the patient our control of the activity of NOVX by supplementing the patient our control of the activity of NOVX by supplementing the patient our control of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by confidential with the cells own genes and preventing their expression. NOVX polymelecules and complementary sequences may also be used as DNA production of antibodies and so which patients may be in need of similar sequences in assays to detect and quantitate the presence of similar sequences in assays to detect and quantitate the presence of similar sequences in assays to detect and antiquity of NOVX. The crestorative therapy. NOVX polypeptides may also be used as antidens and antiquity of NOVX. The anti-NOVX polypeptide and in assays to identify modulators candiance NOVX polypeptide expression and activity of NOVX. The canti-NOVX polypeptide expression and activity of NOVX colypeptides. The anti-NOVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX colypeptides and polymucleotides may be used in this way to prevent, and acceptance and treat: metat: metating disorders, diagnose and treat: metating disorders, diagnose and treat: metating disorders, diagnose and treat: metating disorders, diaberes, observed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, haematopoletic disorders, and the various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
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Claim 1; SEQ ID NO 96; 395pp; English.
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2001US-0327435P.
2001US-0327449P.
2001US-0327917P.
2001US-0328029P.
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|LLPLOILLL 14
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Best Local Similarity
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09-OCT-2001;
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R, Ellerman K, Malyankar UW;
lerson DW, Zhong M, Catterton B;
ne DJ, Pena CEA, Shenoy SG;
MD, Agee ML, Berghs C, Dipippo VA;
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Leach MD, Agee ML, DK, Spaderna SK;

Rieger DK,

Gangolli EA,

Eisen A,

WPI; 2004-213931/20. N-PSDB; ADN62899.

ek KA, Edinger SR, Ellerma Zerhusen BD, Anderson DW, Rastelli L, Stone DJ, Pena

Rastelli L,

Ji W, Miller CE, Rastelli L Shimkets RA, Rothenberg ME,

Patturajan M, Spytek KA, Ort T, Gorman L, Zerhuse

Peyman JA,

Millet I,

Smithson

EISEN A. GANGOLLI E A. AGEE M L. BERGHS C. DIPIPPO V A.

EISE/)

(AGEE/) (BERG/)

RIEGER D K. SPADERNA S K.

(GANG/) (RIEG/) (SPAD/)

MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
LEACH M D.

SHIM/) ROTH/) (LEAC/)

(RAST/) (STON/)

PENA/

SHEN/

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09-OCT-2001; 2001US-0328056P.
15-OCT-2001; 2001US-0328149P.
17-OCT-2001; 2001US-0339144P.
17-OCT-2001; 2001US-0330142P.
28-OCT-2001; 2001US-0330309P.
24-OCT-2001; 2001US-0339266P.
24-OCT-2001; 2001US-0339266P.
29-OCT-2001; 2001US-0349575P.
01-NOV-2001; 2001US-0349575P.
19-APR-2002; 2002US-0373816P.
19-APR-2002; 2002US-0373826P.
19-APR-2002; 2002US-0373826P.
19-APR-2002; 2002US-0373826P.
19-APR-2002; 2002US-0373826P.
19-APR-2002; 2002US-0373826P.
16-MAY-2002; 2002US-0373826P.
16-MAY-2002; 2002US-0381038P.
16-MAY-2002; 2002US-0381042P.
17-MAY-2002; 2002US-0381642P.
25-JUN-2002; 2002US-0381642P.
                                                                                                                                                                01-OCT-2002; 2002US-00262511
                                                                                                                                                                               (CURA-) CURAGEN CORP.
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                                                                                                                                                                                                                                                     N-PSDB; ADA05731.
                                                                                                                                                                                                                                                                                        pharmacogenomics
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Dipippo VA; Catterton E; Guo X; Malyankar UM; Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar U Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Cattert Jiw, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Di Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or

Claim 1; Page 169-170; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising a polypeptide described above; in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a disease associated with altered levels of expression of the above correctly altered levels of expression of the above correctly an encloded a disease associated with altered levels of expression of the above correctly of interesting an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiclogical interactions of the polypeptide described above; (10) a method for addulator of activity or of latency or predisposition to correctening for a modulator of activity or of latency or predisposition to the activity of the polypeptide described above; (12) methods of modulator or preventing a pathology associated with the polypeptide; (12) method for modulating the activity or of latency or predisposition to correct a partology associated with the above polypeptide in a method for producing the above polypeptide in a method for producing the above polypeptide in a crivity of the polypeptide above; (13) methods of correctly infections, captoratic, anoretic, antibacterial, virucide, and antilipaemic activities, and can be used in gene therapy. The colypeptide is useful in manufacturing a medicament for treating a cyndrone associated with a human disease. The polypeptide or the nucleic acid molecule may be used to disease. The protections, cacid molecule may be used to disease. The protecti

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disease, immune disorders, haematopoietic disorders and various dyslighdaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
                                                                                                                                                                                                                                                                                                                                                                   human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
                                                                                                                                    Gaps
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                                                                                                         6; Length 250;
                                                                                                                                   0; Indels
                                                                                                      Score 40; DB Pred. No. 27; 0; Mismatches
                                                                                                                                                                                                                                                        ADN62896 standard; protein; 250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-OCT-2001; 2001US-0327455F.
05-OCT-2001; 2001US-0327455F.
09-OCT-2001; 2001US-0328044P.
09-OCT-2001; 2001US-0328044P.
09-OCT-2001; 2001US-0328044P.
12-OCT-2001; 2001US-0328044P.
11-OCT-2001; 2001US-0328144P.
11-OCT-2001; 2001US-0339144P.
11-OCT-2001; 2001US-0339144P.
12-OCT-2001; 2001US-0319266P.
24-OCT-2001; 2001US-0349575P.
12-APR-2002; 2001US-0345357P.
11-APR-2002; 2001US-0343815P.
11-APR-2002; 2002US-0373815P.
11-APR-2002; 2002US-0373815P.
11-APR-2002; 2002US-0373815P.
11-APR-2002; 2002US-0373815P.
11-APR-2002; 2002US-0373815P.
11-APR-2002; 2002US-0373815P.
12-APR-2002; 2002US-0373815P.
                                                                                                      100.0%;
Similarity 100.0%;
9; Conservative 0
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2002US-0381042P.
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                                                                                                                                                                                                                                                                                                             01-JUL-2004 (first entry)
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|LLPLQILLL 11
                                                                                                                                                            1 LLPLOILLL 9
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                                                                                                        Query Match
Best Local Similarity
                                                      present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                        wasting disorder.
                                                                              Sequence 250 AA;
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                                                                                                                                                                                                                                                                                                                                        Human NOV18a.
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MILIER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHENOY S G.
SHINGERS R A.
ROTHENBERG M E.
LEACH M D.
                         SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
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BERGHS C.
DIPIPPO V A.
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GANGOLLI E A.
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SPADERNA S K.
                     PATTURAJAN M.
                                                  ZERHUSEN B D.
ANDERSON D W.
                                                           ZHONG M.
CATTERTON E.
                                                                                                                                                                         WPI; 2004-213931/20.
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PEYMAN J P
KEKUDA R.
                                               GORMAN L.
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                 GUO X
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(SPAD/)
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(GANG/)
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(ZHON/)
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(MILL/)
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                     PATT/
                          SPYT/
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                                      MALY/
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The invention relates to isolated Novy polypetices and polymucleotides. Novy polypetides and polymucleotides to the invention relates to isolated Novy polypetides and activity of Novy polypetides and activity of Novy polypetides and cativity of Novy polypetides and activity of Novy polypetides and polymucleotides may be used to treat disorders associated with decreased coxpression or activity of Novy by supplementing the patient our coxplaint of Novy bolypetides and production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of Novy polypeptides by binding with the cells own genes and preventing their expression. Novy colymuclectides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and in assays to identify modulators (agonists and antibodies and in assays to identify modulators cantivovy polypeptide antibodies, agonists and antagonists may also be used as diagnostic agents for detecting the presence of NoVx in samples. NoVx polypeptides and polymucleotide may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, and the various dyslipidaemias, metabolic disorders, and the metabolic syndrome X and the Anderson and the metabolic syndrome X and and activity the metabolic syndrome X and Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen A, Gangolli EA, Rieger DK, Spaderna SK; The invention relates to isolated NOVX polypeptides and polynucleotides. Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease. Claim 1; SEQ ID NO 92; 395pp; English.

RESULT 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The enzyme encoded by this sequence is used in pharmaceutical, cosmetic and skin care products, especially to treat and prevent acne, xeroderma, or other hyperkeratotic conditions (e.g. callosities or keratosis pilaris), ichthyoses, paoriasis, eczema, etc. It is produced recombinantly following mammal, insect, plant, or microorganism transformation with plasmid pS507. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and related vectors, transformed cells and polypeptides, useful for treating skin disorders, e.g. acne or psoriasis, and for identification of
wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
                                                                                                                  Gaps
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callosities; keratosis pilaris; ichthyoses; eczema.
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                                                                                                                                                                                                                                                                                                                                                  Human stratum corneum chymotrophic recombinant enzyme (SCCE).
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                                                                                    Length 250;
                                                                                                                  0; Indels
                                                                                       8;
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                                                                                    100.0%; Score 40; DB
100.0%; Pred. No. 27;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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                                                          Sequence 250 AA;
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09-AUG-1995
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                   Human amyloid precursor protein protease (AAW05383) is involved in the processing or clearance of amyloid precursor protein to form beta-amyloid peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783) obtd. from a human lung library. Recombinant protease can be produced in transformed or transfected prokaryotic (partic. E. coli) or eukaryotic partic. AV-120 host cells. It is used to develop products for the design and testing of cods. useful for treating or preventing conditions associated with beta-amyloid peptide, esp. Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
                                                                                                                                                                                                                                                                                           New isolated human amyloid precursor protein protease - used to develop prods. for the treatment or diagnosis of associated conditions, esp.
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                                                                                        Amyloid precursor protein protease; Alzheimer's disease; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 40; DB 2; Length 253; Best Local Similarity 100.0%; Pred. No. 27; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human SCCE protein N-terminal fragment SEQ ID 48.
                                                                     Human amyloid precursor protein protease.
                                                                                                                                                                                                                                            Little SP;
          AAW05383 standard; protein; 253 AA.
                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 44-45; 55pp; English
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                                                                                                                                                                                                   95US-00416257
                                                 (first entry)
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                                                                                                                                                                                                                      (ELIL ) LILLY & CO ELI
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                                                                                                                                                                                                                                                                                                                Alzheimer's disease.
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                                                                                                                                                                                                                                                                        N-PSDB; AAT39783
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 253 AA;
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                                                                                                                                                                               02-APR-1996;
                                                                                                                      Homo sapiens
                                                                                                                                         WO9631122-A1
                                                                                                                                                                                                   04-APR-1995;
                                                 31-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                             10-OCT-1996.
                              AAW05383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB84421;
                                                                                                   therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
ABB8442
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This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneuw chymotryptic enzyme (SCCE) or its variant, or stratum corneuw chymotryptic enzyme (SCCE) or its variant, or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a cosmetic or a pharmaceutical formulation, and for the development of a diagnostic method. It can also be useful for screening or identifying a composation effective for the prevention or treatment of an abnormal or composation effective for the prevention or treatment of an abnormal or composition effective for the prevention or treatment of an approxant or composition effective for the prevention or treatment of an approxant or composition effective for the prevention or treatment of an approxant or composition effective for the prevention or treatment of an approxant or printitus, atopic dermatitis, eccena, acne and inherited skin diseases of inflammatory skin diseases selected from diseases consisting of epidermal hyperkratosis. The mammal of the invention is also useful as a model for further studies of itch mechanisms and the testing of potential compounds and compositions for relieve of various skin diseases where itch is a component. This sequence represents the N-terminal Erragment of the human statatum corneum chymotryptic enzyme, SCCE synonymous with human kallikrein 7 (KLK7), used in the development of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine proteease; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 6; Page 37; 74pp; English
08-FEB-2002; 2002WO-IB001300
                                                                                      09-FEB-2001; 2001CA-02332655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       gelrud T, Hansson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-643380/69.
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                                                                                                                                                                                                                            (EGEL/) EGELRUD T.
(HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 253 AA;
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This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a bratum corneum chymotryptic enzyme (SCCE) or its variant, operably linked to a promoter that drives expression of heterologous scce or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a cosmetic or a pharmaceutical formulation, and for the development of a diagnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an ecomposition effective for the prevention or treatment of an compound or composition effective for the prevention or treatment of inflammatory skin diseases selected from diseases consisting of epidermal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation, puritus, atopic dermatitis, eczema, acne and inherited skin diseases with epidermal hyperkeratosis. The mammal of the invention is also useful as a model for further studies of itch mechanisms and the testing of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               potential compounds and compositions for relieve of various skin diseases where itch is a component. This sequence represents the human stratum corneum chymotryptic enzyme, SCCE which is a serine protease synonymous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; protease; cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder;
                                                                                                                                                                                                                                                                                                                                                                                            Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCE which is a serine protease synonymous and is used in the development of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of novel human protease #39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with human kallikrein 7 (KLK7) and is used in
transgenic mammals described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Page 58-59; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU82740 standard; protein; 253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KLK7)
                                                                                                          08-FEB-2002; 2002WO-IB001300
                                                                                                                                                    09-FEB-2001; 2001CA-02332655.
09-FEB-2001; 2001DK-00000218.
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                                                                                                                                                                                                                                                                                        Egelrud T, Hansson L;
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                                                                                                                                                                                                                     (EGEL/) EGELRUD T.
(HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABQ76226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 253 AA;
                  WO200262135-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-2002
                                                              15-AUG-2002
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AAU82740
ID AAU82X
XX
AC AAU82
XX
XX
DT 23-AP
DE AMINO
XX
HUMAN
KW HUMAN
KW NEUTO
KW NEUTO
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The present invention relates to the isolation of novel human proteases, and the mucleic acids encoding them. The sequences of the invention are condition that the mucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. restenosis and diseases and asthma), cardiovascular diseases (e.g. restenosis and coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. disbettes, obscitzy), inflammatory disorders (e.g. disbettes, pain, sexual dysfunction, mood disorders, attention disorders, pain, sexual dysfunction, mood disorders, attention disorders, hypotension, psychotic disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's disease) and dyskinesias. The nucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. inflammatormal disease (e.g. infections aused as ocular disease (e.g. inflammatormal disease) the novel human proteases of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
hypertension; psychotic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; enzyme.
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                                                                                                                                                                                                                                                                                                    Sudarsanam S, Manning G, Caenepeel S;
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27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein differentially regulated in prostate cancer #43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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100.0%; Pred. No. ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Fig 2N; 313pp; English.
                                                                                                                                                                                         26-JUN-2001; 2001WO-US020171.
                                                                                                                                                                                                                            26-JUN-2000; 2000US-0214047P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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nes 9; Conservative
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                                                                                                                                                                                                                                                                 (SUGE-) SUGEN INC
                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABK31782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 253 AA;
                                                                                                                 WO200200860-A2
                                                                                                                                                                                                                                                                                                      Plowman G, W)
Charydczak G;
                                                                               Homo sapiens.
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                                                                                                                                                      03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders.
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Best Local 9
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The invention describes genes (1) which are differentially regulated in prostate cancer. (2) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (1) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves determining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer. Preferably, the expression levels of at least 10 genes are determined. (1) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells which involves contacting a polypeptide differentially-regulated in prostate cancer. (2) is also useful as moleculate a biological activity of the polypeptide, and certifies a molecular markers, as qualt trader of the polypeptide, and determining whether the test agent modulates the biological activity. (1) is useful as molecular markers, as qualt traders, prognosticating, determining predisposition to diseases and conditions especially relating to prostate cancer. (1) and its expression products are used in the diagnostic test to assay for presence of cancer e.g., in tissue sections, in biopsy sample, in total NN, in lymph, in blood etc. (1) is useful for assessing assessing the polypeptide and thus to blood etc. (1) is useful for assessing as target for thersapy or drug discovery. (1) can also be used for expressing the polypeptide and thus for searching specific binding partners of the polypeptide and these completed and disease pathways and the delineation of targets in these graders and groups of genes, expressed in pathways and the delineation of targets in these completed and disease pathways and the delineation of a product or animal or an early an early program o
                                                                                                                                                                                                                                                                                                                                                                           Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 293-294; 416pp; English.
                                                                                                                                                                                                         (ORIG-) ORIGENE TECHNOLOGIES INC.
                                                                                        08-APR-2002; 2002WO-US010824.
                                                                                                                                      06-APR-2001; 2001US-0281731P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulated in prostate cancer
                                                                                                                                                                                                                                                                                                        WPI; 2003-058520/05.
                                                                                                                                                                                                                                                                                                                               N-PSDB; ABX10343
WO200281638-A2
                                                                                                                                                                                                                                                            Jay G;
                                            17-0CT-2002
                                                                                                                                                                                                                                                          Sun Z,
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Sequence 253 AA;

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Gaps
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       100.0%; Score 40; DB 6; Length 253; 100.0%; Pred. No. 27;
                             0; Indels
                             0; Mismatches
Query Match
Best Local Similarity 100.
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ABU07471 standard; protein; 253 AA ABU07471; RESULT 14
ABU07471
ID ABU07.
XX
AC ABU07.

(first entry) 28-JAN-2003 

Protein differentially regulated in prostate cancer #74.

Prostate cancer; gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer monitoring.

Homo sapiens.

WO200281638-A2.

17-OCT-2002

08-APR-2002; 2002WO-US010824.

06-APR-2001; 2001US-0281731P.

(ORIG-) ORIGENE TECHNOLOGIES INC.

ö Jay Sun Z, WPI; 2003-058520/05. N-PSDB; ABX10375. Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.

Claim 1; Page 351; 416pp; English.

The invention describes genes (1) which are differentially regulated in prostate cancer. (1) Is useful for diagnosing a prostate cancer in a comprising protate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (1) Is useful for assessing a therapeutic or preventive incremention in a subject having a prostate cancer, which involves contention in a subject having a prostate cancer, which involves the expression levels in a sample comprising prostate cancer. (2) Is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells, which involves contacting a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent under conditions effective for the test agent to modulate a biological activity. (1) is useful as molecular markers, as drug targets, and for detecting, cancer cells, withing or prostate cancer. (1) and its expression conditions especially retaining predisposition to diseases and conditions especially retaining to prostate cancer. (1) and its expression conditions especially relating to prostate cancer. (1) and its expression conditions especially relating predisposition to diseases and conditions especially relating partners of the polypeptide and thus for easewing specific genes, and genes, expression conditions especially relating partners of the polypeptide and development, the nature of geneic defect, etc. (2) is useful for assessing cancer e.g., to determine the type conditions in the propertions to be used for expressing the polypeptide and development to prostate cancer. The identification of specific genes, and groups of genes, expressed in pathways which are useful in disease pathways and the delineations. This i

Sequence 253 AA;

Gaps ö Similarity 100.0%; Score 40; DB 6; Length 253; Similarity 100.0%; Pred. No. 27; 9; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches

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The invention relates to a novel isolated polynucleotide. The polynucleotides of the invention have cytostatic activity, and may have a use in gene therapy, and in a vaccine. The composition and methods are useful in diagnosing and/or treating cancer, particularly ovarian cancer. The composition may also be used as a vaccine to prevent cancer. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide and polypeptide useful for diagnosing and/or treating cancer, particularly ovarian cancer, and as a vaccine.
                                                                                                                                                                                            Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
                                                                                                                                                                                                                      Human; cytostatic; gene therapy; vaccine; cancer; ovarian cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0\$; Score 40; DB 6; Length 253; Best Local Similarity 100.0\$; Pred. No. 27; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 157-158; 169pp; English
                                                                                                   ABR58471 standard; protein; 253 AA
                                                                                                                                                                                                                                                                                                                                           02-OCT-2002; 2002WO-US031467.
                                                                                                                                                                                                                                                                                                                                                                        02-OCT-2001; 2001US-0327135P. 30-MAY-2002; 2002US-0384531P.
                                                                                                                                                             07-JUL-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mannion J;
                    6 LLPLQILLL 14
1 LLPLQILLL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 253 AA;
                                                                                                                                                                                                                                                                                 WO2003029468-A1
                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                               10-APR-2003.
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                                                                                                                                 ABR58471;
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                       g
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Gaps

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Search completed: March 11, 2006, 00:24:14 Job time: 87.6667 secs

1 LLPLQILLL 9

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein

March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds (without alignments) 61.367 Million cell updates/sec Run on:

US-09-905-083A-35 Title: Perfect score:

1 LLPLQILLL 9 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pir 80:\*
1: pir1:\*
2: pir2:\*
1: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	serine proteinase	cation transport P	hypothetical prote	conserved hypothet	tax-responsive ele	hepatocarcinogenes	surfactant protein	conglutinin precur	conglutinin - bovi	hypothetical prote	probable permease	hypothetical prote	Mg protoporphyrin	hypothetical prote	cytochrome aa3 con	hypothetical prote	transcription acti	cholera toxin tran	amyloid precursor-	hypothetical prote	transport protein	lipopolysaccharide	chloramphenicol re	probable transport	probable transport	P-selectin glycopr	stromelysin 3 (EC	stromelysin 3 (EC	Na+/H+-exchanging
ΩI		D97163	A71875	B64638	JC7300	JC4857	833603	JN0450	145878	T17215	H82994	T12520	T50904	H75201	H84314	E70890	A25970	E82257	A46362	E75440	AF1535	JQ0708	B43750	B85535	F90684	A57468	JC6197	A44399	AI2088
8	7	7	~	7	~	7	~	Н	7	~	~	7	~	7	~	7	~	~	N	(1	~	N	Н	~	~	N	~	N	7
Query Match Length		845	493	496	266	267	369	371	371	429	539	1092	1236	146	277	282	294	294	653	245	253	256	394	394	394	412	491	492	543
Query Match		90.0	87.5	87.5	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	82.5	82.5	82.5	82.5	82.5	82.5	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0
Score	40	36	35	35	34	34	34	34	34	34	34	34	34	33	33	33	33	33	33	32	32	32	32	32	32	32	32	32	32
Result No.	-1	7	m	4	ហ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	peptidyl-dipeptida	CFTR protein - Afr	probable transcrip	hypothetical prote	hypothetical prote	ELF-1 protein prec	ephrin-A2 - human	hypothetical prote	sugar ABC transpor	acid phosphatase (	insulin-like growt	daunorubicin resis	probable permease	ABC transporter, m	hypothetical prote
T29010	A31759	S23756	A83214	T43766	G65039	A54984	JE0322	C84914	H86811	A41720	A41927	AB3334	A98157	AH3130	T26360
8	-	~	N	~	N	~	N	N	~	-	-	N	N	~	7
1041	1306	1485	157	189	196	209	213	303	306	327	328	370	372	372	388
80.0	80.0	80.0	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5
32	32	32	31	31	31	31	31	31	31	31	31	31	31	31	31
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
CiAccesion: A53968
R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19456, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Reference number: A53968; MUID:94308225; PMID:8034709
A,Accession: A53968
A,Accession: A53968
A,Molecule type: mRNA
A,Residues: 1-253 <HAN>
A,Molecule type: mRNA
A,Residues: 1-253 <HAN>
A,Cross-references: UNIPROT:P49862; UNIPARC:UPI000001BC4; GB:L33404; NID:g521214; PIDN:#
A,Genetics:
A,Genetics:
A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetics: A,Genetic
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                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                         N;Alternate names: stratum corneum chymotryptic enzyme
serine proteinase SCCE precursor - human
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## 6 LLPLQILLL 14

RESULT 2

1 LLPLQILLL 9

ð 셤 Cation transport P-type ATPase CAC2137 [imported] - Clostridium acetobutylicum (;Species: Clostridium acetobutylicum (;Species: Clostridium acetobutylicum (;Species: La-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004 (C)Accession: D97163 RNO11ing, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Kronin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001 Aprile: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: D97163
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-845 < KUR>
A;Cross-references: UNIPROT:Q97H76; UNIPARC:UP100000CA412; GB:AE001437; PIDN:AAK80095.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
A;Gene: CAC2137

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Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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surfactant protein D - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 LLPLQILSL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 LLPLQILSL 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conserved hypothetical integral membrane protein HP0946 - Helicobacter pylori (strain 26 C; Species: Helicobacter pylori
C; Species: Helicobacter pylori
C; Species: Helicobacter pylori
C; Species: Helicobacter pylori
C; Species: Helicobacter pylori
C; Species: Helicobacter pylori
C; Species: Helicobacter pylori
C; Species: Helicobacter pylori
R; Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:025600; UNIPARC:UP100000030BA; GB:AE000604; GB:AE000511; NID
C;Genetics:
A;Start codon: GTG
                                                                                                                                                                                                                                                                                        hypothetical protein jhp0880 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Acrees: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: A71875
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Inves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Altile: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUD:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q9ZKOS; UNIPARC:UPI00000D7271; GB:AE001518; GB:AE001439; NID
A;Experimental source: strain J99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                 Score 36; DB 2; Length 845;
Pred. No. 40;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 2; Length 496;
Pred. No. 37;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.5%; Score 35; DB 2; Length 493; 88.9%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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tax-responsive element-binding protein 5 - mouse
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                    90.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.5%;
Query Match
Best Local Similarity 77. o
Langeryative 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                  670 LLPIQILLI 678
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254 LLPLSILLL 262
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254 LLPLSILL 262
                                                                                                                      1 LLPLQILLL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-493 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: jhp0880
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C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: JC7300
R;Masaki, T.; Noguchi, H.; Kobayashi, M.; Yoshida, M.; Takamatsu, K.
D;NA Res. 7, 187-193, 2000
A;Title: Isolation and characterization of the gene encoding mouse tax-responsive element A;Reference number: JC7300
A;Accession: JC7300
A;Molecule type: mRNA
A;Accession: JC56 <MAS>
A;Cross-references: UNIPROT:Q9ESS3; UNIPARC:UPI0000E73B0; DDBJ:AB036745
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cispecies: Rattus norregicus (Norway fat)
Cispecies: Rattus norregicus (Norway fat)
Cispecies: Rattus norregicus (Norway fat)
Cispecies: Rattus norregicus (Norway fat)
Cispecies: Rattus norregicus (Norway fat)
Cispecies: National Hypes (Norway fat)
Rikishimoto, T.; Kokura, K.; Kumagai, Y.; Makino, Y.; Tamura, T.
Biochem. Biophys. Res. Commun. 224, 746-751, 1996
A,Tiles: HYP: A b.z.ip transcription factor that is closely related to the human XBP/TREB:
A,Reference number: JC4857
A,Reference number: JC4857
A,Residues: 1-267 <KIS>
A,Generics: A,Generics: A,Generics: A,Generics: A,Generics: A,Generics: A,Generics: A,Generics: A,Generics: A,Generics: A,Generics: A,Generics: A,Generics: A,Generics: Leucine zipper; transcription factor
C; Reywords: leucine zipper; transcription factor
F; S8-98/Domain: fos/jun DNA-binding domain homology
F; S8-98/Domain: fos/jun DNA-binding domain homology
F; 89-126/Region: leucine zipper motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cispecies: Bos primigenius taurus (cattle)
Cipate: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
Cipate: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
Cipates 333603 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
Cipates 333603 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
A;Title: Structural similarity between bovine conglutinin and bovine lung surfactant prot A;Reference number: S33603 MuID:93170856; PMID:8436402
A;Reference number: S33603 MuID:93170856; PMID:8436402
A;Residues: 1-369 <LIM
A;Residues: 1-369 <LIM
A;Residues: 1-369 <LIM
A;Residues: UNIPARC:UPI0000177932
C;Superfamily: pulmonary surfactant protein D; C-type lectin homology
F;248-367/Domain: C-type lectin homology <LCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: treb5
C;Superfamily: X box-binding protein 1; fos/jun DNA-binding domain homology
C;Keywords: leucine zipper; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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88.9%; Pred. No. 32;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 2; Length 266
Pred. No. 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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A; Reference number: A29416; MUD:87184551; PMID:3566740
B; Malhotra: annotation
B; Malhotra: R: Lauren, S.B.; Willis, A.C.; Sim, R.B.
Biochem. J. 293, 15-19, 1993
A; Title: Research Communication. Localization of the receptor-binding site in the collect A; Reference number: S34054; MUD:93319501; PMID:8328957
A; Contents: annotation
B; Liou, L.S.; Sastry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarma, T.B.; Tauber, A.I.; Sastry, J. Immunol. 153, 173-180, 1994
A; Title: Bovine conglutinin gene exon structure reveals its evolutionary relationship to A; Reference number: 146010; MUD:94267222; PMID:8207234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: UNIPARC:UP10000127EB3; EMBL:U06860; NID:9507183; PIDN:AAB60624.1; PII Comment: This protein mediates the agglutination of erythrocytes with antibody and comp. Comment: This protein is a Ca2+-dependent serum lectin specific for N-acetylglucosamine.
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775-571/Product: conglutinin-N #status predicted <MA2>
77-571/Product: conglutinin-N #status predicted <MA2>
7248-369/Domain: C-type lectin homology <LCH>
763,87,99,135,141,159,162,198,210/Modified site: carbohydrate (Lys) (covalent) #status production of the construction of 
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A;Molecule type: mRNA
A;Residues: 1.371 <LIO>
A;Croserreferences: UNIPROT: P23805; UNIPARC: UP1000016C2E0; GB: L18871; NID: G495012; PIDN: P;Croperfamily: pulmonary surfactant protein D; C-type lectin homology
F;248-369/Domain: C-type lectin homology <LCH>
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C;Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
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Pred. No. 44;
1; Mismatches 1; Indels
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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LLPLSVLLL 11
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Biochem. 215, 793-799, 1993
A;Title: Structural similarity between lung surfactant protein D and conglutinin. Two di A;Reference number: S35044; MUID:93358905; PMID:8354286
A;Accession: S35044
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Kawasaki, N.; Itoh, N.; Kawasaki, T.
Lochem. Biophys. Res. Commun. 198, 597-604, 1994
Title: Gene organization and 5'-flanking region sequence of conglutinin: A C-type mamm Reference number: JC2396; MUID:94128104; PMID:8297370
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A;Mesidues: 21-209,'S','211-371 <LEE>
A;Residues: 21-209,'S','211-371 <LEE>
A;Kesidues: 21-209,'S','Z11-371 <LEE>
A;Cross-references: UNIPARC:UPI0000140P2A
R;Kawasaki, N.; Yokota, Y.; Kawasaki, T.
Arch. Blochem. Blochya. 305, 533-540, 1993
A;Title: Differentiation of conglutination activity and sugar-binding activity of congluA;Reference number: 836879; MUID:99384312; PMID:8973191
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Residues: 21-54;75-86,'X',88-89,'X',91,'X',93-94;208-209,'X',211-227 <KAW>
Cross-references: UNIPARC:UP100001741A3; UNIPARC:UP100001741A4; UNIPARC:UP100001741A5
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Biol. Chem. 266, 2715-2723, 1991
Title: Primary structure of bovine conglutinin, a member of the C-type animal lectin; Reference number: A23740; MUID:91131556; PMID:1993651
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N'Contains: condutinin.N

C'Species: Bos primigenius taurus (cattle)

C'Accession: 10-Sep # Heequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C'Accession: JN0450; JC2396; S33235; A23740; S36879; S35644; I46010; A22416; S34054

R'Suzuki, Y.; Yin, Y.P.; Makino, M.; Kurimura, T.; Wakamiya, N.

Biochem. Biophys. Res. Commun. 191, 335-342, 1993

A;Title: Cloning and sequencing of a change for bovine conglutinin.

A;Reference number: JN0450; MUID:93213261; PMID:8460993
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;Note: The authors translated the codon GAT for residues 250 and 270 as Glu
;Note: The authors translated the codon GAT for residues 250 and 270 as Glu
icohem. J. 292, 157-162, 1993
;Title: The CDNA cloning of conglutinin and identification of liver as a primary
;Reference number: S33235; MUID:93277452; PMID:7684896
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                   Length 369;
              Score 34; DB 2;
Pred. No. 44;
1; Mismatches
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A;Residues: 75-86,'X',88-89,'X',91,'I' <LUA>
A;Cross-references: UNIPARC:UP100001741A6
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77.8%;
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         Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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LLPLSVLLL 11
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A; Residues: 1-371 <SUZ>
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My protoporphyrin methyl transferase [imported] - Rubrivivax gelatinosus C.Species: Rubrivivax gelatinosus R.J. 10004
C.Accession: T50904
R.Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K. submitted to the EMBL Data Library, November 1999
A.Description: Defermination of Nucleotide Sequences of Rubrivivax gelatinosus Photosynth A.Peference number: Z25270
A.Accession: T50904
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Fesidues: 1-1236 -NAG-
A.Fesidues: 1-1236 -NAG-
A.Fesidues: J.L.SA -NAG-
A.Fesidues: UNIPROT: 09JPA4; UNIPARC: UPI00000B2528; EMBL: AB034704; PIDN: BAA94057.]
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Cibate: 20-Aug-1999 #text_change 09-Jul-2004
Cibate: 20-Aug-1999 #text_change 09-Jul-2004
Cibate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
Cibate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
Cibate: 20-Aug-1999 #sequence_revision 20-Aug-1999
Sibate of the EMBL Data Library, July 1999
A; Reference number: A75001
A; Reference number: A75001
A; Reference number: A75001
A; Reference number: Dreliminary
A; Rolecule type: DNA
A; Residues: 1-146 < KAM>A; Residues: 1-146 < KAM>A; Residues: UNIPROT: Q99ZD5; UNIPARC: UPI0000063243; GB:AJ248283; GB:AL096836; NID:
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C;Species: Halobacterium sp. NRC-1
C;Species: Peb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H84314
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
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C;Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
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C;Superfamily: Pyrococcus abyssi hypothetical protein PAB0088
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87.5%; Pred. No. 1.3e+02;
cive 1; Mismatches 0
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Best Local Similarity 88.9%;
Matches 8; Conservative
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Matches 6; Conservative
                            7; Conservative
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule: 1-539 <STO>
A;Cross-references: UNIPROT:Q9HTX4; UNIPARC:UPI0000C5F5A; GB:AE004934; GB:AE004091; NIE
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: H82994
S;Stover. C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Sture 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor, Reference number: A82950; MUID:20437337; PMID:10984043
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  C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-0C;Accession: T17215
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18723
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-429 < POUS
A; Cross-references: UNIPARC: UPI000000D884; EMBL: AL117404
A; Experimental source: adult testis; clone DKF2p434H2235
A; Note: DKF2p434H2235.1
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A;Residues: 1-1092 <WAM>
A;Cressreferences: UNIPARC;UPI00000711F2; EMBL:AL080133
A;Experimental source: adult testis; clone DKFZp434G173
C;Genetics:
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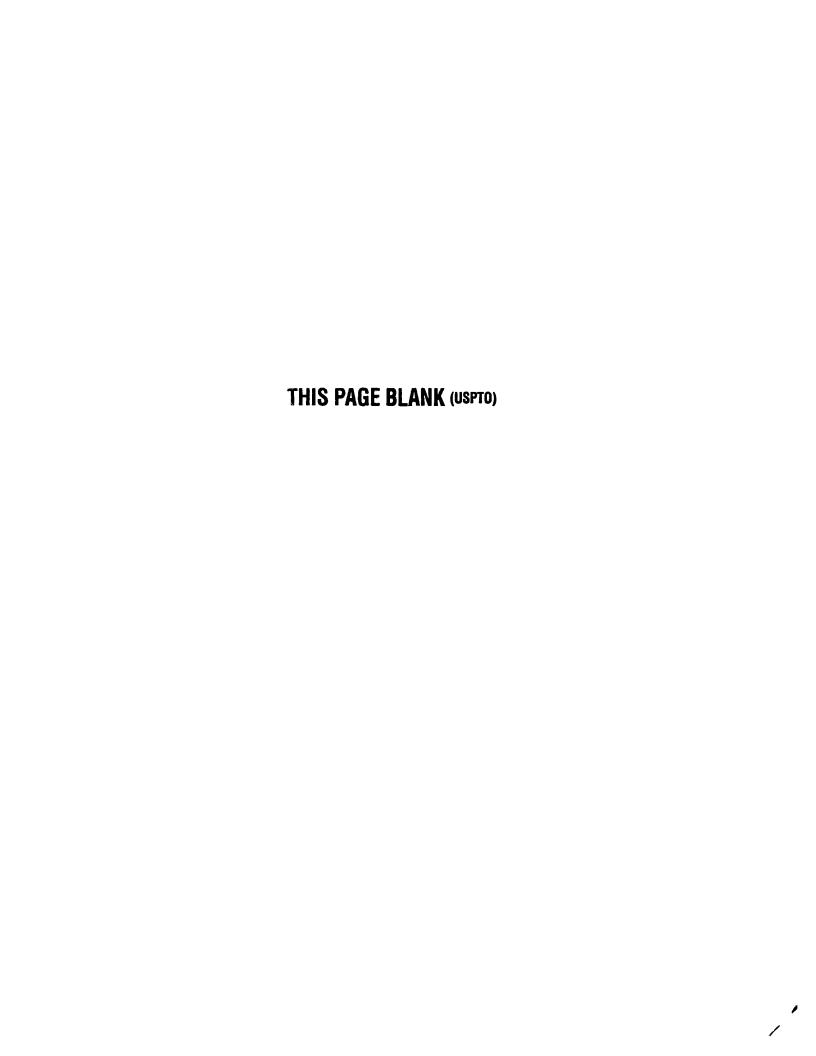
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; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabld Jung, K.H.; Alam, M.; Preitas, T.

Jung, K.H.; Alam, M.; Preitas, T.

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A.Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: H84314
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Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altechul S.F., Zeeberg B. B., Buecow K.H., Schaefer C.F., Bhat N.K.,

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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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Villaton D.K., Muray D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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-!- FUNCTION: May catalyze the degradation of intercellular cohesive structures in the cornified layer of the skin in the continuous shedding of cells from the skin surface. Specific for amino acid residues with aromatic side chains in the PI position. SCCE cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-Phe-|-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the activation of precursors to inflammatory cytokines.
[2]
NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dong Y., Kaushal A., Brattsand M., Nicklin J., Clements J.A.;
"Differential splicing of KLK5 and KLK7 in epithelial ovarian
produces novel variants with potential as cancer biomarkers.";
Clin. Cancer Res. 9:1710-1720(2003).
                                                 TISSUE-Keratinocyte;
PubMed=10974542; DOI=10.1016/S0378-1119(00)00280-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22623266; PubMed=12738725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION.
MEDLINE=95314630; PubMed=7794273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND TISSUE SPECIFICITY.
TISSUE-Ovarian carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 257:119-130(2000).
                                                                                                                                                                                                                                                   Gene 254:119-128(2000).
                                                                                                                                                                                                                              regulation."
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                       LINERNATIVE PRODUCTS:

EVENTEALIZETORY

Name=1; Synonyms=Long;

Squence=Displayed;

Name=2; Synonyms-Short;

Isoid=P49862-1; Squence=USP_013581;

Isoid=P49862-2; Squence=VSP_013581;

LISOIG=P49862-2; Squence=VSP_013581;

TISOIG SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermis. Also expressed in the brain, mammary gland, cerebellum, spinal cord and kidney. Lower levels in salivary gland, uterus, thymus, thyroid, placenta, traches and testis. Up-regulated in ovarian carcinoma, especially late-stage serous carcinoma, compared with normal ovaries and benign adenomas (at the protein level).

Coll INDUCTION: By estrogens and glucocorticoids in a breast carcinoma
SUBCELLULAR LOCATION: Secreted. In ovarian carcinoma, secreted and also observed at the apical membrane and in cytoplasm at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            // similarity).
// similarity).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00200; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
Alternative splicing; Direct protein sequencing; Glycoprotein; Hydrolase; Protease; Serine protease; Signal; Zymogen.
                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Charge relay system (By similari
N-linked (GloNac. .) (Potential
By similarity.
Fill soften 2).
FTIGE-808 (In 180 form 2).
FTIGE-808 (1338 81.
C -> W (In Ref. 6; AAH32005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 604438; -.
GO; GO:0008236; F:serine-type peptidase activity; TAS.
GO; GO:0008544; P:spidermis development; TAS.
InterPro; IPR001254; Peptidase_S1_S6.
InterPro; IPR001314; Peptidase_S1_R.
Pfam; PF00089; Trypsin; 1.
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Charge relay system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Activation peptide.
Kallikrein 7.
                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 1 peptidase S1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, L33404; AAC37551.1; -; mRNA.

EMBL, AF166330; AAD49718.1; -; Genomic_DNA.

EMBL, AF24527; AAG33360.1; -; Genomic_DNA.

EMBL, AF332583; AAK69624.1; -; Genomic_DNA.

EMBL, AF411214; AAN03662.1; -; mRNA.

EMBL, AF411215; AAN03663.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptidase S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ensembl, ENSG0000169035; Homo sapiens.
HGNC; HGNC:6368; KLK7.
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HSSP; P00760; 1EZX.
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253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; S01.300;
                                                                                                                                                                                                                                                                line.
                                                                                                                                                                                                                                                                                          subfamily.
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Manne musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CZECH II;
TISSUE-Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.0%; Score 38; DB 2; Length 104; 88.9%; Pred. No. 19; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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104 AA; 11085 MW; 0534D57467566914 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-UUL-2004 (TrEMBLrel. 27, Last sequence update) 65-UUL-2004 (TrEMBLrel. 27, Last annotation update) 8-Up11 protein.
                                       01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR001179; FKBP_PPIase.
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HSSP; P18203; 1FKL.
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05-JUL-2004 (TrEMBLrel. 27,
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PROSITE; PS50059; FKBP_PF
SEQUENCE 104 AA; 11085
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NCBI_TaxID=10090;
                                                                                                                                                                                                                                                   Muridae; Murinae; Mus.
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les 8; Conserv
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                                                                              protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METAGENER R.L., Feingold E.A., Grouse L.H., Derge J.G.,

MIschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MIschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

MISCHOELO M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

MISCHOLL S.A., McEwan P.J., McKernan K.J., Mallek J.A., Gunaratne P.H.,

MISCHARS S.N., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

MISCHARS S.N., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

MILIAON D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Makesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Motiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Mutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

M. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus muscilus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                              Gaps
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                                   100.0%; Score 40; DB 1; Length 253; 100.0%; Pred. No. 18; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC021345; AAH21345.1; -; mRNA.
MGI; MGI:1913370; Fkbpl1.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
SEQUENCE 73 AA; 7819 MW; 93E8F53399BF3C11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=FVB/N; TISSUE=Salivary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21,
Query Match
Best Local Similarity 100.00
English 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBRSD6 MOUSE PRELIMINARY;
QBRSD6;
                                                                                                                                                                                                                                                                                                                                                                                                             Q8VCA9 MOUSE PRELIMINARY;
Q8VCA9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                σ
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NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fkbp11 protein.
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Q8RSD6 N ID Q8F AC Q8F DT 01-

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CATAINER YOUN NO.

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NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
STRAIN=C57BL/6J; TISSUB=Embryo;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
Mikaido II. Osato N., Saukne H., Yamanaka II., Kiyosawa H., Yangido K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Last sequence update)
10-WAX-2005 (Rel. 47, Last annocation update)
FKS06 binding protein 11 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis-
trans isomerase) (PPIase) (Rotemase) (19 kDa FK506-binding protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus muscilus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEAN; PF00254; FKBP C; 1.
PROSITE; PS50059; FKBP PPIASE; 1.
SEQUENCE 138 AA; 15105 MW; C138B8B0EFDDF59D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005615; C:extracellular space; TAS. GO; GO:0016021; C:integral to membrane; TAS. InterPro; IPR001179; FKBP_PPIase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC002311; AAH02311.1; -; mRNA.
MGI; MGI:1913370; Fkbp11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FKB11 MOUSE STANDARD;
Q9D1M7; Q9CRE4;
28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA sequences."
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NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Fkbp11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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FKB11 MOUSE

AC 09D1M77
DT 28-FEB-7
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DE FKS06 b)
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Registrial I. W., Kanapin D., Mettuda H., Batclow S., Bedsell K.W.,

Bike J.A., Fared D., Brusie V., Cohristo, S., Bedsell K.W.,

Bike J.A., Fared D., Brusie V., Cohristo, S., Bedsell K.W.,

Batch S. M., Brand D., Brusie V., Cohristo, S., Bedsell K.W.,

Batch S. M., Brand D., Brusie V., Cohristo, S., Bedsell K.W.,

Batch S. M., Brand D., Brusie V., Cohristo, M., Brand K., Sough J.,

Batch S. M., Statincian S., Hirdwan M., Cast J., Codzis M., Gough J.,

Batch S. M., Mance K., Controlled M., Cast J., Codzis M., Cast J.,

Batch S. M., Mance K., Controlled M., Cast J., Codzis M., Mith H.,

Batch S. M., Pettinia L., Marchicani L., Mich H.,

Batch S. M., Pettinia L., Marchicani L., Mith H.,

Batch S. M., Pettinia L., Marchicani L., Mith H.,

Batch S. M., Pettinia L., Marchicani L., Mith H.,

Batch S. M., Pettinia L., Marchicani L., Mith H.,

Batch S. M., Pettinia L., Marchicani L., Mith H.,

Batch S. M., Mance L., Wallarend C., Man Y., Sandon M., Shinada K.,

Milland M., Schmidt, C., Sample C.A., Sandon M., Shinada M.,

Batch S. M., March M., Mallarend C., Man Y., Sandon M., Shinada M.,

Batch S. M., March M., Mallarend C., Man Y., Wang J., Vang J., Wang J.,

Milland J. G., Whenhaw Borls A., Zimmer A., Carninol P., Haydrau N.,

Batch S. Maysahlaki Y., Sanda J. A., March M., Mallarend C., Man Y., Sandon M., Shinada S.,

Batch S. Maysahlaki Y., Sanda J., Alaxam K., Atchar M., March M., Mallarend C.,

Batch S., Haysahlaki Y., Sanda J., Alaxam K., Atchar M., Mallan S.,

Milland M., March M., March M., Match M., Mallan M., Sandau M., Mallan M.,

Batch S. Maysahlaki Y., Sanda J., March M., Mallan M., Mallan M.,

Batch S. M., Mark M., Rada J., March M., Sandau M., Mallan M.,

Batch S. M., March M., March M., March M., March M., Mallan M., Mallan M.,

Batch S. M., March 
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR005599; Alg9_trang.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; PD000357; TGFb; 1.
SM00204; TGFB; 1.
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Q75E55;
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65
231
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SIGNAL 1 21
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322
361 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=ABL185C;
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DISULFID
SEQUENCE
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vulpecula).",
J. Mol. Endocrinol. 21:141-152(1998).

J. Mol. Endocrinol. 21:141-152(1998).

Inhibina and activins inhibits and activate,
respectively, the secretion of follitropin by the pituitary gland.
Inhibins/activins are involved in regulating a number of diverse functions such as hypothalamic and pituitary hormone secretion, gonadal hormone secretion, agem cell development and maturation, erythroid differentiation, insulin secretion, nerve cell survival, embryonic axial development or bone growth, depending on their subunit composition. Inhibins appear to oppose the functions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Dimeric, linked by one or more disulfide bonds. Inhibin A is a dimer of alpha and beta-A. Inhibin B is a dimer of alpha and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FTM: Proteolytic processing yields a number of bioactive forms, consisting either solely of the mature alpha chain, of the most Neterninal propeptide linked through a disulfide bond to the mature alpha chain, or of the entire proprotein. SIMILARITY: Belongs to the TGF-beta family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WCLEOTIDE SEQUENCE.
MEDLINE=9907340; PubMed=9801457; DOI=10.1677/jme.0.0210141;
Vanmontfort D., Fidler A.E., Heath D.A., Lawrence S.B., Tiedall D.J.,
Greenwood P.J., McNatty K.;
"cDNA sequence analysis, gene expression and protein localisation of
the inhibin alpha subunit of Australian brushtail possum (Trichosurus
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Metatheria, Diprotodontia, Phalangeridae, Trichosurus.
                                                                                                                                                                                                                                                                                               ö
                                                                                                        PPIase FKBP-type.
S -> F (in Ref. 1; BAB31559).
S -> R (in Ref. 1; BAB31559).
                                                                                                                                                                                                                                        95.0%; Score 38; DB 1; Length 201; 88.9%; Pred. No. 36;
                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                       94D955C57264BD82 CRC64;
                                                                                    FK506 binding protein 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AF033340; AAC63945.1; -; mRNA.
GO; GO:0005576; C:extracellular region; ISS.
GO; GO:0017106; F:activin inhibitor activity; ISS.
GO; GO:0005125; F:cytokine activity; ISS.
GO; GO:0008083; F:growth factor activity; ISS.
GO; GO:0005179; F:hormone activity; ISS.
GO; GO:000515; F:protein binding; ISS.
GO; GO:000515; F:protein binding; ISS.
GO; GO:0007515; F:protein differentiation; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trichosurus vulpecula (Brush-tailed possum)
                                                                                                                                                                                                                                                                 Pred. No. 36;
1; Mismatches
                                                      Potential
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PS50059; FKBP PPIASE; 1.
                                                                                                                                                                                       22137 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibin alpha chain precursor
                                                                                                                                                                                                                                                                 Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                               201
144
53
198
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                                [somerase; Rotamase;
                                                                                                                                                                                       201 AA;
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                                                                               28
57
53
198
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077755;
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                                                                                                        DOMAIN
CONFLICT
CONFLICT
  PROSITE;
                                                                                                                                                                                       SEQUENCE
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removed

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GO; GO:0007166; P:cell surrace control of GO:0007267; P:cell-cell signaling; ISS.
GO; GO:000267; P:cell-cell signaling; ISS.
GO; GO:0002541; P:hemoglobin biosynthesis; ISS.
GO; GO:0042549; P:hemoglobin biosynthesis; ISS.
GO; GO:0045786; P:hemoglobin biosynthesis; ISS.
GO; GO:0045786; P:negative regulation of B cell differentiation; ISS.
GO; GO:0045786; P:negative regulation of follicle-stimulating. .; ISS.
GO; GO:0045779; P:negative regulation of interferon-gamma bio. .; ISS.
GO; GO:004550; P:negative regulation of interferon-gamma bio. .; ISS.
GO; GO:0004236; P:negative regulation of phosphorylation; ISS.
A GO; GO:0001541; P:ovarian follicle development; ISS.
B GO; GO:0046881; P:positive regulation of follicle-stimulating. .; ISS
InterPro; IPR002405; Inhibin_alpha.

InterPro; IPR00189; TGF.

**Control of the control of
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Cleavage (By similarity).
Cleavage (Glowac...) (Potential).
N-linked (Glowac...) (Potential).
N-linked (Glowac...) (By similarity).
By similarity.
By similarity.
By similarity.
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Science 304:304-307(2004).
AGD; ABL185C: -, Genomic_DNA.
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By similarity.
Inhibin alpha N-terminal region (By
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Last annotation update)
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Inhibin alpha chain.
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Virol. 75:11811-11820(2001)
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Lo C.-F., Kou G.-H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
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                                                         NUCLEOTIDE SEQUENCE
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                                                                                              STRAIN=Taiwan
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Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
Quail M.A., Ormond D., Dogett J., Trueman H.E., Mendoza J.,
Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
"A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";
Science 307:82-86(2005).
--- CAUTION: The sequence shown here is derived from an
EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.

EMBL, CAAJ0104512; CAH81670.1; -; Genomic_DNA.
                                                                                                                                                                                                                                          Gaps
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MEDLINE=21548311; PubMed=11689662;
DOI=10.1128/JVI.75.23.11811-11820.2001;
Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
"Complete genome sequence of the shrimp white spot bacilliform virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium chabaudi.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
                                                                                                                                                                             Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.0%; Score 36; DB 2; Length 71;
100.0%; Pred. No. 32;
tive 0; Mismatches 0; Indels
                                                                                                                                                                       92.5%; Score 37; DB 2; Length 552
77.8%; Pred. No. 1.5e+02;
ive 2; Mismatches 0; Indels
                                                                                                                   62708 MW; 62A8842023DEEA04 CRC64;
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13-SEP-2005 (TYEMBLrel. 31, Last sequence update)
13-SEP-2005 (TYEMBLrel. 31, Last annotation update)
Hypothetical protein (Fragment).
ORFNames=PC108599.00.0;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
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InterPro; IPR001202; WW_Rsp5_WWP.
Pfam; PF03901; Glyco_transf_Z2; 1.
PROSITE; PS01159; WW_DOMAIN_1; UNKNOWN_1.
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                                                                                                                                                                                                                                       7; Conservative
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Q8VB59;
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67 LMPLQVLLL 75
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NUCLEOTIDE SEQUENCE.
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                                                                                           Complete proteome.
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SEQUENCE
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STRAIN=Taiwan;
MEDLINE=21844071; PubMed=11853398; DOI=10.1006/viro.2001.1273;
MEDLINE=21840771; PubMed=11853398; DOI=10.1006/viro.2001.1273;
LO C. E., Kou G. H.,
Indentification of a nucleocapsid protein (VP35) gene of shrimp white spot syndrome virus and characterization of the motif important for targeting VP35 to the nuclei of transfected insect cells.";
Virology 293:44-53(2002).
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PubMed=12504569; DOI=10.1006/viro.2002.1696;
Lin S.T., Chang Y.S., Wang H.C., Tzeng H.F., Chang Z.F., Lin J.Y.,
Wang C.H., Lo C.F., Kou G.H.;
Wang C.H., Lo C.F., Kou G.H.;
Wang C.H., and colored colored of shrimp white spot syndrome virus (WSSV):
expression and enzymatic activity in a baculovirus/insect cell system
and WSSV-infected shrimp.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genomic and proteomic analysis of thirty-nine structural proteins of shrimp white spot syndrome virus.";
J. Virol. 78:11360-11370(2004).
MEDLINE=20517548; PubMed=11062040; DOI=10.1006/viro.2000.0597; Tsai M.F., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J., Lin J.Y., Kou G.H., Lo C.F.; Identification and characterization of a shrimp white spot syndrome virus (WSN) gene that encodes a novel chimeric polypeptide of cellular-type thymidine kinase and thymidylate kinase."; virology 277:100-110(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=12359454; DOI=10.1006/viro.2002.1536;
Chen L.L., Wang H.C., Huang C.J., Penng S.E., Chen Y.G., Lin S.J.,
Chen W.Y., Dai C.F., Yu H.T., Wang C.H., Lo C.F., Kou G.H.;
"Transcriptional analysis of the DNA polymerase gene of shrimp white
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Chimeric polypeptide of thymidine kinase and thymidylate kinase of shrimp white spot syndrome virus: thymidine kinase activity of the recombinant protein expressed in a baculovirus/insect cell system."; Virology 299:248-255(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tzeng H.F., Chang Z.F., Peng S.E., Wang C.H., Lin J.Y., Kou G.H.,
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syndrome virus virion are formed by the major structural protein
VP664, the largest viral structural protein ever found.";
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PubMed=15452257; DOI=10.1128/JVI.78.20.11360-11370.2004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Taiwan;
PubMed=12202227; DOI=10.1006/viro.2002.1480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rology 301:136-147(2002).
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SEQUENCE 845 AA
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A Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
A Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
A Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
A Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
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A Carucci D.J.;
"Genome sequence and comparative analysis of the model rodent malaria
T parasite Plasmodium yoelli yoelii.";
Mature 419:512-519(2002).
C -! CAUTION: The sequence shown here is derived from an EMBL/Genbank_DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                               Gaps
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097H36 CLOAB PRELIMINARY; PRT; 845 AA.
097H36;
01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLRel. 18, Clostridiaceae;
01-MAR-2004 (TrEMBLRel. 18, Created)
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Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                      90.0%; Score 36; DB 2; Length 79; 77.8%; Pred. No. 35; 0; Indels ive 2; Mismatches 0; Indels
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AR332093; AAL33116-1; Genomic DNA. EMBL, AF440570; AAL89055.1; -; Genomic DNA. SEQUENCE 79 AA; 9287 MM; 800910C7FFA0EC7E CRC64;
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EMBL; ABBL01000328; BA20540.1; -; Genomic_DNA.
GO; GO; 0016020; C: membrane; IEA.
InterPro; IPR004316; MtN3_81v.
PANTHER; PTHR0791; MtN3_81v.
PEANTHER; PTHR0313 81v; 2.
SEQUENCE 637 AA; 70992 MW; BC506320B2AEIFE5 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Name=PY01249;
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QTRQ54 PLAYO PRELIMINARY;
Q7RQ54;
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Matches 7, Conservative
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1es 8; Conservative
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LPLQILLL 14
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                                                                                                         DOI=10.1128/JB.183.16.4823-4838.2001;

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"Genome sequence and comparative analysis of the solvent-producing

bacterium Clostridium acetobutylicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGO; GO:0016020; C:membrane; IEA.

RGO; GO:0015524; F:ATP binding; IEA.

GO; GO:0015524; F:ATP binding; IEA.

GO; GO:0015624; F:ATP binding; IEA.

GO; GO:0015624; F:ATP binding; IEA.

GO; GO:0015629; F:CatLou transport; IEA.

GO; GO:0016812; P:CatLou transport; IEA.

GO; GO:0016912; P:metabolism; IEA.

GO; GO:0015992; P:proton transport; IEA.

R InterPro; IPR00157; ATPase E1-E2.

INTERPRO; IPR001608; Catlon ATPase C.

INTERPRO; IPR0014; Catlon ATPase C.

INTERPRO; IPR0014; Catlon ATPase C.

INTERPRO; IPR001591; DEAD I like hydro.

INTERPRO; IPR005894; Dehal like hydro.

R InterPro; IPR005895; H-E2_ATPase C.

R InterPro; IPR00689; Catlon ATPase C.

R Pfam; PF001699; Catlon ATPase C.

R Pfam; PF00172; BI-E2 ATPASE C.

R Pfam; PF0017
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Cation transporter P-ATPase (EC 3.6.1.).
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EMBL; AE007714; AAK80095.1; -; Genomic_DNA.
PIR; D97163; D97163.
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STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
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QSFMG7;
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Matches 7; Conservative
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                                  RESULT 15
Q8MZZ0_HELAU
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RL Proc. Natl. Acad. Sci. U.S.A. 102:3906-3912 (2005).

BRBL; CP000033; AAV42107.1; -; Genomic_DNA.

BR GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016220; F:XTP binding; IEA.

GO; GO:0016820; F:Mydrolase activity; IEA.

GO; GO:0016820; F:hydrolase activity; acting on acid anhydrid. .; IEA.

GO; GO:0016820; F:hydrolase activity; IEA.

GO; GO:0016820; F:hydrolase activity; IEA.

GO; GO:0016820; F:magnesium-importing Arpase activity; IEA.

GO; GO:001592; P:metabolism; IEA.

BR InterPro; IPR004014; Cation_Arpase. N.

InterPro; IPR008205; H.Arpase.

InterPro; IPR008205; H.Arpase.

InterPro; IPR008205; H.Arpase.

InterPro; IPR008205; H.Arpase.

InterPro; IPR00122; H.Arpase.

INTERPRO; IPR00122; H.Arpase.

INTERPRO; IPR00122; H.Arpase.

INTERPRO; IPR00120; HARPASE.

BR RINTS; PR001120; HARPASE.

BR RINTS; PR001120; HARPASE.
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RX Pubmed-14704707; DOI=10.1038/nbt923;

RX Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,

RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,

RA Larimer F.W., Tabian T.E., Bober C., Torres J.E., Peres C.,

RA Harrison F.H., Gibson J., Harwood C.S.;

RA Harrison F.H., Gibson J., Harwood C.S.;

RY "Complete genome sequence of the metabolically versatile

RT "Complete genome sequence of the metabolically versatile

RT photosynthetic bacterium Rhodopseudomonas palustris.";

RL Nat. Biotechnol. 22:55-61(2004).

RM EMBL; BX72595; GAZ26376.1; -; Genomic_DNA.

KW Complete protecome; Hypothetical protein.

RO SEQUENCE 181 AA; 19632 MW; CD844D8210E565D1 CRC64;
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Bradyrhizobiaceae; Rhodopseudomonas.
NCBI_TaxID=1076;
                                                                                                                                                                                                                                                                                                                                                                                                                                         90.0%; Score 36; DB 2; Length 887; 77.8%; Pred. No. 3.8e+02; ive 2; Mismatches 0; Indels
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87.5%; Pred. No. 1.2e+02;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             99091 MW; 9071A032A09BE9CE CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 AA
                                                                                                                                                                                                                                                                                                                                              TIGRFAMs; TIGRO1524; ATPASS-IIIB MG; 1.
TIGRFAMS; TIGRO1494; ATPASSE P-type; 1.
PROSITE; PSO1154; ATPASSE E1 E2; UNKNOWN 1.
CCMPLETE PTOLEOME; Hydrolase.
SEQUENCE 887 AA; 99091 MW; 9071A032A091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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OrderedLocusNames-RPA0932;
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QENB96;
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Matches 7; Conservative
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24 LLPLOVLL 31

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   o. - - - 1002 (TrEMBLrel. 22, Created)
01-077-2002 (TrEMBLrel. 22, Last sequence update)
01-077-2003 (TrEMBLrel. 26, Last annotation update)
Acyl-CoA desaturase HassPPAE (Fragment).
Helicoverpa assulta (Oriental tobacco budworm).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Nooptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Heliothinae; Helicoverpa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics 162:1737-1752(2002).

R Genetics 162:1737-1752(2002).

R GO; GO:0005734; C:nendoplasmic reticulum; IEA.

GO; GO:0005634; C:nendbrane; IEA.

GO; GO:0005634; C:nencleus; IEA.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0006491; F:oxidoreductase activity; IEA.

R GO; GO:0004768; F:stearcyl-CoA 9-desaturase activity; IEA.

R GO; GO:000633; P:fatty acid biosynthesis; IEA.

R GO; GO:000633; P:fatty acid biosynthesis; IEA.

R GO; GO:000635; P:fatty acid biosynthesis; IEA.

R InterPro; IPR001525; Desaturase.

R InterPro; IPR001525; Homecobox.
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Knipple D.C., Rosenfield C.L., Nielsen R., You K.M., Jeong S.E.;
"Evolution of the integral membrane desaturase gene family in moths
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fatty acid biosynthesis; Iron; Lipid synthesis; Oxidoreductase;
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87.5%; Pred. No. 1.3e+02;
tive 1; Mismatches 0;
183 AA
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Job time : 98.3333 secs
PRT;
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QBMZZO_HELAU PRELIMINARY;
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nes 7; Conservative
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14 LPLQVLLL 21
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US-09-502-600-35
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US-09-918-243-35
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Sequence 2, Appli
Sequence 3, Appli
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Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 31, Appli
Sequence 33, Appli
Sequence 33, Appli
Sequence 1083, Appli
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Sequence 42872, A
Sequence 19, Appl
Sequence 6, Appli
Sequence 6, Appli
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Sequence 99, Appl
Sequence 5, Appli
Sequence 99, Appli
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                                                                                                                            March 11, 2006, 00:41:16; Search time 21.222 Seconds (without alignments) 35.061 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-08-557-146-2
US-08-557-146-2
US-08-918-243-35
US-09-154-34-2
US-09-154-344-2
US-09-154-344-2
US-09-154-344-2
US-09-10-10-13-2
US-09-20-10-13-3
US-09-20-10-716
US-09-18-243-33
US-09-918-243-33
US-09-918-243-33
US-09-205-258-1083
US-09-205-258-1079
US-09-333-61-1079
US-09-333-61-1079
US-09-252-9918-22870
US-09-252-9918-22870
US-09-252-9918-22870
US-09-252-9918-22870
US-08-319-12075
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US-08-319-12075
US-08-319-12075
US-08-319-12075
US-08-319-12275
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US-08-319-12075
US-08-319-12075
US-08-319-12275
US-08-2120-9918-6
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-09-991-181-99
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                                                                                                                                                                                                                                                                                                                                                                        572060 seqs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                      protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                         US-09-905-083A-35
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Maximum DB seq length: 2000000000
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US-09-502-600-35

Sequence 35, Application US/09502600A

Fatent No. 6294344

Fatent No. 6294344

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer

TITLE OF INVENTION: Ovarian Cancer

TITLE OF INVENTION: Ovarian Cancer

CURRENT FILING DATE: 2000-02-11

CURRENT APPLICATION NUMBER: US/09/502,600A

PRIOR FILING DATE: 03-14-1998

FRIOR FILING DATE: 03-14-1998

NUMBER OF SEQ ID NOS: 136

LENGTH: 9
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                       Sequence 36, Appl
Sequence 17, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 1574, Appl
Sequence 1574, Appl
Sequence 1574, Appl
Sequence 1574, Appl
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| Patent No. 6627403
| Fatent No. 6627403
| GENERAL INFORMATION:
| APPLICANT: O'Brien, Timothy J.
| APPLICANT: Cannon, Martin J.
| APPLICANT: Santin, Alessandro
| TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer:
| TILE PRINCES: D6223CHP/C/D/CIP
| CURRENT APPLICATION NUMBER: US/09/918,243
| FRIOR PILING DATE: 2001-07-30
| FRIOR PILING DATE: 2001-07-13
| NUMBER OF SEQ ID NOS: 136
| SEQ ID NO 35
| TYPE: PRT
| ORGANISM: Homo sapiens
                                                                                                                                                                                                                 Sequence 52836,
Sequence 21399,
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Sequence 9 Sequence 9 Sequence 9 Sequence 1 Sequence 1 Sequence 1 Sequence 3 Sequence 1 Sequence 1 Sequence 2 Sequence 2 Sequence 2 Sequence 3 Sequence 2 Sequence 3 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2
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                                                                                                                                                                                       US-09-605-703B-1574
US-09-270-767-37619
US-09-270-767-52836
US-09-248-796A-21399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 40; DB 2; L Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 9; Conservative 0; Mismatches 0;
                                   US-08-339-152A-17
US-08-339-152A-16
US-08-607-998-3
US-09-245-041-15
US-09-358-058-15
US-09-502-600-36
US-09-502-600-36
US-09-502-600-28
US-09-502-600-28
US-09-502-600-28
US-09-918-243-28
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201
201
232
634
653
653
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2787
2787
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ORGANISM: Homo sapiens
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Patent No. 5834290
GENERAL INFORMATION:
APPLICANT: Beglind, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Bazyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New YOLK
STATE: New YORK
COUNTRY: U.S.A.
ZIP: 10036-2787
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible

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                                                                                                                                                                                             Query Match 100.0%; Score 40; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 9; Conservative 0; Mismatches 0; Indels
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-918-243-35
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Patent No. 5962300
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
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LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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US-08-557-146-2
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US-08-824-874-3
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100.0%; Score 40; DB 2; Length 253; larity 100.0%; Pred. No. 4.4; Conservative 0; Mismatches 0: Indels
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                                                                                                                                                                                        US-09-210-084-3
; Sequence 3, Application US/09210084
; Patent No. 619711
; GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE INCYTE Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/824,874
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0252 US
TELECOMMUNICATION INPORMATION:
TELEFRENS: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09764762
Patent No. 6472195
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TILE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
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                                                                                                                    6 LLPLQILLL 14
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                                                                                   1 LLPLQILLL 9
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IMMEDIATE SOURCE:
LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid STRANDEDNESS: si
         Query Match
Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             94304
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                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/930,188
                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                         NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEFHONE: (212) 819-8783
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARCTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REPERENCE/POCKET NUMBER: X9239
TELECOMMUNICATION IN TELECOMMUNICATION:
TELEPHONE: 317-277-1090
     APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08930188 Patent No. 6093397
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INFORMATION FOR SEQ ID NO: 2:
                       FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-154-344-2
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MOLECULE TYPE: protein

US-08-930-188-2
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LLPLOILLL 14
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COUNTRY: Unite
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US-08-930-188-2
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Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-949-016-7716
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GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Johnstone, Edward M.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 40; DB 2; Length 253; Best Local Similarity 100.0%; Pred. No. 4.4; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                          ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 18/99/764,762
FILING DATE: 16-Jan-2001
CLASSIFICATION: <UNknown>
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CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/210,084
FILING DATE: (UNKNOWN)
FILING DATE: (UNKNOWN)
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 96,749
REGISTRATION INFORMATION:
TELEPAN 415-845-4166
INFORMATION FOR SEC ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE: 532504
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Elilily and Company STREET: Lilly Corporate Center CITY: Indianapolis STATE: Indiana COUNTRY: United States of America ZIP: 46285 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: IBM PC COMPASSIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
LIBRARY: GenBank
                                                                                                                    COUNTRY: USA
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PCT-US96-04294-2
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FARENAL NO. SELIZAS);
FARENAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERBUCE: CLOOL307;
CURRENT FILING DATE: 2000-04-14
FRICH APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PELICATION NUMBER: 60/231,498
PRIOR PELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTESE FASTESE FOR Windows Version 4.0
SEQ ID NO 7716
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APPLICANT: O'BELION:
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Ovarian Cancer
FILE REFERENCE: D6223CIP-C
CURRENT FILING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: US/09/502,600A
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTAATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X239
TELECOMMUNICATION INFORMATION:
TELEPHORE: 317-277-1090
TELEFAX: 317-277-3861
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acide
TYPE: amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7716, Application US/09949016 Patent No. 6812339
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US-09-502-600-33
; Sequence 33, Application US/09502600A
; Patent No. 6294344
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: O'BRIEN, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro.
TITLB OF INVENTION: Methods for the early diagnosis of ovarian cancer FILE REFERENCE: D6223CIP/C/D/CIP
CURRENT APPLICATION NUMBER: US/09/918,243
CURRENT FILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 33
LENGTH: 9
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                                                                                                                                                                                                                                                             90.0%; Score 36; DB 2; Length 9; 100.0%; Pred. No. 4.6e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                            ) OTHER INFORMATION: Residues 5-13 of the SCCE protein US-09-502-600-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: CHAIN
STATE INFORMATION: Residues 5-13 of the SCCE protein US-09-918-243-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-09-205-258-1083

Sequence 1083, Application US/09205258

Patent No. 6225174

GENERAL INFORMATION:
APPLICANT: Young et al.
CURENT APPLICATION 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1

CURRENT APPLICATION NUMBER: US/09/205,258

CURRENT APPLICATION NUMBER: US/09/205,258

CURRENT RELING DATE: 1998-06-04

EARLIER PILING DATE: 1998-06-06

EARLIER APPLICATION NUMBER: 60/048,885

EARLIER APPLICATION NUMBER: 60/049,375

EARLIER APPLICATION NUMBER: 60/049,375

EARLIER APPLICATION NUMBER: 60/049,375

EARLIER APPLICATION NUMBER: 60/049,881

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 09/039,211
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 33
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 33, Application US/09918243
Patent No. 6627403
GENERAL INFORMATION:
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-918-243-33
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EARLIER APPLICATION NUMBER: 60/049,020
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER APPLICATION NUMBER: 60/049,036
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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                                                               FEATURE:

NAME/KEX: SITE

LOCATION: (8)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-004-860-1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
APPLICANT: Ryba, Nick
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: He Regents of the University of California
APPLICANT: The Regents of the United States of America
APPLICANT: The Regents of the United States of America
APPLICANT: Department of the United States of America
APPLICANT: Department of Health and Human Services
ITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
FILE REFERENCE: 02307E-09800005
CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT PILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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85.0%; Score 34; DB 2; Length 73;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                           Score 34; DB 2; Length 73;
Pred. No. 16;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-10-004-860-1083
; Sequence 1083, Application US/10004860
; Patent No. 6914047
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT FILING DATE: 2001-12-07
; CURRENT FILING DATE: 2001-12-07
; WUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1083
; LENGTH: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 37, Application US/09393634 Patent No. 6558910
                                                                                                                                                                                           Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
LENGTH: 73
TYPE: PRT
ORGANISM: Homo sapiens
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25 LPLQLLLL 32
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25 LPLQLLLL 32
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APPLICANT: Zuker, Ch
APPLICANT: APLICANT: Ryba, Nic
APPLICANT: Ryba, Nic
APPLICANT: Hoon, Mar
APPLICANT: Hoen, Mar
APPLICANT: The Regen
APPLICANT: The Gover
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NAME/KEY: SITE
LOCATION: (8)
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US-09-393-634-37
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LENGTH: 302
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; ORGANISM: Homo sapiens
; PEATURE:
; OTHER INPORMATION: human GR02
; NAME/KEY: MOD_RES
; LOCATION: (143)
; OTHER INPORMATION: Xaa = any amino acid
US-09-393-634-37

Query Match
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps

Qy 1 LLPLQILLL 9

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Db 42 LMPIQILLM 50

Search completed: March 11, 2006, 01:24:26
Job time: :22.2222 secs
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Mon Mar 13 12:27:57 2006
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FILLY FILLING DAILS: 2000-02.
WUMBER OF SEQ ID NOS: 136
LENGTH: 9
TYPE: PRT
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Sequence 35, Appl
Sequence 35, Appl
Sequence 53737, A
Sequence 92, Appl
Sequence 92, Appl
Sequence 98, Appl
Sequence 2, Appl
Sequence 48, Appl
Sequence 95, Appl
Sequence 38, Appl
Sequence 95, Appl
Sequence 95, Appl
Sequence 38, Appl
Sequence 95, Appl
Sequence 38, Appl
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Sequence 33, Appl
Sequence 33, Appl
Sequence 207950,
Sequence 928, Appl
Sequence 51875, A
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                                                                                     March 11, 2006, 01:24:47; Search time 69.444 Seconds (without alignments) 54.151 Million cell updates/sec
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Sequence
Sequence
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-372-521-35

US-10-372-521-35

US-10-450-765-53737

US-10-262-511-96

US-10-262-511-96

US-10-262-511-96

US-10-262-511-96

US-10-071-214-48

US-10-071-214-48

US-10-071-214-48

US-10-071-214-48

US-10-255-027-498

US-10-264-293

US-10-264-294-8

US-10-264-39-95

US-10-348-518-95

US-10-348-518-95

US-10-348-518-95

US-10-348-518-95

US-10-348-518-95

US-10-348-518-95

US-10-348-518-95

US-10-373-958-95

US-10-373-928-95

US-10-373-928-95

US-10-373-923-928
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                                                                                                                                                                                                                                                            1867569 seqs, 417829326 residues
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Maximum Match 1008
Listing first 45 summaries
                                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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		of ovarian .n	Length 9; Indels	Barly I
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0-369-493-10255 9-864-761-46097 0-424-5915-115-284317 0-335-977-6098 0-335-977-6098 0-335-977-6097 0-335-977-6097 0-335-977-6101 0-35-913A-92 0-425-114-70206 0-425-115-29449 0-425-115-29449 0-425-115-21842 0-097-863-1215-2949 0-097-863-1215-2949 0-097-863-1215-2949 0-097-863-1215-2949 0-097-863-1215-2949 0-097-863-1215-2949 0-097-863-1215-2949 0-097-863-1215-2949 0-097-863-1215-2949 0-097-863-1215-2949 0-097-863-1215-2949	SNTS	dias	DB 1.7e	hods 3
-100-369-869-869-869-869-869-869-869-869-899-89	ALIGNMENTS	243 the early 9/918,243	Score 40; D Pred. No. 1. Mismatches;	и Ö,
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868 23 23 305 305 306 330 477 477 480 637 637 637 70 70 70		tion US/0991 3317A1 Timothy J. Martin J. Alessandor for Methods fo	100.0%; 100.0%; vative 9	ion US/09905083 708A1 Timothy J. Compositions an Ovarian Cancer 321P/C/103 201-07-13 MBER: US/09/9
990.0 87.5 87.5 87.5 87.5 87.5 87.5 87.5 887.5 885.0 885.0		pplicat 002014 monology monolo	Similarity 9; Conservat 1 LLPLQILL 9	SULT 2 Sequence 35, Application US/09905083 Sequence 35, Application US/09905083 Patent No. US20020146708A1 APPLICAMT: O'Brien, Timochy J. TITLE OF INVENTION: Compositions and Met. FILE OF INVENTION: Compositions and Met. FILE OF INVENTION: Owarian Cancer FILE PREFERENCE: D6223CIP/C/biv CURRENT APPLICATION NUMBER: US/09/905,08 CURRENT FILING DATE: 2001-07-13 PRIOR APPLICATION NUMBER: US/09/502,600 PRIOR FILING DATE: 2000-02-11
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~		SEQUENCE 35, Applica Patent No. US2002014 SERENT NO. US2002014 SERENT INFORMATION. APPLICANT: Camon, APPLICANT: Camon, APPLICANT: Santin, TITLE OF INVENTION: SANTIN, CURRENT FILING DATE: PRIOR PILING DATE: NUMBER OF SEQ ID NO	sal sal	i. 083-35 No. US2002014 No. US2002014 INDORMATION: OF INVENTION: OF INVENTION: THERERED THE APPLICATION THE FILING DATE THE
8 0 0 0 H B B B B B B B B B B B B B B B B		RESULT 1 Sequence 35 Sequence 35 Sequence 35 Patent No. GENERAL INF. APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: PITUE OF IT. FILE REFER. CURRENT PIP FILE REFER. CURRENT PIP CREATURE: CREATURE C	Query Match Best Local Matches Oy 1	RESULT 2 US-09-905 Sequence: Patent GENERAL TITLE: TUREN CURREN PRIOR: PRIOR:

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                                                                                                                                                                                                                                                                                                                                                                         Sequence 35, Application US/10372521
; Sequence 35, Application US/10372521
; Publication No. US20030223973A1
; GRNERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer; FILE REFERENCE: D6223CIP/C/D/CIP/C)
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR PELICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-831-075-35
) Sequence 35, Application US/10831075
) Sequence 35, Application US/10831075
) Publication No. US20040224891A1
) GENERAL INFORMATION:
) APPLICANT: Cannon, Martin J.
) APPLICANT: Cannon, Martin J.
) TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
) TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
) FILE REPRENENCE: D6223.CIP/C/D/CIP3
) CURRENT APPLICATION NUMBER: US 10/372,521
) PRIOR FILING DATE: 2004-04-23
) PRIOR FILING DATE: 2003-02-21
) NUMBER OF SEQ ID NOS: 140
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                                                                                                                                              Query Match 100.0%; Score 40; DB 3; Length 9; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 9; Conservative 0; Mismatches 0; Indels
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                                              ; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-905-083-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:

NAME/KEY: CHAIN

OTHER INCRNATION: Residues 6-14 of the SCCE protein US-10-372-521-35
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OTHER INFORMATION: Residues 6-14 of the SCCE protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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100.0%; Score 40; DB 5; Length 9;

Query Match

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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOWAIN
COTHER INFORMATION: Serine proteases trypsin family, histidine proteins. domain
OTHER INFORMATION: 20, raw score of 11.96
FEATURE:
NAME/KEY: DOWAIN
COTHER INFORMATION: 20, raw score of 11.96
FEATURE:
OTHER INFORMATION: (36). (133)
OTHER INFORMATION: COMPANION: COMPANION: (36). (133)
OTHER INFORMATION: Trypsin domain identified by PFam, accession name trypsin, E-
OTHER INFORMATION: value=3.2e-31, PFam score of 101.0
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                                                                                                                                                                                                                                                              ABPELICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 53737
LENGTH: 136
                   Indele
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                    Sequence 53737, Application US/10450763 Publication No. US20050196754A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 96, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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Malyankar, Uriel M.
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Zerhusen, Bryan D.
Anderson, David W.
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Matches 9; Conservative
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                                                                                                  1 LLPLQILLL 9
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                                                            1 LLPLQILLL
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US-10-262-511-96
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APPLICANT:
APPLICANT:
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APPLICANT:
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FILE OF INVENTION: NOWEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
FILE APPLICATION NUMBER: US/10/262,511
FRICA APPLICATION NUMBER: 60/336,483
PRIOR FILING DATE: 2001-10-02
PRIOR PLICATION NUMBER: 60/337,917
PRIOR PLICATION NUMBER: 60/337,917
PRIOR PLILING DATE: 2001-10-09
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-05-17
PRIOR FILING DATE: 2002-05-17
PRIOR FILING DATE: 2002-05-17
PRIOR FILING DATE: 2002-05-16
PRIOR FILING DATE: 2002-05-16
PRIOR FILING DATE: 2002-05-16
PRIOR PLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR PLICATION NUMBER: 60/333,260
PRIOR FILING DATE: 2002-04-17
PRIOR PLICATION NUMBER: 60/373,260
PRIOR PLICATION NUMBER: 60/373,260
PRIOR PLING DATE: 2002-04-17
PRIOR PRIOR PRIOR PRIOR DATE: 2002-04-17
PRIOR 
                                                                                                                            APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Reactelli, Luca
APPLICANT: Stene, David J.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkets, Atchard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Agee, Michele L.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
Zerhusen, Bryan D.
Anderson, David W.
Zhong, Mei
                                                                                                Catterton, Elina
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US-10-262-511-92
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Best Local Similarity
Matches 9; Conserv
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERBENCE: 12402-4462C
CURRENT APPLICATION NUMBER: 60/326,483
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR APPLICATION NUMBER: 60/373,917
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR PILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR PILING DATE: 2002-05-16
PRIOR PILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR PILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/313,260
PRIOR PILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR PILING DATE: 2002-04-17
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NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
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                                                                                                                                                                                                                             Shimkets, Richard A. Rothenberg, Mark E. Leach, Martin D. Agee, Michele L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guo, Xiaojia (Sasha)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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Malyankar, Uriel M.
Ort, Tatiana
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Rewida, Ramesh
APPLICANT: Li, Li
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sasha
                               i, Weizhen
iller, Charles E.
                                                                                                                                Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
Catterton, Elina
                                                                                   Rastelli, Luca
Stone, David J.
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Best Local Similarity 100
Matches 9; Conservative
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; ORGANISM: Homo sapiens
US-10-262-511-96
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APPLICANT:
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APPLICANT:
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ö Gaps ö 100.0%; Score 40; DB 4; Length 250; illarity 100.0%; Pred. No. 36; Conservative 0; Mismatches 0; Indels Sequence 98, Application US/09888615
Patent No. US20020064856A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: CAENEPEL, SEAN
APPLICANT: CAENEPEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION NOVEL PROTEASES
TITLE OF INVENTION NOVEL PROTEASES
FILE REPERBNCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26

Mon Mar 13 12:27:57 2006

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                                                                                                                                                                                          100.0%; Score 40; DB 3; Length 253; 100.0%; Pred. No. 36; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
US-09-764-762-3
Sequence 3, Application US/09764762
Fatent No. US20020066341A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CORRESPONDENCE 3:
CORRESPONDENCE ADDRESS:
ADDRESSE:
STREET: 3174 POTTER Drive
COUNTY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/210,084
FILING DATE: cUnknown:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTATION NUMBER: 36,749
REPRENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-855-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 98
LENGTH: 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: GenBank
                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-888-615-98
                                                                                                                                                                                                                                                                                                              6 LLPLOILLL 14
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Best Local Similarity
Matches 9; Conserv
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                                                                                              LENGTH: 25.
TYPE: PRT
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LLPLQILLL 14

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Sequence 2, Application US/10071214

Publication No. US20030066099A1

Publication No. US20030066099A1

REDREAL INCORMATION:
THIS DEFENDENCE: FORCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
TITLE OF INVENTION: SCOEE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
FILE REFERENCE: HANSSON-3A

CURRENT APPLICATION NUMBER: US/10/071,214

PRIOR APPLICATION NUMBER: US 60/267,422

PRIOR PELING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-071-214-48

US-10-071-214-48

US-10-071-214-48

Squence 48, Application US/10071214

Publication No. US2030066099A1

GENERAL INFORMATION:

APPLICANT: HANSSON, Lennart

APPLICANT: EGELRUD, Torbjorn

TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN

TITLE OF INVENTION SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN

FILE REFERENCE: HANSSONA

CURRENT PAPLICATION NUMBER: US 60/267,422

PRIOR PILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin version 3.1

SEQ ID NO 48

LENGTH 253

MANDER. DELENGTH 253

MANDER. DELENGTH 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 40; DB 4; ilarity 100.0%; Pred. No. 36; Conservative 0; Mismatches 0
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US-10-264-283-90
; Sequence 90, Application US/10264283
; Publication No. US20030144494A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LLPLOILL 14
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Best Local Similarity
Matches 9; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 253
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                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2
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US-10-173-999-48
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APPLICANT: G19TH, KUIT C.
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Matson, Susan R.
APPLICANT: Matson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Bos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US 09/663,733
RRIOR APPLICATION NUMBER: US 60/350,666
RRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-12
PRIOR FILING DATE: 2001-11-12
PRIOR FILING DATE: 2001-11-12
PRIOR FILING DATE: 2001-11-21
PRIOR PLILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-02-03
PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR P
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NUMBER OF SEQ ID NOS: 1386
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 498
LENGTH: 253
                              APPLICANT: Mannion, Jane:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210.21.590
CURRENT APPLICATION NUMBER: US/10/264,283
CURRENT FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 111
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 90
LENGTH: 253
TYPE: PRT
CREEN: Homo gapiens
US-10-264-283-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 40; DB 4; Length 253; 100.0%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Afar, Daniel
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurr C.
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Best Local Similarity 100.
Matches 9; Conservative
APPLICANT: Algate, Paul A.
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US-10-295-027-498
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US-10-295-027-498
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| Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match | Query Match |
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Query Match
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: March 11, 2006, 01:37:23 Job time : 69.4444 secs

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Kabouni (19-12-748-14)
Sequence 14, Application US/10412748
Sequence 14, Application US/10412748
Publication No. US20060035219A1
GENERAL INFORMATION:
APPLICANT: Queensland University of Technology
TITLE OF INVENTION: Aberrant Kallikrein Expression
FILE REFERENCE: DAVI172.003AUS
CURRENT APPLICATION NUMBER: US/10/412,748
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: AU PSI616/02
PRIOR FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
SEQ ID NO 14
SEQ ID NO 14
TYPE: PRT
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ORGANISM: Human
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  RESULT 2
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Sequence 14, Appl
Sequence 17, Appl
Sequence 98, Appl
Sequence 409, App
Sequence 27354, Appl
Sequence 27354, Appl
Sequence 27351, Appl
Sequence 17351, Appl
Sequence 1124, Appl
Sequence 1124, Appl
Sequence 1147, Appl
Sequence 1347, Appl
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                                                                            March 11, 2006, 01:27:17; Search time 8 Seconds (without alignments) 31.314 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
            GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-412-748-14

US-10-412-748-14

US-11-037-243-98

US-11-000-463-881

US-11-000-463-881

US-11-096-568A-27354

US-11-096-568A-27390

US-11-230-180-124

US-11-230-188-136

US-10-131-826A-136

US-10-131-826A-136

US-11-169-041-227

US-11-169-041-227

US-11-169-041-227

US-11-169-041-227

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US-11-17-216-216
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US-10-821-234-1465
US-11-051-720-1355
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Maximum Match 100%
Listing first 45 summaries
                                                       protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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2533
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93
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Sequence 94, Appl Sequence 1357, Ap Sequence 1350, Ap Sequence 2089, A Sequence 1352, Ap Sequence 1354, Ap Sequence 1354, Ap Sequence 1354, Ap Sequence 2216, Ap Sequence 2216, Ap Sequence 27, Appli Sequence 7, Appli Sequence 2385, Ap Sequence 2316, Ap Sequence 231
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Sequence 5641, Ap
Sequence 5640, Ap
Sequence 14701, A
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US-10-412-748-11

Sequence 11, Application US/10412748

Publication No. US20060035219A1

GENERAL INFORMATION:

APPLICANT: Queensland University of Technology

APPLICANT: Queensland University of Technology

TITLE OF INVENTION: Aberrant Kallikrein Expression

FILE REFERRINCE: DAVI172.003AUS

CURRENT APPLICATION NUMBER: US/10/412,748

CURRENT FILING DATE: 2003-04-09

PRIOR PILING DATE: 2002-04-09

NUMBER OF SEQ 1D NOS: 41

SOFTWARE: Patentin version 3.2

ENGIN NO 11

TYPE: RRI
                                 US-11-051-720-1357
US-11-051-720-1357
US-11-051-720-1350
US-11-096-568A-20889
US-11-051-720-1356
US-11-051-720-1356
US-11-051-720-1354
US-11-051-720-1353
US-11-072-5155
US-11-072-5155
US-11-072-5155
US-11-097-2515
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US-11-096-568A-26217
US-11-096-568A-23862
US-11-096-568A-5642
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US-11-096-568A-5640
US-11-096-568A-14701
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Query Match 82.5
Best Local Similarity 77.8
Matches 7; Conservative
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ORGANISM: Homo sapiens
                        1 LLPLQILLL 9
    1 LLPLOILLL
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US-11-000-463-409
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                                                           Query Match 100.0%; Score 40; DB 6; Length 253; Best Local Similarity 100.0%; Pred. No. 1.7; Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                    Sequence 17, Application US/10412748

Publication No. US20060035219A1

GENERAL INFORMATION:
APPLICANT: Queensland University of Technology
APPLICANT: Clements, Judith A
TITLE OF INVENTION: Aberrant Kallikrein Expression
FILE REFERENCE: DAVI172. 003AUS
CURRENT PILIGATION NUMBER: US/10/412,748
CURRENT FILING DATE: 2003-04-09
PRIOR FILING DATE: 2002-04-09
NUMBER: OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
SEQ ID NO 17.
LENGTH: 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: WHYTE, DAVID
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CHANYDCZAK, GLEN
APPLICANT: CHANYDCZAK, GLEN
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/11/037,243
CURRENT APPLICATION NUMBER: US/09/808,615
PRIOR APPLICATION NUMBER: US/09/808,615
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PALENTIN VOICE: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 98, Application US/11037243; Publication No. US20050287546A1; GENERAL INFORMATION: APPLICANT: PLOWMAN, GREGORY APPLICANT: WHYTE, DAVID
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Best Local Similarity 100.
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ORGANISM: Homo sapiens
                                                                                                                                                   1 LIPLOILLE 9
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; ORGANISM: Human
US-10-412-748-14
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US-11-037-243-98
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Sequence 27391, Application US/11096568A
Publication No. US20660048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REPERENCE: 2750-1592PUS2
CURRENT REPERENCE: 2750-1592PUS2
CURRENT REPLICATION NUMBER: US/11/096,568A
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 27391
LENGTH: 71
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| Sequence 27353, Application US/11096568A
| Sequence 27353, Application US/11096568A
| Publication No. US20060048240A1
| GENERAL INFORMATION:
| APPLICANT: Alexandrov, Nickolai et al.
| TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides |
| TITLE OF INVENTION: Therby
| FILE REPERENCE: 2750-1592PUS2
| CURRENT APPLICATION NUMBER: US/11/096,568A
| CURRENT APPLICATION NUMBER: US/11/096,568A
| CURRENT FILING DATE: 2005-04-01
| SEQ ID NOS: 34471
| LENGTH: 85
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80.0%; Score 32; DB 7; Length 71;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels
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NAME/KEY: misc_feature

LOCATION: (1)...(71)

TOTHER INPORMATION: Ceres Seq. ID no. 13500184
US-11-096-568A-27391
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FRATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(71)
; LOCATION: (1)..(71)
; UTHER INFORMATION: Ceres Seq. ID no. 5677704
US-11-096-568A-27354
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| LOCATION: (1)..(85)
| TOTER INORMATION: Ceres Seq. ID no. 5677703
| US-11-096-568A-27353
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ORGANISM: Arabidopsis thaliana
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity
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2 LLPLQIL 8
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US-11-096-568A-27391
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Sequence 27354, Application US/11096568A

Publication No. US20060048240A1

GENERAL INPORMATION:

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

FILE REFERENCE: 2750-15929US2

CURRENT PPLICATION UNDER: US/11/096,568A

CURRENT PAPLICATION NOWBER: US/11/096,568A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7; Length 181; 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6768, Application US/11087099
Publication No. US20060041961A1
Publication No. US20060041961A1
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EP
CURRENT FILIAND NUMBER: US/11/087,099
CURRENT PLICATION NUMBER: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 7
Pred. No. 23;
1; Mismatches
                                           CURRENT AFFILMS DATE: 2004-11-29
PRIOR APPLICATION NUMBER: 10/291,265
PRIOR APPLICATION NUMBER: 10/291,265
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR PILING DATE: 2001-01-25
PRIOR PLING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR PLING DATE: 2000-01-25
PRIOR PLING DATE: 2000-01-37
PRIOR PLING DATE: 2000-01-37
PRIOR PLING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR STLING DATE: 2000-09-15
  FILE REFERENCE: 785CIP4CN
CURRENT APPLICATION NUMBER: US/11/000,463
CURRENT FILING DATE: 2004-11-29
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Best Local Similarity 77.0
Tr Conservative
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Best Local Similarity 77.8
T. Conservative
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CORGANISM: Homo sapiens
US-11-000-463-409
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7 LLPLHLLLL 15
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39 LLPLSLLLL 47
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ORGANISM: Zea mays
US-11-087-099-8768
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LENGTH: 181
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Sequence 93, Application US/11203251A
Publication No. US20060039904A1
GENERAL INFORMATION:
APPLICANT: Mediamune inc.
TITLE OF INVENTION: CELL-MEDIATED CYTOTOXICITY ACTIVITY
FILE REFERENCE: AE702US
CURRENT FILING DATE: 2005-08-15
PRIOR APPLICATION NUMBER: US/11/203,251A
PRIOR PELING DATE: 2004-08-16
PRIOR FILING DATE: 2004-08-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Andermani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REPERBURE: 821A
CURRENT APPLICATION WUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR PAPLICATION NUMBER: US 60/462,047
PRIOR PILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704-07
SEQ ID NO 1347
LENGTH: 140
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APPLICANT: Samad, Tarek A.

TITLE OF INVENTION: DRG11-RESPONSIVE (DRAGON) GENE FAMILY
FILE REFERENCE: 00786/419002

CURRENT APPLICATION NUMBER: US/11/230,180

CURRENT FILING DATE: 2005-09-19
PRIOR APPLICATION NUMBER: US/10/419,296

PRIOR APPLICATION NUMBER: 60/373,519
PRIOR APPLICATION NUMBER: 60/373,519
PRIOR FILING DATE: 2002-04-18

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 12

LENTH: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.5%; Score 31; DB 6; Length 140; 77.8%; Pred. No. 42; tive 1; Mismatches 1; Indels
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Pred. No. 28;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
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Matches 7; Conservative
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9 LLPLLLLLL 17
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US-10-821-234-1347
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Publication No. US20060048240A1

GENERAL INFORMATION:
ACRIECANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 27390
LENGTH: 85
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Sequence 1024, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THERROF FILE REPRENCE: CLOUSES9
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1024
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                  Indels
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LOCATION: (1)..(85)

OTHER INFORMATION: Ceres Seq. ID no. 13500183

US-11-096-568A-27390
                  Mismatches
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Best Local Similarity 100...
7; Conservative
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                  7; Conservative
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LLPLPLLLL 21
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16 LLPLQIL 22
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Best Local Similarity
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US-11-096-568A-27390
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US-11-230-180-12
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## PRIOR APPLICATION NUMBER: 60/608,852
| PRIOR FILING DATE: 2004-09-13 |
| NUMBER OF SEQ ID NOS: 101 |
| SOFTWARE: Patentin version 3.3 |
| SEQ ID NO 93 |
| TYPE: PRT |
| ORGANISM: Homo sapiens |
| ORGANISM: Homo sapiens |
| TYPE: PRT |
| ORGANISM: Homo sapiens |
| ORGANISM: Homo sapiens |
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March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds (without alignments) 45.628 Million cell updates/sec Run on:

US-09-905-083A-36

1 SLLLPLQIL 9 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2443163 segs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

geneseqp1980s:\* A\_Geneseq\_1 Database

geneseqp1990s: \*
geneseqp2000s: \*
geneseqp2001s: \*
geneseqp2001s: \*
geneseqp2003as: \*
geneseqp2003bs: \*
geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## CITAMADIES

		de			SUMMARIES	
Result	C	Query		1	:	
9	Score	Match	Length	80	ID	Description
-	40	100.0	o,	4	AAE08241	Aae08241 Human str
73	40	100.0	o,	œ	ADR68797	Adr68797 Human str
m	40	100.0	136	4	ABG23378	Abg23378 Novel hum
4	40	100.0	198	9	ADA05736	Ada05736 Human NOV
Ŋ	40	100.0	198	80	ADN62900	
9	40	100.0	250	9	ADA05732	Ada05732 Human NOV
7	40	100.0	250	œ	ADN62896	Adn62896 Human NOV
80	40	100.0	253	N	AAR67888	Aar67888 Human str
თ	40	100.0	253	N	AAW05383	Aaw05383 Human amy
10	40	100.0	253	ഗ	ABB84421	Abb84421 Human SCC
11	40	100.0	253	Ŋ	ABB84406	Abb84406 Human SCC
12	40	100.0	253	ហ	AAU82740	Aau82740 Amino aci
13	40	100.0	253	9	ABU07440	Abu07440 Protein d
14	40	100.0	253	9	ABU07471	Abu07471 Protein d
15	40	100.0	253	9	ABR58471	Abr58471 Human str
16	40	100.0	253	7	ADB80484	Adb80484 Ovarian c
17	40	100.0	253	7	ADJ68833	Adj68833 Human hea
18	40	100.0	253	7	ADN39180	Adn39180 Cancer/an
19	40	100.0	253	œ	ADL06515	
20	40	100.0	253	œ	ADN04182	Adn04182 Antipsori
21	40	100.0	253	œ	ADR72880	
22	40	100.0	253	σ	ADY67588	Ady67588 Human kal
23	40	100.0	253	σ	AEC00353	Aec00353 Human kal

	Adb65713 Human pro Adj92327 Mouse hai Aaw22303 Rat CRTI. Adl27274 Amino aci Add30604 Plant yie
AAE08238 ADR68794 ADX80484 ADX201222 AA012472 AB0171036 AB071036 ABP70828 AAE08240 AAE08240 AAE08240 AAE08370 ADR68977 ADR68977 ADR691991	ADB65713 ADJ92327 AAW22303 ADL27274 ADD30604
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88 8 8 8 7 7 7 9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	00000
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22222222222222222222222222222222222222	4 4 4 4 4 1 4 6 4 6

## ALIGNMENTS

RESULT 1 AAE08241

AAE08241 standard; peptide; 9 AA.

AAE08241;

01-NOV-2001 (first entry)

Human stratum corneum chymotrypsin enzyme peptide #6 (residues 4-12).

Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia. 

Homo sapiens

WO200159158-A1.

16-AUG-2001.

07-FEB-2001; 2001WO-US003977.

11-FEB-2000; 2000US-00502600.

(UYAR-) UNIV ARKANSAS

O'brien TJ;

WPI; 2001-514676/56.

Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.

Claim 25; Page 103; 127pp; English.

The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCB). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCB oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCB peptide

Sequence 9 AA;

Aab21326 Human HSC

3 AAB21326

257

40 100.0

24

Human, chromosome mapping, gene mapping, gene therapy, forensic; food supplement, medical imaging, diagnostic; genetic disorder.

30-MAR-2001; 2001WO-US008631. 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

WO200175067-A2 Homo sapiens.

11-OCT-2001

Novel human diagnostic protein #23369.

Human; chromosome

(first entry)

18-FEB-2002

ABG23378;

ABG23378 standard; protein; 136 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel method for vaccinating an individual against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating an individual with a SCCE peptide, which elicite an immune response in the individual. A peptide of the invention acts as a stratum corneum chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or a risk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligonucleotide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or peptides are also useful in the monitoring and development of immunotherapies for ovarian and other malignancies. The present sequence represents a peptide fragment of serine protease SCCE (stratum corneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
                                                                                                                                                                                                                                                                                                                                                                                                                 Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:36.
                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              serine protease; stratum corneum chymotrytic enzyme; SCCE; immune response; ovarian cancer; lung cancer; prostate cancer; pancreatic cancer; colon cancer.
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       100.0%; Score 40; DB 4; Length 9; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                      ADR68797 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                     02-DEC-2004 (first entry)
                                                      9; Conservative
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                                                                                                        SLLLPLQIL 9
                                                                                                                                   1 SLLLPLQIL 9
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Query Match
Best Local Similarity
Matches 9: Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

biodiversity.

Tang YT;

Drmanac RT, Liu C, WPI; 2001-639362/73

N-PSDB; AAS87565

(HYSE-) HYSEQ INC

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCK) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). (II) epolymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food of sites expressing (II). (I) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders or layopeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              patent did not appear in the printed specification, but was obtained in
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Claim 20; SEQ ID NO 53737; 103pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA05736 standard; protein; 198 AA.
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Best Local Similarity
Matches 9; Conserv
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Gaps

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Best Local Similarity 100. Matches 9; Conservative

1 SULLPLOIL 9 

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New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                  immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obseity; infection; cachexia; cancer;
ineurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                      human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                         Human NOV18c protein SEQ ID NO:96.
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                                                                                                                                                                                                                                                                                                                                          05-0CT-2001; 20010S-0327449P.

09-0CT-2001; 20010S-0327417P.

09-0CT-2001; 20010S-0328029P.

09-0CT-2001; 20010S-0328049P.

12-0CT-2001; 20010S-0328849P.

15-0CT-2001; 20010S-0328849P.

17-0CT-2001; 20010S-0330849P.

18-0CT-2001; 20010S-03308P.

22-0CT-2001; 20010S-0341058P.

24-0CT-2001; 20010S-0341058P.

24-0CT-2001; 20010S-0341058P.

25-0CT-2001; 20010S-034058P.

26-0CT-2001; 20010S-034957P.

17-APR-2002; 20020S-0373260P.
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19-APR-2002; 2002US-0373884P.
22-APR-2002; 2002US-0374977P.
16-MAY-2002; 2002US-0381037P.
16-MAY-2002; 2002US-0381039P.
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17-MAY-2002; 2002US-0381642P.
28-MAY-2002; 2002US-0383656P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-APR-2002; 2002US-0373815P.
                                                                                                                                                                                                                                                                                     02-OCT-2002; 2002WO-US031373
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                            (first entry)
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N-PSDB; ADA05735.
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                             06-NOV-2003
                                                                                                                                                                                             Homo sapiens
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29-MAY-2002;
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ADA05736;
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described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell indeator the polypeptide described above; (7) methods for determining the binds to the polypeptide described above; (7) methods for determining the sample; (8) methods for determining the presence of a mount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for aberrant physicological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for screening for a modulator of activity or of latency or predisposition to a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a method for producing the above polypeptide or the nucleic and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid acid molecule may be used to diagnose, treat or prevent metabolic adjusted with a human disease. The polypeptide or the nucleic acids can an also be used as hybridisation and conferent and an also be used by probes, in chromosom
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2001US-0327435P.
2001US-0327449P.
2001US-0327917P.
2001US-0328029P.
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05-OCT-2001; 2
05-OCT-2001; 2
09-OCT-2001; 2
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Matches
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Dipippo VA;

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide

Claim 1; SEQ ID NO 96; 395pp; English.

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Smithson G, marter L, -- Sdinger SR, Ellerman K, maryammer. Patturajan M, Spytek KA, Edinger SR, Ellerman K, maryammer. Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Pigen A. Gangolli EA, Rieger DK, Spaderna SK;
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A, Edinger SR, Ellerman K, Malyankar UM;
      09-0CT-2001; 2001US-0328056P.
12-0CT-2001; 2001US-0328849P.
15-0CT-2001; 2001US-0339142P.
18-0CT-2001; 2001US-0330142P.
18-0CT-2001; 2001US-0341058P.
24-0CT-2001; 2001US-0341058P.
24-0CT-2001; 2001US-034955P.
29-0CT-2001; 2001US-0349557P.
01-NOV-2001; 2001US-0349557P.
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19-APR-2002; 2002US-0373817P.
19-APR-2002; 2002US-0373826P.
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16-MAY-2002; 2002US-0381037P.
16-MAY-2002; 2002US-0381038P.
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17-MAY-2002; 2002US-0381642P
28-MAY-2002; 2002US-0383656P
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25-JUN-2002; 2002US-0391335P
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EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
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RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
LEACH M D.
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GANGOLLI E A.
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SPADERNA S K.
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PATTURAJAN M.
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ANDERSON D W
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PEYMAN J A.
KEKUDA R.
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BERGHS C.
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(GANG/)
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Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

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The invention relates to isolated NOVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and collaborate associated with decreased polymucleotides may be used to treat disorders associated with decreased compared to dwm regulate expression of NOVX polypeptides by production or to rectify mutations. Conversely, antisense NA molecules may be administered to dwm regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polypurcleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of crestorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. The anti-NOVX polypeptides and polymucleotide expression and activity of NOVX collapoptides. The anti-NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polypeptide antibodies may be used in this way to prevent, clasquese, anorexia, cancer, cancer disperses, obesity, infectious disperses, anorexia, cancer, cancer associated cachexia, neurodegenerative dispenses and treat: metabolic disorders, disberder, immune dispenser. The matalopiet in the various dyslipidaemias, metabolic wasting disorders associated with obesity, the metabolic syndrome X and charactory of the pating dispense and the various dyslipidaemias, metabolic contexts. The year and the various dyslipidaemias, metabolic contexts. The year and the various dyslipidaemias, metabolic contexts. The year and the various dyslipidaemias and various cancer. The year and the various dyslipidaemias and various cancer. The year and the various cancer cancer cancer 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                They may also be used as antibacterial agents. The present represents the amino acid sequence of a human NOVX protein.
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2001US-0327449P.
2001US-0327917P.
2001US-0328029P.
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Matches 9; Conserv
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05-OCT-2001;
09-OCT-2001;
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us-09-905-083a-36.rag

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09-OCT-2001; 2001US-0328056P.
15-OCT-2001; 2001US-0328849P.
15-OCT-2001; 2001US-0339142P.
18-OCT-2001; 2001US-0330142P.
18-OCT-2001; 2001US-0330169P.
24-OCT-2001; 2001US-0341058P.
24-OCT-2001; 2001US-0343629P.
24-OCT-2001; 2001US-0343629P.
11-APR-2002; 2001US-0349575P.
11-APR-2002; 2001US-0373815P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373816P.
19-APR-2002; 2002US-0373816P.
19-APR-2002; 2002US-0373816P.
16-MAY-2002; 2002US-0381037P.
16-MAY-2002; 2002US-0381032P.
16-MAY-2002; 2002US-0381042P.
17-MAY-2002; 2002US-0381042P.
18-MAY-2002; 2002US-0381642P.
28-MAY-2002; 2002US-0381642P.
                                                                                                                                                             25-JUN-2002; 2002US-0391335P
01-OCT-2002; 2002US-00262511
                                                                                                                                                                                   (CURA-) CURAGEN CORP.
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Dipippo VA; Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK; New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics

Claim 1; Page 169-170; 586pp; English

The present into present the present through a polypeptide described above and a carrier; (2) a kit comprising a polypeptide described above and a carrier; (2) a kit comprising a polypeptide described above; (3) an isolated mucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or a pathology associated with the above polypeptide. NovX sequences have antidiabetic, nootropic, neuroprotective, antiparkinsonian and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a polypeptide in manufacturing a medicament for treating a polypeptide of an above polypeptide is useful in manufacturing a medicament for treating a polypeptide. acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's The present invention describes NOVX proteins, where X can be 1 to 55

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                                                                                                                                                                                                                                                                                                                     human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; meurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
disease, immune disorders, haematopoietic disorders and various dyslighdaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
                                                                                                                     Gaps
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                                                                                           100.0%; Score 40; DB 6; Length 250; 100.0%; Pred. No. 17; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                           ADN62896 standard; protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-OCT-2001; 2001US-0330309P.
22-OCT-2001; 2001US-0339266P.
24-OCT-2001; 2001US-0343629P.
29-OCT-2001; 2001US-0343629P.
10-NOV-2001; 2001US-0349575P.
17-APR-2002; 2002US-0373815P.
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2001US-0328849P.
2001US-0329414P.
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2001US-0328029P.
2001US-0328044P.
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2002US-0373826P.
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2002US-0381042P.
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                                                                                                                   9; Conservative
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                                                                                           Query Match
Best Local Similarity
Matches 9; Conserv
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                                                present invention.
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                                                                                                                                                                                                                                                                                                                                                                      wasting disorder.
                                                                      Sequence 250 AA;
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09-001-2001; 2
09-001-2001; 2
112-001-2001; 2
115-001-2001; 2
117-001-2001; 2
118-001-2001; 2
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22-APR-2002; 2
16-MAY-2002; 2
16-MAY-2002; 2
                                                                                                                                                                                                                                                                                                Human NOV18a.
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05-OCT-2001;
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19-APR-2002;
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wasting disorders associated with chronic diseases and various cance They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.

Sequence 250 AA;

8,5093

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MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E.
                                    MALYANKAR U M.
                                                                                                 LEACH M D.
AGEE M L.
BERGHS C.
DIPIPPO V A.
                                                                                                                 EISEN A.
GANGOLLI E A.
                                                ZERHUSEN B D. ANDERSON D W.
                                                                                                                             SPADERNA S K.
                GUO X.
PATTURAJAN M.
                            EDINGER S R.
ELLERMAN K.
                                                        ZHONG M.
CATTERTON E.
                                                                                                                                                                  WPI; 2004-213931/20.
Ä.
                        SPYTEK K A.
                                                                                                                          RIEGER D K.
PEYMAN J A
KEKUDA R.
                                            GORMAN L.
                                                                                                                                                                      N-PSDB, ADN62895
                                                                                                                 (EISE/)
(GANG/)
(RIEG/)
(SPAD/)
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(LEAC/)
(AGEE/)
(BERG/)
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(SHEN/)
(SHIM/)
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(CATT/
                Guox/
                    PATT/
                                    MALY/
                                        ORTT/
                        SPYT/
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Cort T, Gorman L, Zerhusen BD, Anderson DW, Ehong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen A, Gangolli EA, Rieger DK, Spaderna SK;

Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease

Claim 1; SEQ ID NO 92; 395pp; English.

The invention relates to isolated NOVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the abstrant expression and activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of suppeptides by binding with the cells own genes and preventing their expression. NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polypeptides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as DNA probes and antagonists of the expression and activity of NOVX. The anti-NOVX polypeptides and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. Colypeptides antibodies, agonists and antagonists may also be used as anti-NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polypeptide expression and activity of NOVX polypeptides and polymucleotide expression and activity of NOVX polypeptides and polymucleotide expression and activity of NOVX polypeptides and polymucleotides may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, anorexia, cancer, cancer associated cachexia, neurodegenerative disorders, and the various dyslipidaemias, metabolic disorders, haematopoietic disorders, parkinson's Disease, Parkinson's Disease, mathematopoietic disorders, and the various dyslipidaemias, metabolic disturbances associated authobuse type the metabolic syndrome X and

RESULT 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and talated vectors, transformed cells and polypeptides, useful for treating skin disorders, e.g. acne or psoriasis, and for identification of specific inhibitors.
                           Gaps
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                                                                                                                                                                                                                                               Human stratum corneum chymotrophic recombinant enzyme (SCCE).
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 Length 250;
                           0; Indels
100.0%; Score 40; DB 8; 100.0%; Pred. No. 17;
                           0; Mismatches
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                                                                                                                                                  AAR67888 standard; protein; 253 AA
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(first entry)
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Best Local Similarity 100...
9, Conservative
              Best Local Similarity 100.
Matches 9; Conservative
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                                                       1 SLLLPLQIL
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                                                                                                                                                                                                                                                                                                                                             WO9500651-A1.
                                                                                                                                                                                                                                                                                                                   Homo sapiens
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09-AUG-1995
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This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide equence comprising at least a significant part of a nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneuw chymotryptic enzyme (SCCE) or its variant, or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a cosmetic or a pharmaceutical formulation, and for the development of a diagnostic method. It can also be useful for screening or identifying a composition effective for the prevention or treatment of an abnormal or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal for unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of thyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation, pruritus, atopic dermatitis, eczema, ache and inherited skin diseases with epidermal hyperkeratosis. The mammal of the invention is also useful as a model for further studies of itch mechanisms and the testing of potential compounds and compositions for relieve of various skin diseases where itch is a component. This sequence represents the N-terminal Ergement of the human stratum corneum chymotryptic enzyme, SCCE synonymous with human kallikrein 7 (KLK7), used in the development of the themselvention of the invention of the synonymous with human kallikrein 7 (KLK7), used in the development of the human per an envelopment.
                                                                                                                                                                                                                                                                                                                                                                                                   Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
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                                                                            08-FEB-2002; 2002WO-IB001300
                                                                                                                               09-FEB-2001; 2001CA-02332655
09-FEB-2001; 2001DK-00000218
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Matches 9; Conservative
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                                                                                                                                                                                                              (EGEL/) EGELRUD T.
(HANS/) HANSSON L.
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                      15-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human amyloid precursor protein protease (AAW05383) is involved in the processing or clearance of amyloid precursor protein to form beta-amyloid peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783) obtd. from a human lung library. Recombinant protease can be produced in transformed or transfected prokaryotic (partic. B. coli) or eukaryotic and testing of cpds. useful for develop products for the design and testing of cpds. useful for treating or preventing conditions associated with beta-amyloid peptide, esp. Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serin disease; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human amyloid precursor protein protease - used to develop prods. for the treatment or diagnosis of associated conditions, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                    Amyloid precursor protein protease; Alzheimer's disease; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 40; DB 2; Length 253; 100.0%; Pred. No. 17; or Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human SCCE protein N-terminal fragment SEQ ID 48.
                                                                                                                                                                                  Human amyloid precursor protein protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Little SP;
                   AAW05383 standard; protein; 253 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 44-45; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB84421 standard, peptide, 253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-US004294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-00416257
                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dixon EP, Johnstone EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ELIL ) LILLY & CO ELI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-464694/46.
N-PSDB; AAT39783.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                         WO9631122-A1.
                                                                                                                                                                                                                                                                                                                      Ното варіеля
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-APR-1995;
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                                                                                                                               31-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                               10-0CT-1996.
                                                                         AAW05383;
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Gaps

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0; Indels

Matches

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ABB84421 11D ABB8 AX ABB XX SCC; XW SCC; XW SCC; XW PTU XX YW PTU XX XX NW PTU XX XX XX NW PTU XX XX NW PTU

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This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, operably linked to a promoter that drives expression of heterologous scce or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a commette or a pharmaceutical formulation, and for the development of a diagnostic method. It can also be used as a model for skin disease or skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of inflammatory skin diseases selected from diseases consisting of epidermal compounds accompliance for the invention is also useful sea a model for further studies of itch mechanisms and the testing of sevention or pruritus, atopic dermatitis, eczema, acne and inherited skin diseases where itch is a component. This sequence represents the human stratum corneum chymotryptic enzyme, sore medical service protesses service protesses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; protease; cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder;
                                                                                                                                                                                                                                                                                                                                                                               Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and is used in the development of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of novel human protease #39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transgenic mammals described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 58-59; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU82740 standard; protein; 253 AA.
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                                                                                                        08-FEB-2002; 2002WO-IB001300
                                                                                                                                                  09-FEB-2001; 2001CA-02332655.
09-FEB-2001; 2001DK-00000218.
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                                                                                                                                                                                                                                                                           Egelrud T, Hansson L;
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                                                                                                                                                                                                             (EGEL/) EGELRUD T.
(HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABQ76226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 253 AA;
                      WO200262135-A2
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                                                           15-AUG-2002.
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AAU82740
ID AAU82
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DT 23-AP
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KW Human
KW Human
KW neuro
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Gaps

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The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. inflammatory diseases and asthma), brain or neuronal-associated diseases, metabolic coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory diseases (e.g. diabetes, obesity), inflammatory disorders (e.g. diseases, migraines, pain, sexual dysfunction, mood disorders, attention disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's disease) and dyskinsesiar. The mucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel
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hypertension; psychotic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                         Whyte D, Sudarsanam S, Manning G, Caenepeel S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 40; DB 5; Length 253; 100.0%; Pred. No. 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein differentially regulated in prostate cancer #43.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human proteases of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Fig 2N; 313pp; English.
                                                                                                                                                                                                       26-JUN-2001; 2001WO-US020171.
                                                                                                                                                                                                                                            26-JUN-2000; 2000US-0214047P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JAN-2003 (first entry)
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-139913/18.
                                                                                                                                                                                                                                                                                    (SUGE-) SUGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABK31782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 253 AA;
                                                                                                                          WO200200860-A2
                                                                                                                                                                                                                                                                                                                           Plowman G, WP
Charydczak G;
                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                               03-JAN-2002
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AC ABUC
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DE Prot
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KW Prot
KW MOLION
KW Can
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KW Can
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The invention describes genes (I) which are differentially regulated in protected cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample comprises prostate cancer. (I) Is useful for assessing a therapeutic or preventive content on in a subject having a prostate cancer, which involves the expression levels in a sample comprising prostate cancer. (I) Is useful for assessing a therapeutic or preventive content on the expression levels in a sample comprising prostate cancer. (I) the apple the expression levels of at least 10 genes are determined. (I) the also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer. (I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells, which involves contacting a polypeptide differentially-regulated in prostate cancer cells, which involves contacting a polypeptide differentially regulated in prostate cancer cells, which involves contacting a polypeptide differential of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, cancer cells, useful as molecular markers, as drug targets, and for detecting, promosticating, promosticating, promosticating, promosticating, promosticating, promosticating, producer center. (I) and its sage and in the diagnostic test to assay for presence of cancer center, its stage of development, the nature of genetic defect, etc. (The polypeptide encoded by (I) can be used as target for therapy or drug for cancer, its stage of development, the nature of genetic defect, etc. (The polypeptide encoded by (I) can be used as target for therapeutic applications to treat prostate cancer. The identification of searching specific panes, and groups of genese, and
                                                                                                                                                                                                                                                                                                                                                                            Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 293-294; 416pp; English.
                                                                                                                                                                                                          (ORIG-) ORIGENE TECHNOLOGIES INC.
                                                                                           08-APR-2002; 2002WO-US010824.
                                                                                                                                       06-APR-2001; 2001US-0281731P-06-APR-2001; 2001US-0281732P-
                                                                                                                                                                                                                                                                                                       2003-058520/05.
                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABX10343.
WO200281638-A2
                                                                                                                                                                                                                                                        Sun Z, Jay G;
                                            17-OCT-2002.
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100.0%; Score 40; DB 6; Length 253; 100.0%; Pred. No. 17; Local Similarity 100. nes 9; Conservative Sequence 253 AA; Query Match

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Gaps ö

0; Indels

0; Mismatches

Matches

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1 SLLLPLQIL 9

RESULT 14
ABU07471
ID ABU07
XX
AC ABU07

ABU07471 standard; protein; 253 AA. ABU07471;

28-JAN-2003 (first entry) 

Protein differentially regulated in prostate cancer #74.

molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer assessing; cancer monitoring. Prostate cancer; gene expression; differential regulation;

Homo sapiens.

40200281638-A2

17-OCT-2002.

08-APR-2002; 2002WO-US010824.

06-APR-2001; 2001US-0281731P. 06-APR-2001; 2001US-0281732P.

(ORIG-) ORIGENE TECHNOLOGIES INC.

ö Jay Sun Z, WPI; 2003-058520/05. N-PSDB; ABX10375. Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.

Claim 1; Page 351; 416pp; English.

The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves determining the expression levels of at least 10 genes are determined. (C) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer. (I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, assessing predisposition to diseases and conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer. (C) is useful for assessing cancer. e.g., to determine the type of conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer. (C) is used to the diagnostic test to assay for presence of cancer. (C) to an also be used as target for therapy or drug discovery. (I) can also be used for expressing the polypeptide and coded by (I) can be used as target for therapy or drug for esarching specific binding partners of the polypeptide and discovery. (I) is an adjourned to prostate cancer. The identification of specific binding partners of the polypeptide in therapeutic applications to treat prostate cancer. The identification of the polypeptide and discov pathways which are useful in diagnostic, therapeutic, and clinical applications. This is the amino acid sequence of a protein diferentially regulated in prostate cancer

Sequence 253 AA;

Gaps ; 0 100.0%; Score 40; DB 6; Length 253; 100.0%; Pred. No. 17; Indels tive 0; Mismatches 0; Indels Conservative Best Local Similarity Matches 9; Conserv Query Match

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The invention relates to a novel isolated polynucleotide. The polynucleotides of the invention have cytostatic activity, and may have a use in gene therapy, and in a vaccine. The composition and methods are useful in diagnosing and/or treating cancer, particularly ovarian cancer. The composition may also be used as a vaccine to prevent cancer. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide and polypeptide useful for diagnosing and/or treating cancer, particularly ovarian cancer, and as a vaccine.
                                                                                                                                                                                      Human stratum corneum chymotryptic enzyme - ovarian cancer clone 01676P.
                                                                                                                                                                                                                   Human; cytostatic; gene therapy; vaccine; cancer; ovarian cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 40; DB 6; Length 253; Best Local Similarity 100.0%; Pred. No. 17; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 157-158; 169pp; English
                                                                                                 ABR58471 standard; protein; 253 AA.
                                                                                                                                                                                                                                                                                                                                02-OCT-2002; 2002WO-US031467.
                                                                                                                                                                                                                                                                                                                                                            02-OCT-2001; 2001US-0327135P. 30-MAY-2002; 2002US-0384531P.
                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mannion J;
                   SLLLPLQIL 12
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SLLLPLQIL
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Gaps

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Search completed: March 11, 2006, 00:24:16 Job time : 88.6667 secs

SLLLPLQIL 12

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March 11, 2006, 00:24:40; Search time 14.1111 Seconds (without alignments) 61.367 Million cell updates/sec Run on:

US-09-905-083A-36 1 SLLLPLQIL 9 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARIES

Result No.	Score	& Query Match	y h Length	DB t	SUMMAKIES	Description
!	40	100.0	0 253		A53968	serine proteinase
	38	95.0	7		H75201	
	33	82.		7	AB3334	
	32		0 218		T02912	
	32	80.	0	-	C97402	
	32	80.	0		AC2620	1-acyl-sn-glycerol
	32	80.	0		JC7300	tax-responsive ele
	32	80.	0		JC4857	hepatocarcinogenes
	32	80.	0		B85327	probable transcrip
	32	80.	0		C49349	
	32	80.	0		B95976	
	32	80.	0		S40176	
	32		0		S61692	Ω
	31		196		G65039	hypothetical prote
	31				C84914	hypothetical prote
	31				T48649	æ
	31				A98157	probable permease
	31				AH3130	ABC transporter, m
	31				D83934	hypothetical prote
	31				D69779	antibiotic resista
	31		5 398		C91063	hypothetical prote
	31	77.			B90120	SNF1-related prote
	31	77.			AC0834	ш
	31		5 470		A90083	hypothetical prote
	31				A69149	ro
	31				AE0614	probable competenc
	31	•	5 783		A46136	myosin-heavy-chain
	31				AC2445	
	30	75.		~	145913	interleukin-2 prec

interleukin-2 - go interleukin-2 prec	probable membrane hypothetical prote probable phosphate	NADH2 dehydrogenas hypothetical prote	cytochrome aa3 con probable high affi Tooll surface alv	conserved hypothet surfactant protein	<pre>conglutinin precur conglutinin - bovi hypothetical 41.1K</pre>
S38662 S11488	E96979 T43766 T39622	T17092 G69798 F83598	H84314 T43663 H1H175	E82656 S33603	JN0450 145878 S47704
01 01	000	210	100-	100	1 2 2
155 155	168 189 190	208 214 224	277	349 349 69	371 371 375
75.0	75.0 75.0 75.0	75.0	75.0	75.0	75.0 75.0 75.0
30	0 0 0	300	9000	000	000
30 31	332 332 4	35 36 37	9 E E E	. 4 4 5 H S	44 44 45 T

## ALIGNMENTS

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CyAccession: A53968
Rihansson, L.; Stroemyrist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A; Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A; Reference numbor: A53968; MUD: 94308225; PMID: 8034709
A; Rocession: A53968
A; Ratus: preliminary
A; Molecule type: mRNA
A; Residues: 1-253 cHAN>
C; Genetics: Corners of the corners of 
                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53968
                                                                                                                                                                                                                                                                                                                   N;Alternate names: stratum corneum chymotryptic enzyme
RESULT 1
A53968
serine proteinase SCCE precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Gene: GDB:PRSS6; SCCE
A,Cross-references: GDB:377730
A,Map position: 7q35-7q35
C,Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology
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Similarity 100.0%; Score 40; DB 2; Length 253; Similarity 100.0%; Pred. No. 1.7; 9; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches 9; Conserv

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RESULT 2

Accession: H7501
Access

A;Gene: PAB0088 C;Superfamily: Pyrococcus abyssi hypothetical protein PAB0088

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80.0%; Score 32; DB 2; Length 218;
100.0%; Pred. No. 55;
.ive 0; Mismatches 0; Indela
                                                                                                                       7; Conservative
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19 ILLPLQLL 26
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Best Local Similarity
Matches 7; Conserv
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Matches 6; Conserv
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A; Residues: 1-218 -BNA
A; Residues: 1-218 -BNA
A; Residues: 1-218 -BNA
A; Residues: 1-218 -BNA
A; Croser-references: UNIPROT: 092TE3; UNIPARC: UPI00000A46AC; EMBL: AL035524
A; Croser-references: ULIVAR Columbia; BAC clone T13.08
B; Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Greco, R.; Jin, H.; Kranz, H.J.; Greco, R.; Jin, H.J.; Kranz, H.J.; Greco, R.; Jin, H.; Grec
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NyAlternate names: protein T13J8.220
NyAlternate names: protein T13J8.220
Cyspecies: Arabidopsis thaliana (mouse-ear cress)
Cybete: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 05-Oct-2004
CyAccession: T02912; T51654
CyAccession: T02912; T51654
Submitted to the Protein Sequence Database, February 1999
A.Reference number: Z14766
A.Accession: T02912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       daunorubicin resistance transmembrane protein (imported) - Brucella melitensis (strain in Species: Brucella melitensis (c) Species: Brucella (c) Species: Brucella (c) Species: Appleace (c) Species: Appleace (c) Species: Brucella (c) Species: Brucella (c) Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis A; Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-370 <KUR>
A;Cross-references: UNIPROT:Q8YHY9; UNIPROT:Q8FZX1; UNIPARC:UPI0000057D7A; GB:AE008917;
A;Experimental source: strain 16M
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                                     Score 38; DB 2; Length 146;
Pred. No. 2.3;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.5%; Score 33; DB 2; Length 370; 75.0%; Pred. No. 60;
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A;Map position: 4
A;Note: T1346.220
A;Note: intron positions not resolved
                                         95.0%;
Ouery Match
Best Local Similarity 8b.>
Best Local Similarity 6b.>
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66 SLLLPLOII 74
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293 ILLPLQVL 300
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probable acyltransferase (AF232919) [imported] - Agrobacterium tumefaciens (strain C58, C5pecies: Agrobacterium tumefaciens (Species: Agrobacterium tumefaciens) (Species: Agrobacterium tumefaciens) (Species: Agrobacterium tumefaciens) (Agrobacterium tumefacience number: Agrobacterium tumefa
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C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 16-Aug-2004
C;Accession: Ac2220
C;Accession: Ac2220
C;Accession: Ac2220
C;Accession: Ac2220
C;Accession: Acap, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellf, Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: C97402
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-264 «KUR»
A;Cross-references: UNIPROT:QBUIE2; UNIPARC:UPI0000D17A6; GB:AE007869; PIDN:AAK86172.1;
C;Genetics:
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-264 <KUR>
A,Cross-references: UNIPROT:QBUIE2; UNIPARC:UPI00000D17A6; GB:AE008688; PIDN:AAL41377.1;
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; WUID:21608550; PMID:11743193
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80.0%; Score 32; DB 2; Length 264;
Best Local Similarity 75.0%; Pred. No. 67;
Matches 6; Conservative 2; Mismatches 0; Indels
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A;Map positIon: circular chromosome
C;Superfamily: 1-acyl-sn-glycerol-3-phosphate acyltransferase
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A;Map position: circular chromosome
C;Superfamily: 1-acyl-sn-glycerol-3-phosphate acyltransferase
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A;Cross-references: UNIPROT:Q9M0J5; UNIPARC:UPI000000BD4E; GB:NC_001268; NID:g7269665; PJ C;Genetics: A;Generics: A;Gene: AT4g28110
A;Map position: 4
C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: C49349
R;Glucksmann, M.A; Reuber, T.L.; Walker, G.C.
J. Bacteriol. 175, 7045-7055, 1993
A;Title: Genes needed for the modification, polymerization, export, and processing of suc A;Reference number: A49349; MUID:94042870; PMID:8226646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-494 <GLU>
A;Residues: 1-494 <GLU>
A;Cross-references: UNIPROT:P33699; UNIPARC:UPI000012A381; GB:L20758; NID:g393240; PIDN:#
C;Superfamily: hypothetical protein b2046
C;Keywords: transmembrane protein
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A; Residues: 1-94 «KUR»
A; Cross-references: UNIPROT:P33699; UNIPPARC:UPI000012A381; GB:AL591985; PIDN:CAC49474.1;
A; Experimental source: strain 1021, megaplasmid pSymB
R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable succinoglycan transport protein ExoT - Rhizobium meliloti
C;Species: Rhizobium meliloti
C;Date: 03-May.1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: C49349
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Pred. No. 1.3e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                           80.0%; Score 32; DB 2; Length 282; 100.0%; Pred. No. 71; of Indels ive 0; Mismatches 0; Indels
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Similarity 75.0%;
6; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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122 SLLIPLQL 129
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Best Local Similarity
Matches 6; Conserv
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A;Status: preliminary
A;Molecule type: DNA
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                                                                                    tax-responsive element-binding protein 5 - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: JC7300
R;Masaki, T.; Noguchi, H.; Kobayashi, M.; Yoshida, M.; Takamatsu, K.
A;Masaki, T.; Noguchi, H.; Kobayashi, M.; Yoshida, M.; Takamatsu, K.
A;Title: Isolation and characterization of the gene encoding mouse tax-responsive elemen
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C;Ade: 11-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
C;Accession: JG4857
R;Kishimoto, T.; Kokura, K.; Kumagai, Y.; Makino, Y.; Tamura, T.
R;Kishimoto, T.; Kokura, Z.; Y.; Kumagai, Y.; Makino, Y.; Tamura, T.
R;Kishimoto, T.; Kokura, Z.; Y.; Mackino, Y.; Tamura, T.
R;Kishimoto, T.; Kokura, K.; Kumagai, Y.; Makino, Y.; Tamura, T.
R;Kishimoto, T.; Kokura, K.; Kumagai, Y.; Makino, Y.; Tamura, T.
R;Kishimoto, T.; Kokura, K.; Kumagai, Y.; Makino, Y.; Tamura, T.
A;Reference number: JC4857
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A;Residues: 1-267 <KIS>
A;Cross-references: UNIPROT:Q9R1S4; UNIPARC:UPI00000E80AD
C;Comment: This is a basic-leucine zipper type transcription factor involved in hepatoce
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C;Superfamily: X box-binding protein 1; fos/jun DNA-binding domain homology
C;Keywords: leucine zipper; transcription factor
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A;Molecule type: mRNA
A;Residues: 1-266 <MAS>
A;Kesidues: 1-266 <MAS>
Cross-references: UNIPROT:Q9ESS3; UNIPARC:UPI0000E73B0; DDBJ:AB036745
C;Genetics:
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JC4857
hepatocarcinogenesis-related transcription factor - rat
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Matches 7; Conservative 0; Mismatches
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A;Molecule type: mR
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Cispecies: Escherichia coli
Cipate: 12-58p-1997 #sequence_revision 17-5ep-1997 #text_change 01-Mar-2002
Cipatesion: G65039
R.Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 145-1462, 1997
Science 277, 145-1462, 1997
A.Title: The complete genome sequence of Escherichia coli K-12.
A.Reference number: A64720; MUID: 97426617; PMID: 9278503
A.Accession: G65039
A.Accession: G65039
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Residues: 1-196 - SEATP.
A.Kose-references: UNIPARC: UPI000016ED74; GB: AE0000347; GB: U00096; NID: 92367142; PIDN: AAK
A.; Krose-references: UNIPARC: UPI0AD16ED74; GB: AE0000347; GB: U00096; NID: 92367142; PIDN: AAK
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: C84914
C;Accession: C84914
C;Accession: C84914
C;Accession: C84914
C;Accession: C85.; Cronin, L.A.; Shen, M.I.; Town, C.D.; Fujii, C.Y.; h
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Miscrman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUD:20083487; PMID:10617197
A;Actus: preliminary
A;Accession: C84914
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-303 <STO>
A;Cross-references: UNIPROT:022910; UNIPARC:UPI00000A2116; GB:AE002093; NID:g2275214; PII
A;Man roatifon: 2
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 77.5%; Score 31; DB 2; Length 196; Best Local Similarity 87.5%; Pred. No. 78; Matches 7; Conservative 0; Mismatches 1; Indels
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                                                                                      hypothetical protein b2612 - Escherichia coli (strain K-12)
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Best Local Similarity 77.8
Matches 7; Conservative
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N.Alternate names: hypothetical protein 03329; hypothetical protein YOR3329c
C.Species Saccharomyces cerevisiae
C.Species Saccharomyces cerevisiae
C.Species Saccharomyces cerevisiae
C.Species Sachoz
C.Saccesion: S61692; S67022
C.Accession: S61692; S67022
SAPEnes, V.; Andrade, W.A.; Rechmann, S.; Teodoru, C.; Banrevi, A.; Sander, C.; Valencia submitted to the EMBL Data Library, December 1995
A.Description: Nucleotide sequence and analysis of a 130 kb fragment of yeast chromosome A.Mceference number: S61643
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: NA
A.
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A;Realdues: 1-622 <VOS>
A;Cross-references: UNIPARC:UPI00006BE6F; EMBL:Z75045; NID:g1420348; PID:e252028; PID:g
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ExoT protein - Rhizoblum meliloti
C;Species: Rhizoblum meliloti
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 19-May-2000
C;Accession: 840176
K;Becker, A.; Klackcmann, A.; Kuester, H.; Keller, M.; Arnold, W.; Puehler, A.
submitted to the EMBL Data Library, April 1993
A;Description: Analysis of the Rhizoblum meliloti genes exoU, exoW, exoW, and exoI
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Pred. No. 1.5e+02;
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A;Residues: 1-582 xBEA
A;Cross-references: UNIPARC:UPI00001787F9; EMBL:Z22646
C;Superfamily: hypothetical protein b2046
75.0%; Pred. No. 1.3e+02; vative 2; Mismatches 0;
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F;11-27/Domain: transmembrane #status predicted <TMM>
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MEDLINE=94308225; PubMed=8034709;
Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A., Egelrud T.;
"Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase.";
J. Biol. Chem. 269:19420-19426(1994).
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                                                                                                                                           2166443 segs, 705528306 residues
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Q91184
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Kishi T., Michael I.P., Diamandis B.P.;
Kishi T., Michael I.P., Diamandis B.P.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY646152; AAT66047.1; -; mRNA.
SEQUENCE 66 AA; 7171 MW; 82EIC392BC822FDB CRC64;
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Pred. No. 2.8;
Mismatches 0; Indel
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Q8UIE2_AGRT5
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Q9D226_MOUSB
Q653Z3_ORYSA
Q9ZTE3_ARATH
Q5AXD4_EMENI
Q876R3_EMENI
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25-0CT-2004 (TrEMBLrel. 28, Ls
25-0CT-2004 (TrEMBLrel. 28, Ls
Kallikrein 7 splice variant 3
Homo sapiens (Human)
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  TISSUB-Skin,

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubborg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Rataubborg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Ratauberg R.L., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Carpieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B Cherration and initial analysis of more than 15,000 full-length human
                                                                                                      Diamandis E.P.;
"The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic enzyme is a new member of the human kallikrein gene family - genomic characterization, mapping, tissue expression and hormonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dong Y., Kaushal A., Brattsand M., Nicklin J., Clements J.A.; "Differential splicing of KLK5 and KLK7 in epithelial ovarian cancer produces novel variants with potential as cancer biomarkers."; clin. Cancer Res. 9:1710-1720(2003).
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Biochem. Biophys. Res. Commun. 211:586-589(1995).

-!- FUNCTION: May catalyze the degradation of intercellular cohesive structures in the corrilided layer of the skin in the continuous shedding of cells from the skin surface. Specific for amino acid residues with aromatic side chains in the PI position. SCCE cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-Phe-|-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the activation of precursors to inflammatory cytokines.
[2]
NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLECTIDE SEQUENCE [GENOMIC DNA].

Hansson L., Baeckman A., Ny A., Edlund M., Edholm B., Tornell J.,
Wallbrandt P., Egelrud T.,
"Epidermal overexpression of stratum corneum chymotryptic enzyme in
mice; a model for chronic ithchy dermatitis.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION.
MEDLINE=95314630; PubMed=7794273;
Skytt A., Stroemgyist M., Egelrud T.;
"Primary substrate specificity of recombinant human stratum corneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                           PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6; Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paeper B., Wang K.; Squencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region."; Gene 257:119-130(2000).
                                                                                        Yousef G.M., Scorilas A., Magklara A., Soosaipillai A.,
                                          TISSUE=Keratinocyte;
PubMed=10974542; DOI=10.1016/S0378-1119(00)00280-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22623266; PubMed=12738725;
                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND TISSUE SPECIFICITY.
TISSUE-Ovarian carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.
                                                                                                                                                                                                                           Gene 254:119-128(2000).
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LINERANTIVE PRODUCTS:

Byent=Alternative splicing; Named isoforms=2;

Byent=Alternative splicing; Named isoforms=2;

Rame=1; Synonyms=Long;

Isoid=P49862-1; Sequence=Displayed;

Name=2; Synonyms=Short;

Isoid=P49862-1; Sequence=USP_013581;

Isoid=P49862-1; Sequence=USP_013581;

Isoid=P49862-1; Sequence=VSP_013581;

Isoid=P49862-1; Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED GUESTALON - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
SUBCELLULAR LOCATION: Secreted. In ovarian carcinoma, secreted and also observed at the apical membrane and in cytoplasm at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M. Min; 60438; -...

R. Min; 60438; -...

R. GO; GO:0008236; F:serine-type peptidase activity; TAS.

R. GO; GO:0008244; P:epidermis development; TAS.

R. GO; GO:0008544; P:epidermis development; TAS.

R. InterPro; IPR001314; Peptidase_S1Ā.

R. InterPro; IPR001314; Peptidase_S1Ā.

R. Fran; PR00129; TYP9511, 1.

R. PRINTS; PR00722; CHYMOTYPENIN.

DR. RART; SM00020; TYP SPC; 1.

DR. RART; SM00020; TYP SPC; 1.

DR. ROSITE; PS00134; TRYPSIN_EN; 1.

DR. PROSITE; PS00135; TRYPSIN_EN; 1.

DR. Alternative splicing; Direct protein sequencing; Glycoprotein; KW Hydrolase; Protease; Serine protease; Signal; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       // similarity).
// similarity).
(Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Charge relay system (By similari
N-linked (GloNac. .) (Potential
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
Missing (in isoform 2).
FrId=VSP_013581.
C -> W (in Ref. 6; AAH32005).
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Charge relay system
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Kallikrein 7.
Peptidase S1.
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EMBL; AF166330; AAD49718.1; -; Genomic_DNA.
EMBL; AF243527; AAG33360.1; -; Genomic_DNA.
EMBL; AF332583; AAK69624.1; -; Genomic_DNA.
EMBL; AF411214; AAN03662.1; -; mRNA.
EMBL; AF411215; AAN03662.1; -; mRNA.
EMBL; BC023005; AAN32005.1; -; mRNA.
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HGNC; HGNC:6368; KLK7.
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HSSP; P00760; 1EZX.
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253 AA;
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Leishmania major.
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MEDINE=2521545; PubMed=12622808;

MEDINE=2521545; PubMed=12622808;

A DOI=10.1046/j.1365-2959.2003.03381.x;

Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,

Cohen G.N., Parieur D., Querellou J., Ripp R., Thierry J.-C.,

Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;

An integrated analysis of the genome of the hyperthermophilic

archaeon Pyrococcus abyssi.";

Mol. Microbiol. 471499-1512(2003).

REMBL, AJ248283; CAB49063.1; -; Genomic_DNA.

PIR, H75201; H75201.

RICEPTPO: IPRO08237; DUPB19.

RICEPTPO: IPRO08237; DUPB19.

REPERPORTED FOOSE MW; 7182941371258CIF CRC64;
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Arvicolinae; Clethrionomys.
NCBI_TaxID=56223;
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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NUCLEOTIDE SEQUENCE.

MEDLINE=98152303; PubMed=9491603;

Engel S.R., Hogan K.M., Taylor J.F., Davis S.K.;

"Molecular systematics and paleobiogeography of the South American sigmodontine rodents.";

Mol. Biol. Evol. 15:35-49(1998).

EMBL; U83808; AAB871681; -; Genomic DNA.

GO: 0005739; C:mitochondrion; IEA.
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                    100.0%; Score 40; DB 1; Length 253; 100.0%; Pred. No. 11; 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=ND4;
Clethrionomys gapperi (Southern red-backed vole).
                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
OrderedLocusNames=PYRAB01390; ORFNames=PAB0088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 38; DB 2;
88.9%; Pred. No. 16;
iive 1; Mismatches
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                                                                                                                                                                                                                                                                PRT;
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Q9V2D5;
Query Match
Best Local Similarity 100.
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=29292;
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1000205 PY
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GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0042773; P:ATP synthesis coupled electron transport; IEA.
GO; GO:0042773; P:ATP synthesis coupled electron transport; IEA.
InterPro; IPR003918; NADHub_oxred4.
InterPro; IPR00056; Oxidored_G5_N.
Pfam; PF01059; Oxidored_G5_N; 1.
PRINTS; PR01437; NUOXDRDTASE4.
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ACCOUNTING SUCCESS.

ACCOUNTING M., FOSKER N., Harris D., Oliver K., O'Neil J.,

Banth D., Collins M., Fosker N., Harris D., Oliver K., O'Neil S.,

Saunders D., Seeger K., Waren T., Rajandream M., and Barrell B.G.,

Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.

IN BRBL, CT005272, CAJ09256.1; -; GenOmic_DNA.

InterPro; IPR001547; Glyco hydro S.

InterPro; IPR00403; P13/4_kinase_cat.

R Fam; PR0454; P13_P14 kinase; 1.

R SMART; SM00146; P13 K.; AINBAS; 1.

R ROSITE; PS00659; GLYCOSYL HYDROL F5; UNKNOWN_I.

R ROSITE; PS0016; P13 4_KINASE 3; 1.

R HYDCHCHEICAL DIOCECHI; Nucleocide-binding.

CW HYDCHCLEAL DIOCECHI; Nucleocide-binding.
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NCBI_TaxID=5664;
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Pred. No. 1.1e+03;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                              92.5%; Score 37; DB 2; Length 208; 88.9%; Pred. No. 36; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OrderedLocusNames=syc1910 c;
Synechococcus sp. (strain PCC 6301) (Anacystis nidulans)
                                                                                                                                                                                                                                                                            208 AA; 23967 MW; 8AF1788697AED6A2 CRC64;
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NCBI_TaxID=269084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0401C5;
13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
OKFNames-LmjF36.2940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01.FEB-2005 (TrEMBLrel. 29, Created)
01.FEB-2005 (TrEMBLrel. 29, Last sequence update)
01.FEB-2005 (TrEMBLrel. 29, Last annotation update)
Probable Na+/H+-exchanging protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4183 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    545 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OSNOSO SYNP6 PRELIMINARY;
OSNOSO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q4Q1C5_LEIMA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 77.0
77.0
                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||:|||:|
2801 SLLVPLQVL 2809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 SLLVPLQIL 105
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Gaps

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Length 73; Indels

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93E8F53399BF3C11 CRC64;
                                Score 34; DB 2;
Pred. No. 51;
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HSSP, P18203; 1FKL.
HSSP, P18203; 1FKL.
G0; G0:0005615; C:extracellular space; TAS.
G0; G0:0016021; C:integral to membrane; TAS.
InterPro; IPR001179; FKBP_PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.0%; Score 34; DB
87.5%; Pred. No. 73;
iive 1; Mismatches
                                                                    1; Mismatches
73 AA; 7819 MW;
                                85.0%;
87.5%;
                                                                                                                                                                                                                 QBRSD6_MOUSE PRELIMINARY;
QBRSD6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00254; FKBP C; 1
PROSITE, PS50059; FKBP PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                               Muridae; Murinae; Mus.
            Query Match
Best Local Similarity
7, Conserve
                                                                                                                                      6 LLLPLOLL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 LLLPLOLL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
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                                                                                                  2 LLLPLOIL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LLLPLQIL 9
                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                              Fkbp11 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
                                                                                                                                                                                                                                                                                                                                Name=Fkbp11;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                          MOUSE
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STRAIN=FVB/N; TISSUE=Salivary gland;

NUCLEOTIDE SEQUENCE.

A LESSUES-28.24. FubMed=1247932. DoI=10.1073/pnas.242603899;

A Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Lacchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.R.,

A Lacchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.R.,

A Dischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Strapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Tonaldo M.F., Casavant T.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Tonaldo M.F., Casavant T.L., Scheetz T.B.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garrancin P., Prange C.,

Richards S., Worley K.C., Hale S., Garrancin P., Prange C.,

N. Hilton D.K., Murny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Nhiting M., Madan A., Young A.C., Shevchenko Y., Boutfaud G.G.,

Nhiting M., Madan A., Young A.C., Shevchenko Y., Boutfaud G.G.,

Blakebley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalsa U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalsa U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                ö
                                       Name=Pkbpl1;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                           Length 545;
                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021345; AAH21345.1; -; mRNA.
MGI: 913370; Fkbpl1.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
                                                                                                                                                                                                                                                            545 AA; 58143 MW; 2DB84E920CD7DEDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                           Score 35; DB 2; I Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=FVB/N; TISSUE=Salivary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                            87.5%;
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBVCA9 MOUSE PRELIMINARY;
Q8VCA9;
                                                                                                                                                                                                                                                                                                                              7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muridae, Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                 193 LLLPLOVL 200
                                                                                                                                                                                                                                                                                                                                                               2 LLLPLQIL 9
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NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                            Complete proteome. SEQUENCE 545 AA;
                 STRAIN=PCC6301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fkbp11 protein.
                                   Sugita M.;
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TISSUE-Mammary tumor metastatized to lung. Tumor arose spontaneously;

KX TISSUE-Mammary tumor metastatized to lung. Tumor arose spontaneously;

RA Strausberg R.L.; Feingold E.A.; Grouse L.H., Derge J.G.;

RA Klausher R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Batchenco L., Marusins K., Farmer A.A., Rubin G.M., Hong L.,

RA Staplecon M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Hahey J., Helton B., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smilus D.E.,

RA Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smilus D.E.,

RA Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smilus D.E.,

RA Manner C.N. Assiminate C.N. Amalysis of more than 15,000 full-length human mercen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                         Mus muscilus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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EMBL; BC022900; AAH22900.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 AA; 11085 MW; 0534D57467566914 CRC64;
01-UUN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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10-MAY-2005 (Rel. 47, Last annotation update)
FK506 binding protein 11 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis-
trans isomerase) (PPIase) (Rotamase) (19 kDa FK506-binding protein)
                                                                                                                                                                                                                                                                                                                                                                                                       Virgin mouse. Taken by biopsy.

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METAUSPORT R.D., Feingold E.A., Grouse L.H., Derge d.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MISCHORLO, L., Marusina K.R., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

MEDRAS S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

MISCHORLO, M., Soderson K.J., Malek J.A., Guaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Milalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Metterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Metterfield S., Sherman M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.0%; Score 34; DB 2; Length 138; 87.5%; Pred. No. 96; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virgin mouse. Taken by biopsy.;
Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       00254; FKBP C; 1.
PS50059; FKBP PPIASE; 1.
138 AA; 15105 MW; C138B8B0EFDDF59D CRC64;
                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC002311; AAH02311.1; -; mENA.
MGI; MGI:1913370; Fkbp11.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR001179; FKBP_PPIase.
                                                                                   PRT;
                                                                                                                         Created)
                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                      QEPKE2_MOUSE PRELIMINARY;
QEPKE2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 87.5
les 7; Conservative
                                                                                                                                                                                                                                                                                       Muridae, Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                         (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
STRAIN=FVB/N;
                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00254; FKBP
PROSITE; PS50059; FF
                                                                                                                                                                                     Fkbp11 protein.
                                                                                                                                                                                                                              musculus
                                                                                                                                                                                                    Name=Fkbp11;
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Best Local S
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RC STEALNE-CTIDE SEQUENCE LLAKGES SCALE MKNAI.

RC STEALNE-CTIDE SEQUENCE LLAKGES SCALE MKNAI.

RX OKAZAKI Y., FUTUNO M., KABURKWA T., Adachi J., BOON H., KONDGO S.,

RA MAZAKI Y., FUTUNO M., KABURKWA T., Adachi J., BOON H., KONDGO S.,

RA MAGIOLI., OBSTON M., SAITO R., SUZUKI H., YAMANDKA I., KIYOSBWA H.,

RA BAIDARCHIR R., HILL D.P., BULT C., HUME D.A., QUACKENDUSH J.,

RA BAIDAR J., Bradt D., BILBIC V., HUME D.A., QUACKENDUSH J.,

RA GASTERIAL I.M., KANADIN A., MATSUGA H., FRAZER K.S.,

RA GASTERIAL T., GATIONIA M., GISSI C., GODZIK A., GOUGHIB S.,

RA GASTERIAL T., A., Fletcher C.F., FOTTEST A., Frazer K.S.,

RA GASTERIAL T., MALDIA S., HITCHER R.M., KING B.L.,

RA KANAJI H., KAWASAWA Y., KECZIETSKI R.M., KING B.L.,

RA KOMAGAYA NINCOKHIM I.V., Lee Y., Lenhard B., Lyons P.A.,

MAGIOTT D.R., MALTAIS L., MARCHIONNI L., MCKENZIE L., MIKH H.,

RA BARCONSKY N., PILLAIS L., MARCHIONNI L., MCKENZIE L., MIKH H.,

RA BARCONSKY N., PILLAIS R., PONTIUS J.U., QI D., RAMACHANTAR S.,

RA ANDELIA R., SCHNEIGER C., SEMPLE C.A., SECTO M., SHIMMAD K.,

RA SULTANA R., MADIOLIS A., YANAGHANA M., YANG I., YANG L.,

RA WLIMING L.G., WANDHAW-BOTIS A., YANGARAURA M., SARAZUME N., SALO K.,

RA HIROZANE K., WASHIK W., MANDHAW-BOTIS R., ARAKAWA T., FUKUGA S.,

RA HIROZANE K., WASHIK K., KAWAI J., SARAZUME N., SALO K.,

RA MINAZAKI A., SAKAI K., KAWAI J., SALOWA T., SALOMA T.,

RA MINAZAKI A., SAKAI K., KAWAI J., SALOWA T., SALOWA T.,

RA MINAZAKI R., SAKAIK K., KAWAI J., SALOWA T., SALOWA T.,

RA MINAZAKI R., SAKAIK K., KAWAI J., SALOWA T., SALOWA T.,

RA MINAZAKI R., SAKAIK K., KAWAI J., SALOWA T., SALOWA T.,

RA MINAZAKI R., SAKAIK K., KAWAI J., SALOWA T.,

RA MINAZAKI R., SAKAIK K., KAWAI J., SALOWA T.,

RA MINAMA S., TAKANA T.,

RA MANDHA S., SAKAIK K., KAWAI J., SALOWA T.,

RA MINAMA S., TAKANA T.,

RA MANDHA S., SAKAIK K., KAWAI J., SAKAIK K., SAKAIK R.,

RA MINAMA S., SAKAIK K., KAWAI J., SAKAIK K., SAKAIK R.,

RA MINAMA S., TAKANA M.,

RA MANDHA S., SAKAIK K., KAWAI J., SAKAIK K.,

RA MANDHA S., PANDHA W., IMOLANI K., INDALAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Fkbpl1;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (omega=0).
-!- SIMILARITY: Belongs to the FKBP-type PPIase family.
-!- SIMILARITY: Contains 1 PPIase FKBP-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 420:563-573 (2002)
                                                                                                                                                                  NCBI_TaxID=10090;
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FKB11 MOUSE STANDARD; PRT; 201 AA. AC Q9D1M7; Q9CRE4; DT S8-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

||||||||||| 6 ELLPLQLL 13

RESULT 10

LLLPLQIL 9

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2 LLLPLQIL
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                                                                                                                                              INHA TRIVU
077755;
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                                                                                                                                                                    This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                  the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Ghedin B., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
Shallom J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,
Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trypanosoma brucei.
Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma
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0
                                                                                                                                                                                                                                                                                                                                                                        28 201 FK506 binding protein 11.
57 144 PPIase FKBP-type.
53 53 S -> F (in Ref. 1; BAB31559).
198 198 S -> R (in Ref. 1; BAB31559).
201 AA; 22137 MW; 94D955C57264BD82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 1; Length 201;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 2; Length 246
Pred. No. 1.7e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       El-Sayed N.M., Khalak H., Adams M.D.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=GUTat10.1;
Haas B., Blandin G., El-Sayed N.;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, AC009259; AX80785.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 246 AA; 27875 MW; 706DD83BA6BB46AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                         EMBL; AK003331; BAB22719.1; -; mRNA.
EMBL; AK019132; BAB31559.1; -; mRNA.
EMBL; BC03796; AAH37596.1; -; mRNA.
HSSP; P20071; 1TCO.
Ensembl; ENSMUSG0000003355; Mus musculus.
MGI; MGI:191370; FKDP11.
GO; GO:0016021; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
HILLETPO: IPRO01179; FKBP_PPIRSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                          Potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                             PEam; PP00254; FKBP C; 1.
PROSITE; PS50059; FKBP PPIASE; 1.
Isomerase; Rotamase; SIgnal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 87.5%;
7; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q585W6_9TRYP PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
ORFNames=Tb927.6.3680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LLLPLOLL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=GUTat10.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5691;
                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                            removed.
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                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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058 546
076 976
076 876
076 876
077 10-MJ
077
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### RMBL; AF033340; AAC63945.1; -; mRNA.

### GO; GO:000576; C:extracellular region; ISS.

### GO; GO:000125; F:cytokine activity; ISS.

### GO; GO:000125; F:cytokine activity; ISS.

### GO; GO:000125; F:cytokine activity; ISS.

### GO; GO:0001279; F:cytokine activity; ISS.

### GO; GO:000176; F:cytokine activity; ISS.

### GO; GO:000176; F:cytokine activity; ISS.

### GO; GO:000176; F:cytokine activity; ISS.

### GO; GO:00016; F:coll airferentiation; ISS.

### GO; GO:00016; P:coll surface receptor linked signal transdu. . ,; ISS.

### GO; GO:00016; P:coll surface receptor linked signal transdu. . ,; ISS.

### GO; GO:00016; P:coll signaling; ISS.

### GO; GO:00016; P:coll surface receptor linked signal transdu. . ,; ISS.

### GO; GO:00016; P:coll surface receptor linked signal transdu. . ,; ISS.

### GO; GO:00016; P:coll surface receptor linked signal transdu. . ,; ISS.

### GO; GO:00016; P:coll surface regulation of fellicle-stimulation; ISS.

### GO; GO:0004578; P:negative regulation of fellicle-stimulating . ,; ISS.

### GO; GO:0004586; P:negative regulation of interferon-gamma bio. . ,; ISS.

### GO; GO:0004566; P:negative regulation of phosphorylation; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vulpecula).";
J. Mol. Endocrinol. 21:141-152(1998).

J. Mol. Endocrinol. 21:141-152(1998).

Individual Inhibins and activins inhibit and activate, respectively, the secretion of follitropin by the pituitary gland. Inhibins/activins are involved in regulating a number of diverse functions such as hypothalamic and pituitary hormone secretion, gorm cell development and maturation, erythorid differentiation, inalin secretion, nerve cell survival, embryonic axial development or bone growth, depending on their subunit composition. Inhibins appear to oppose the functions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: Proteolytic processing yields a number of bioactive forms, consisting either solely of the mature alpha chain, of the most Neterminal propeptide linked through a disulfide bond to the mature alpha chain, or of the entire propercial. SIMILARITY: Belongs to the TGF-beta family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
MEDIATE=99027340; Pubmed=9801457; DOI=10.1677/jme.0.0210141;
MARMONTÉCRT D., Fidler A.E., Heath D.A., Lawrence S.B., Tisdall D.J.,
Greenwood P.J., McNatty K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "cDNA sequence analysis, gene expression and protein localisation of the inhibin alpha subunit of Australian brushtail possum (Trichosurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Dimeric, linked by one or more disulfide bonds. Inhibin is a dimer of alpha and beta-A. Inhibin B is a dimer of alpha and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
NCBI_TaxID=9337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                        361 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trichosurus vulpecula (Brush-tailed possum)
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GO:0045077; P:negative regulation
GO:0045550; P:negative regulation
GO:0042326; P:negative regulation
GO:0007399; P:neurogenesis; ISS.
                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibin alpha chain precursor.
Name=INHA;
                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                               163 LMLPLQIL 170
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Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=99883;
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GO; GO:0001541; P:ovarian follicle development; ISS.
GO; GO:0046881; P:positive regulation of follicle-stimulating. . .; ISS.
InterPro; PR002405; Inhibin_alpha.
InterPro; IPR001895; TGFD.
Pfam; PF00019; TGF_beta; 1.
Propon; PR00609; TMIBINA.
Probon; PR00609; TGFEP; 1.
SMART; SM00204; TGFEP; 1.
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GO; GO: 0016020; C: membrane; IEA.
GO; GO: 0005524; F: ATP binding; IEA.
GO; GO: 0042626; F: ATPase activity, coupled to transmembrane m. . .; IEA.
GO; GO: 000610; P: transport; IEA.
InterPro; IPR000412; ABC_2.
Pfam; PF01061; ABC2 membrane; 1.
PROSITE; PS51012; ABC_TM2; 1.
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PubMed=14671304; DOI=10.1126/science.1088727;

Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C., Meidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J., Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Gwinn M.L., Kolonay J.F., Sullivan S.A., Haff D.H., Selengut J., Meiden T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A., Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleavage (By similarity).
Cleavage (By similarity).
N-linked (GlCNAc. . .) (Potential).
N-linked (GlCNAc. . .) (Potential).
N-linked (GlCNAc. . .) (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Geobacter sulfurreducens.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
                                                                                                                                                                                                                                                                                                                                                                                              Inhibin alpha N-terminal region (By
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 1; Length 361;
Pred. No. 2.5e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fnterchain (By similarity).
D661CDF93CDAA87D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 373 AA; 40412 MW; 94B9D6AFF570D4A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibin alpha chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 AA.
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By similarity.
By similarity.
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By similarity.
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EMBL; AE017180; AAR36057.1; -; Genomic_DNA.
TIGR; GSU2695; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38945 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-201, putative. OrderedLocusNames=GSU2685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Geobacteraceae; Geobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEOSL PRELIMINARY;
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Auceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

Ra Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

Ra Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

Ra Nicaud S., Jaffe D., Fisher S., Iutfalla G., Dossat C., Segurens B.,

Ra Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

Ra Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Ra Biemort C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

Ra Biemort C., Shalli Z., Cattolico L., Poulain J., De Berardinis V.,

Ra Arrad C., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

Ra Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

A Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

Waincker P., Lander E.S., Weisenbach J., Roest Crollius H.;

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals

"The early vertebrate proto-karyotype.";
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                                                                                                           Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Actinopterygli, Neopterygli, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygli, Percomorpha, Tetraodontiformes;
Tetraodontoidea, Tetraodontidae, Tetraodon.
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Submitted (FBE-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Pred. No. 5.2e+02;
1; Mismatches 1; Indels
Score 34; DB 2; Length 373;
Pred. No. 2.6e+02;
L; Mismatches 0; Indels
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 5 SCAF15026, whole genome shotgun sequence.
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05-JUL-2004 (TrEMBLrel. 27, Las
05-JUL-2004 (TrEMBLrel. 27, Las
Hypothetical protein precursor.
orderedLocusNames=RPA1183;
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Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
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Q6N500 RHOPA PRELIMINARY;
1D G6N500 RHOPA PRELIMINARY;
DT 05-JUL-2004 (TEMBLrel. 27,
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Q4RKR8;
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293 ILLPLQIL 300
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
NCBI_TaxID=1076;
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82.5%; Score 33; DB 2; Length 148;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels
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Search completed: March 11, 2006, 00:38:50 Job time: 97.3333 secs

us-09-905-083a-36.rup

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LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 2, Appli
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                                                                                     March 11, 2006, 00:41:16; Search time 21.2222 Seconds (without alignments) 35.061 Million cell updates/sec
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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(cgn2_6/ptodata/1/iaa/5_COMB.pep:*
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US-09-518-243-36
US-08-557-146-2
US-08-824-874-3
US-08-9154-344-2
US-08-930-188-2
US-09-930-188-2
US-09-930-188-2
US-09-930-018-3
US-09-949-016-7716
US-09-918-244-2
US-09-918-243-33
US-09-918-243-33
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US-10-012-3338-338
US-10-015-3338-338
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                                                                                                                                                                                                                                                                              572060 seqs, 82675679 residues
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Listing first 45 summaries
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		2-600-36 ce 36, Application US/09502600A NO. 629434 L. INFORMATION: CANT: O'Brien, Timothy J. CANT: O'Brien, Compositions a OF INVENTION: Compositions a OF INVENTION: Compositions NT FILING DATE: 2000-02-11 NT APPLICATION NUMBER: 2000-02-11 NT APPLICATION NUMBER: 09/099,2 RIING DATE: 03-14-1998 NO 36 NO 3	h Simila 9, C	1 SL 1 SL	9-243-36 No. 6627403 No. 6627403 No. 6627403 - INFORMATION: Timoci ZANT: Cannon, Martii ZANT: Cannon, Martii CANT: SANTIN, Martii ANT: SANTIN, Methook REFERENCE: D6223CIP/( RY APPLICATION NUMBER: TILING DATE: 2001-07 APPLICATION NUMBER: FILING DATE: 2001-07 ROF SEQ ID NOS: 136 NO 36
		ESULT 1 Sequence 36, Application US/05 Sequence 36, Application US/05 Patent No. 6294344 THILE No. 6294344 TITLE OF INVENTION: CompositiVENTE OF INVENTION: CompositIE REFERENCE: D6223CIP-CURRENT FILING DATE: 2000-02 CURRENT APPLICATION NUMBER: UPRIOR APPLICATION NUMBER: CRIMBER: OF SEQ ID NOS: 136 SEQ ID NO 36 LENGTH: 9 TYPE: PRT ORGANISM: Homo sapiens FEATURE: CHERRY HOMO sapiens FEATURE: CHERRY HOMO sapiens FEATURE: CHERRY HOMO sapiens FEATURE: CHERRY HOMO sapiens	Match Local		RESULT 2 US-09-918-243-36 1 Sequence 36, Application US/09918; Patent No. 6627403 1 GENERAL INFORMATION: APPLICANT: O'Brien, Timothy J. APPLICANT: Cannon, Martin J. APPLICANT: Santin, Alessandro, FILLE REPERENCE: D6223CIP/C/D/CIP; CURRENT APPLICATION WUMBER: US/O: CURRENT FILING DATE: 2001-07-30; PRIOR FILING DATE: 2001-07-30; PRIOR FILING DATE: 2001-07-31; NUMBER OF SEQ ID NOS: 136 1 LENGTH: 9
00000000000000000000000000000000000000		SULT 1 -09-502-6 Sequence Sequence Sequence Tipus OF TITLE OF TITL	Query Ma Best Loc Matches		SULT 2 -09-918-2. Sequence: Patent No GENERAL IN APPLICAN APPLICAN TITLE OF FILE REFI CURRENT J CURRENT J PRIOR PII PRIOR PII PRIOR PII SEGUENCO D NO LENGTH:
		RESULTANGE OF THE SECTOR OF TH	Sag	දු දු	RESULT US-09-09-09-09-09-09-09-09-09-09-09-09-09-

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CORRESPONDENCE ADDRESS:
                                                                                                                                        94304
                                                                    CITY: Pa]
STATE: C/
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-824-874-3
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APPLICANT: Egelrud, Torbjorn
APPLICANT: Egelrud, Torbjorn
APPLICANT: Egelrud, Torbjorn
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 40; DB 1; Length 253; Best Local Similarity 100.0%; Pred. No. 2.7; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER: U.S.A.
ZIP: 10036-2787
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/88/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 354-813
TELECHONE: (212) 354-813
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: allocat
                                                                                                               Query Match 100.0%; Score 40; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 9; Conservative 0; Mismatches 0; Indels
                                   CTHER INFORMATION: Residues 4-12 of the SCCE protein US-09-918-243-36
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Patent No. 5962300
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-08-557-146-2
'Sequence 2, Application US/08557146
'Fatent No. 5834290
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                      NAME/KEY: CHAIN
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US-08-824-874-3
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DORESTEEN 13.47 Porter Drive

TOTTY: Raid Alto

CITY: Raid Alto

CITY: Baid Alto

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CITY: Baid Alto

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CITY: Baid Alto

CITY: Baid Alto

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CITY: Baid Alto

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Query Match 100.0%; Score 40; DB 2; Length 253; Best Local Similarity 100.0%; Pred. No. 2.7; Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                    US-09-210-084-3

US-09-210-084-3

Sequence 3, Application US/09210084

Patent No. 619/710:
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
ITILE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
ADDRESSE:
ATREFT: 3174 Porter Drive
STRRET: ATA Porter Drive
STRRET: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SUFUMARE: FastSEQ for Windows Version 2.0
SURRENT APPLICATION DAY:
APPLICATION NUMBER: US/09/210,084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELEPRICE/DOCKET NUMBER: PF-0252 US
TELEPRICE/DOCKET NUMBER: PF-0252 US
TELEPRICE/TON INFORMATION:
TELEPRICE/DOCKET NUMBER: SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid strype: amino acid strype: amino acid strype: amino acid strype: Inmear Inmediate SOUNCE:
ILMEDIATE SOUNCE:
LIBRARY: GenBank
CLONE: 532504
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Patent No. 6472195
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Lal, Preeti
TILE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOPTWARE: FASESE FOR WIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                             4 SLLLPLOIL 12
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US-09-764-762-3
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Patent No. 6093397

GENERAL INPORMATION:

APPLICANT: Dixon, Eric P.

APPLICANT: Dixon, Eric P.

APPLICANT: Little, Sheila P.

ITILE OF INVENTION: RELATED NUCLEIC ACIDS

NUMBER OF SEQUENCES: 3

CORRESPONDENCE 3

CORRESPONDENCE BILLILLY and Company

STREET: Lilly Corporate Center

CITY: Indianapolis

STREET: Indianapolis

STREET: United States of America

COUNTRY: United States of America

STREET: Exabable FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: DATE FORM:

MEDIUM TYPE: PLOPPY DISK

COMPUTER: DATE FORM:

MEDIUM TYPE: PLOPPY DISK

COMPUTER: DATE COMPATION

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/930,188
                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 40; DB 1; Length 253; 100.0%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
PILING DATE: 04-APPL-1995
ATTORNEY, AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
TELECOMMUNICATION INPORMATION:
TELEPAX: 317-27-1090
TELEFAX: 317-27-1090
TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                     TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                : 253 amino acids
amino acid
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 10U..
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MOLECULE TYPE: protein

US-09-154-344-2
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Query Match
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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MOLECULE TYPE: protein
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-949-016-7716
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTESSE AND TITLE OF INVENTION: RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Bli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                     ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMpatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04294
ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

ATIONED BATE: «Unknown.

ATTORNEY AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTATION UNDERR: 36,749

REFERENCE/DOCKET NUMBER: PF-0252 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-85-0555

TELEPHONE: 415-845-4166

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 40; DB 2
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 SLLLPLQIL 12
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Sequence 716, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR PLILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SEQ ID NOS: 207012

SEQ ID NO 7716
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APPLICANT: O'BAILEN, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer FILE REFERENCE: D622321P-C
CURRENT FILING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: US/09/502,600A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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PRIOR APPLICATION NUMBER: US 08/410,22.

APPLICATION NUMBER: US 08/410,22.

FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/COKET NUMBER: X9239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-27-1090
TELEPHONE: 317-27-1090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                          US 08/416,257
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US-09-502-600-33
; Sequence 33, Application US/09502600A
; Patent No. 629344
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WS-09-502-600-35

| Sequence 35, Application US/09502600A
| Patent No. 62944404
| Patent No. 62944404
| GENERAL INFORMATION:
| APPLICANT: O'Brien, Timothy J.
| TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: O'Asrian Cancer
| FILE REFERENCE: D6223CIP-C
| CURRENT APPLICATION NUMBER: US/09/502,600A
| PRIOR FILING DATE: 03-14-1998
| NUMBER OF SEQ ID NOS: 136
| SEQ ID NO 35
| LENGTH: 9
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Pagenence 16.24344

GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer
FILE REFERENCE: D6223CIP-C
CURRENT PILING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: US/09/502,600A
PRIOR PELICATION NUMBER: US/09/502,600A
PRIOR FILING DATE: 03-14-1998
SEQ ID NO 116
LENGTH: 9
LENGTH: 9
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                                           Gaps
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Query Match 85.0%; Score 34; DB 2; Length 812; Best Local Similarity 87.5%; Pred. No. 1.4e+02; Matches 7; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.0%; Score 32; DB 2; Length 9;
100.0%; Pred. No. 4.6e+05;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: Residues 6-14 of the SCCE protein US-09-502-600-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Residues 2-10 of the SCCE protein US-09-502-600-116
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Best Local Similarity 100.0
Matches 7; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                           429 LLLPLOLL 436
                                                                                   2 LLLPLOIL 9
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US-09-502-600-116
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US-09-489-019A-12075
i Sequence 12075, Application US/09489019A
j Sequence 12075, Application US/09489019A
j Patent No. 6610836
j GENERAL INFORMATION:
j APPLICANT: Gary Breton et. al
j APPLICANT: Gary Breton et. al
j TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
j TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
j TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
j TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
j CURRENT FILLING DATE: 2000-01-27
j PRIOR FILLING DATE: 1999-01-29
j NUMBER OF SEQ ID NOS: 14342
j SEQ ID NO 12075
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                                                                                                                                                                                                                                Query Match 90.0%; Score 36; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                              FEATURE:
; OTHER INFORMATION: Residues 5-13 of the SCCE protein US-09-502-600-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein US-09-918-243-33
PRIOR APPLICATION NUMBER: 09/039,211
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12075
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ORGANISM: Homo sapiens
                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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                                                               SEQ ID NO 33
LENGTH: 9
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RESULT 2
US-09-905-083-36
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                                                                                                                 March 11, 2006, 01:24:47; Search time 69.444 Seconds (without alignments) 54.151 Million cell updates/sec
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-375-521-36

US-10-450-76--53737

US-10-450-76--53737

US-10-262-511-96

US-10-262-511-96

US-10-262-511-96

US-10-071-214-48

US-10-071-214-48

US-10-071-214-48

US-10-071-214-48

US-10-071-214-48

US-10-256-027-498

US-10-264-283-90

US-10-173-999-48

US-10-173-933

US-10-173-521-33

US-10-172-521-33

US-10-172-521-33

US-10-172-521-33

US-10-172-521-33

US-10-44-599-164977

US-10-424-599-164977
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                                                                                                                                                                                                                                                                                                                                                   1867569 seqs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Fatent No. US20020146708A1

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer; TITLE OF INVENTION: Ovarian Cancer; TITLE OF INVENTION Ovarian Cancer; FILE REPERBNCE: D6223CIP/C/Div

CURRENT APPLICATION NUMBER: US/09/905,083

CURRENT FILING DATE: 2001-07-13

FRIOR PILING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 36

LENGTH: 9

TYPE: PRT
                                                                                                                                                                                                                                                                                         28, Appl
35, Appl
35, Appl
116, App
35, Appl
35, Appl
116, App
116, App
116, Appl
116, Appl
36, Appl
116, Appl
36, Appl
37, Appl
38, Appl
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Sequence 49706, A
Sequence 252879,
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US-09-918-243-36

US-09-918-243-36

Sequence 36, Application US/09918243

Patent No. US20020142317A1

GENERAL INFORMATION:

APPLICANT: Cannon, Martin J.

APPLICANT: Santin, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

FILE REPERENCE: D6223CIP/C/D/CIP

CURRENT FILING DATE: 2001-07-30

PRIOR PELICATION NUMBER: US

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 36

LENGTH: 9

MATHOR PELICATION NUMBER: US

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100.0%; Score 40; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-09-918-243-36
                                                                                        US-10-424-599-199921
US-10-425-115-264649
US-10-425-115-264649
US-10-408-765A-2842
US-10-236-055A-2842
US-09-918-243-116
US-09-918-243-116
US-09-905-083-116
US-10-372-521-116
US-10-372-521-135
US-10-372-521-16
US-10-31-075-35
US-10-831-075-31
US-10-831-075-31
US-10-450-763-49706
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STELPLOIL 9
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Best Local Similarity 100.0%; Fred. No. 1.7e+06; Matches 9; Conservative 0; Mismatches 0;
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Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Bllerman, Karen
Malyankar, Uriel M.
Ort, Tatiana
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Zerhusen, Bryan D.
Anderson, David W.
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Li, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 9; Conserva
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US-10-262-511-96
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Sequence 36, Application US/10831075

Sequence 36, Deplication US/10831075

Publication No. US20040224891A1

SERMERAL INFORMATION:

APPLICANT: Cannon, Marthn J.

APPLICANT: Santin, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

FILE REPERENCE: D6223CIP/C/D/CIP3

FURENT APPLICATION NUMBER: US 10/331,075

CURRENT APPLICATION NUMBER: US 10/372,521

PRIOR PILING DATE: 2003-02-21

SEQ ID NO 36

SEQ ID NO 36
                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                             Sequence 36, Application US/10372521

Sequence 36, Application US/10372521

GENERAL INFORMATION: Timothy J.

APPLICANT: Gennon, Martin J.

APPLICANT: Santin, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

FILE REFERENCE: D6223CIP/C/D/CIP2

FULE REFERENCE: D6223CIP/C/D/CIP2

CURRENT APPLICATION NUMBER: US 09/918,243

PRIOR APPLICATION NUMBER: US 09/918,243

FRIOR APPLICATION NUMBER: US 09/918,243

NUMBER OF SEQ ID NOS: 136
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                                                                                                               100.0%; Score 40; DB 3; Length 9; 100.0%; Pred. No. 1.7e+06; Attive 0; Mismatches 0; Indels
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                            ; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-09-905-083-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , NAME/KEY: CHAIN
, OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-10-372-521-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CHAIN
OTHER INFORMATION: Residues 4-12 of the SCCE protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
                                                                                                             Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
                                                                                                                                                                                             1 SLLLPLOIL 9
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US-10-372-521-36
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FEATURE:
NAME/KEX: DOWAIN
(51). (78)
OTHER INFORMATION: Serine proteases trypsin family, histidine proteins. domain
OTHER INFORMATION: Johntified by eMATRIX, accession number BL00134A, p-value=6.143e-
OTHER INFORMATION: 20, raw score of 11.96
FEATURE:
NAME/KEY: DOWAIN
LOCATION: (36)..(133)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (36)..(133)
; OTHER INFORMATION: Trypsin domain identified by PFam, accession name trypsin,
; OTHER INFORMATION: value=3.2e-31, PFam score of 101.0
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Gapa
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                                                                                                                                                                                                            Sequence 53737, Application US/10450763

Publication No. US20050196754A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES;
FILE RERERENCE: 790C193/US

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR PELING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

PRIOR SEQ ID NOS: 60736

SOFTWARE: Custom

SEQ ID NO 53737

LENTH: 136
Indels
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0; Mismatches
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Patent No. US20020064856A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: CAENEPEL, SEAN
APPLICANT: CAENEPEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
TITLE OF INVENTION: NOVEL PROTEASES
FILE REPERRNCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 2100-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
                                                                                                                            Ji, Weizhen
Miller, Charles E.
Rastelli, Luca
                                 Zerhusen, Bryan D.
Anderson, David W.
                                                                                                                                                                                         Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
                                                                                                           Catterton, Elina
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Best Local Similarity 100.
Matches 9; Conservative
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFRENCE.
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT PILING DATE: 2003-05-28
FRIOR PELLING DATE: 2001-10-8
FRIOR APPLICATION NUMBER: 60/373,815
FRIOR APPLICATION NUMBER: 60/373,917
FRIOR PILING DATE: 2001-10-9
FRIOR FILING DATE: 2002-04-19
FRIOR PILING DATE: 2002-05-17
FRIOR PILING DATE: 2002-05-17
FRIOR PILING DATE: 2002-05-17
FRIOR PILING DATE: 2002-05-17
FRIOR PILING DATE: 2002-05-16
FRIOR PILING DATE: 2002-05-16
FRIOR PILING DATE: 2002-05-17
FRIOR PILING DATE: 2002-05-17
FRIOR PILING DATE: 2002-05-17
FRIOR PILING DATE: 2002-04-17
FRIOR PILING DATE: 2002-04-17
FRIOR PILING DATE: 2002-04-17
FRIOR FILING DATE: 2002-04-17
FRIOR FILING DATE: 2002-04-17
FRIOR FILING DATE: 2002-04-19
FRIOR APPLICATION NUMBER: 60/373, 260
FRIOR FILING DATE: 2002-04-19
FRIOR PILING DATE: 2002-04-19
FRIOR FILING DATE: 2002-04-19
FRIOR PILING DATE: 2002-04-19
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NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
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100.0%; Score 40; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 0; Indels
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
                                                                                                                                                                                                            Shimkets, Richard A.
Rothenberg, Mark E.
Leach, Martin D.
Agee, Michele L.
                                                 Ji, Weizhen
Miller, Charles B.
Rastelli, Luca
Stone, David J.
Pena, Carol B. A.
Shenoy, Suresh G.
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Malyankar, Uriel M.
Ort, Tatiana
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
Zhong, Mei
Catterton, Elina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-96
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LENGTH: 198
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APPLICANT:
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APPLICANT:
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Gaps
APPLICANT: Shimkets, Richard A.
APPLICANT: Rothenberg, Mark B.
APPLICANT: Leach, Martin D.
APPLICANT: Begh, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
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COMPUTER: IBM COMPACTE
SOFTWARE: FASESED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILING DATE: IG-Jan-2001
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/210,084
FILING DATE: «Unknown»
ATTORNEY/AGENT INPORMATION:
NAME: Billings, Lucy J.
REGISTRATION UNMBER: 36,749
REGISTRATION UNMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: AS REGISTRATION NUMBER: AS REGISTRATION NUMBER: AS REGISTRATION NUMBER: AS REGISTRATION NUMBER: AS REGISTRATION NUMBER: AS REGISTRATION NUMBER: AS REGISTRATION NUMBER: AS REGISTRATION NUMBER: AS REGISTRATION NUMBER: AS REGISTRATION NUMBER: AS REGISTRATION NUMBER: AS REFREENCE/DOCKET NUMBER: AS REGISTRATION N
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Patent No. US20020068341A1

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
ITILE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSE:
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLONE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
## PRIOR APPLICATION NUMBER: 60/214,047
| PRIOR FILING DATE: 2000-06-26
| NUMBER OF SEQ ID NOS: 150
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 98
| LENGTH: 253
| TYPE: PRT | CREAMING SAPIENS | CREAMING SA
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TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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STRANDEDNESS: single
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-09-764-762-3
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SLLLPLOIL 12

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Sequence 2, Application US/10071214
Sequence 2, Application US/10071214
Publication No. US20030066099A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HANSSON, Lennart
APPLICANT: HANSSON, Lennart
APPLICANT: HANSSON-3A
CURRENT APPLICATION NUMBER: US/10/071,214
CURRENT PILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,422
PRIOR PELING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
SOFTWARE PLEATION NUMBER: US 001 00218
PRIOR PILING DATE: 2001-02-09
SOFTWARE: PATENTING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTING DATE: 2001-02-09
SOFTWARE: PATENTING DATE: 2001-02-09
SOFTWARE: PATENTING DATE: 2001-02-09
SOFTWARE: PATENTING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTING DATE: 2001-02-09
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; Sequence 48, Application US/10071214
; Sequence 48, Application US/10071214
; PUBLICATION NO. US20030066099A1
; GENERAL INFORMATION.
; APPLICAMT: HANSON, Lennart
; APPLICAMT: BGELKUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSON-3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT PELING DATE: 2002-02-11
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Deduced amino acid sequence from the C-terminal part of SCCE from OTHER INFORMATION: homo sapiens.
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100.0%; Pred. No. 28;
tive 0; Mismatches 0
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100.0%; Pred. No. 28;
tive 0; Mismatches 0
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US-10-264-283-90
Sequence 90, Application US/10264283
; Publication No. US200301449941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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; ORGANISM: Homo sapiens
US-10-071-214-2
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Best Local Similarity
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LENGTH: 253
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APPLICANT: G17me, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Ros Biotechnology, Inc.
APPLICANT: Ros Biotechnology, Inc.
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
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NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 498
LENGTH: 253
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                                                     APPLICANT: Mannion, Jane
TITLE OF INVENTION: Jane
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.590
CURRENT APPLICATION NUMBER: US/10/264,283
CURRENT FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 111
SOFTWARE: CORIXA Invention Disclosure Database
SEQ ID NO 90
LENGTH: 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR PELLING DATE: 2002-11-13
PRIOR PELLING DATE: 2000-09-15
PRIOR PELLING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR PELLING DATE: 2001-11-15
PRIOR PELLING DATE: 2001-11-15
PRIOR PELLING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR PILING DATE: 2001-11-29
PRIOR PELLING DATE: 2001-11-29
PRIOR PELLING DATE: 2001-11-29
PRIOR PELLING DATE: 2001-12-14
PRIOR PELLING DATE: 2001-12-14
PRIOR PELLING DATE: 2002-01-08
PRIOR PELLING DATE: 2002-01-08
PRIOR PELLING DATE: 2002-01-09
PRIOR PELLING DATE: 2002-01-09
PRIOR PELLING DATE: 2002-01-09
PRIOR PELLING DATE: 2002-01-09
PRIOR PELLING DATE: 2002-01-00
PRIOR PELLING DATE: 2002-01-00
PRIOR PELLING DATE: 2002-01-00
PRIOR PELLING DATE: 2002-01-00
PRIOR PELLING DATE: 2002-02-03
PRIOR PELLING DATE: 2002-02-03
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Publication No. US2003022350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-283-90
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; ORGANISM: Homo sapiens
US-10-295-027-498
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RESULT 14
US-10-173-999-48
is Sequence 48, Application US/10173999
is Sequence 48, Application US/20173999
is QENERAL INFORMATION:
is APPLICANT: Mack, David H.
is APPLICANT: Gish, Kurt C.
is APPLICANT: Concern C.
is TITLE OF INVENTION: Methods of Screening for Modulators of Ovarian in TITLE OF INVENTION: Cancer in Sol C.
is FILE REFERENCE: 018501-002420US
is CURRENT FILING DATE: 2001-06-18
is PRIOR APPLICATION NUMBER: US 60/215,287
is PRIOR FILING DATE: 2001-08-27
is PRIOR FILING DATE: 2001-08-27
is PRIOR FILING DATE: 2001-04-12
is NUMBER OF SEQ ID NOS: 163
is SOFTWARE: PatentIn Ver. 2.1
is SEQ ID NO 48
is LENGTH: 253
is URWAREN FOR SEQ ID NOS: 163
is LENGTH: 253
is URWAREN FOR SEQ ID NOS: 163
is ERWAREN F
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                                                                                              Gaps
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APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Garn, Gary M.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROFECME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SEQ ID NO 639
LENGTH: 253
Query Match 100.0%; Score 40; DB 4; Length 253; Best Local Similarity 100.0%; Pred. No. 28; Matches 9; Conservative 0; Mismatches 0; Indels
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Pred. No. 28;
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APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Boin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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Best Local Similarity 100.
Matches 9; Conservative
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CORGANISM: Homo sapiens
US-10-408-765A-639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 1 SLLLPLQIL 9
Db 4 SLLLPLQIL 12

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Search completed: March 11, 2006, 01:37:24 Job time: 70.4444 Becs

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RESULT 2
US-10-412-748-14

i Sequence 14, Application US/10412748

sequence 14, Application US/10412748

publication No. US20060035219A1

GENERAL INFORMATION:
APPLICANT: Clements, Judith A

TITLE OF INVENTION: Aberrant Kallikrein Expression
FILE REFERENCE: DAVI172.003AUS

CURRENT APPLICATION NUMBER: US/10/412,748

CURRENT FILING DATE: 2003-04-09

PRIOR APPLICATION NUMBER: W PS1616/02

PRIOR APPLICATION NUMBER: W PS1616/02

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn version 3.2

LENGTH: 253
 4 SLLLPLOIL 12
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ORGANISM: Human
US-10-412-748-11
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US-10-412-748-11
 TYPE: PRT
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Sequence 14, Appl
Sequence 17, Appl
Sequence 27354, A
Sequence 27351, A
Sequence 27351, A
Sequence 27351, A
Sequence 27351, A
Sequence 2642, Ap
Sequence 6642, Ap
Sequence 6642, Ap
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10163, A
7, Appli
6331, Ap
6330, Ap
23862, A
20656, A
30760, A
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30759, A
80, Appl
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Sequence 176, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                            Sequence 5, Sequence 7, Sequence 63. Sequence 63. Sequence 20. Sequence 30. Sequence 30. Sequence 30. Sequence 30.
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1: /cgn2_6/ptodata/2/pubpaa/USO8 NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6 NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7 NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7 NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USIO NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USIO NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
               GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-412-748-11
US-10-412-748-17
US-11-03-243-98
US-11-096-568A-27391
US-11-096-568A-27391
US-11-096-568A-27391
US-11-096-568A-27391
US-11-096-6642
US-11-121-612-95
US-11-1181-234-5
US-11-181-234-5
US-11-096-568A-6331
US-11-096-568A-6331
US-11-096-568A-6331
US-11-096-568A-3065
US-11-096-568A-3065
US-11-096-568A-3065
US-11-096-568A-3065
US-11-096-568A-3065
US-11-096-568A-3065
US-11-096-568A-3065
US-11-096-568A-3065
US-11-096-568A-30761
US-11-096-568A-30761
US-11-096-568A-30761
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US-11-096-568A-30761
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US-11-121-612-144
US-11-121-612-176
                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                  161667 seqs, 27834885 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                  OM protein - protein search, using sw model
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seq length: 200000000
                                                                                                                                                                                  US-09-905-083A-36
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Perfect score:
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Maximum DB
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                                                                                                                   Run on:
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Sequence 246, App Sequence 247, App Sequence 248, App Sequence 320, App Sequence 349, App Sequence 349, App Sequence 270, App Sequence 631, App Sequence 631, App Sequence 2866, App Sequence 2266, App Seq
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Sequence 12300, A
Sequence 2, Appli
Sequence 18598, A
Sequence 18597, A
Sequence 4, Appli
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100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels
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; Publication No. US20060035219A1
; GENERAL INPORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVIT2.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFWARE: Patentin version 3.2
; LENOTH: 253
; TYPE: PRT
                                                                                                                                                                                                                                    US-11-121-512-342
US-11-121-612-349
US-11-121-612-349
US-11-121-612-100
US-10-895-064-631
US-10-895-064-631
US-10-467-657-3826
US-11-205-2266
US-11-205-225-8
US-11-205-225-8
US-11-205-225-8
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US-11-096-568A-18597
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TYPE: PRT
ORGANISM: Arabidopsis thaliana
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 87.5
Matches 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
                                           4 SLLLPLOIL 12
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US-11-096-568A-27391
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                                                                Query Match 100.0%; Score 40; DB 6; Length 253; Best Local Similarity 100.0%; Pred. No. 1.1; Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                              US-10-412-748-17

Sequence 17, Application US/10412748

Sequence 17, Application US/10412748

Publication No. US20060035219A1

GENERAL INCRMATION:

APPLICANT: Queensland University of Technology

APPLICANT: Clements, Judith A

TITLE OF INVENTION: Aberrant Kallikrein Expression
FILE REFERENCE: DAV1172.003AUS

CURRENT APPLICATION NUMBER: US/10/412,748

CURRENT FILING DATE: 2003-04-09

PRIOR APPLICATION NUMBER: AU PS1616/02

PRIOR FILING DATE: 2002-04-09

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn version 3.2

LENTH: 253
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APPLICANT: CHARTEL, SEAN
APPLICANT: CHARTEL, SEAN
APPLICANT: CHARTOCZAK, GLEN
APPLICANT: MANNING, GERARD
APPLICANT: MANNING, GERARD
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2000-06-26
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PATENTING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PATENTING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PATENTING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PATENTING DATE: 211
SEQ ID NO 98
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US-11-037-243-98
US-11-037-243-98
; Sequence 99, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT

ORGANISM: Homo sapiens

US-11-037-243-98
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ORGANISM: Human
; ORGANISM: Human
US-10-412-748-14
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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I
TITLE OF INVENTION: Therby
FILE REPERENCE: 2750-1592PUG2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
LENGTH: 71
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| Publication No. US2060048240A1 | GENERAL INFORMATION: GENERAL INFORMATION: The Control of Control o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.0%; Score 34; DB 7; Length 71; 87.5%; Pred. No. 4.2; tive 1; Mismatches 0; Indels
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NAME/KEY: misc feature
LOCATION: (1)...(71)
LOTHER INFORMATION: Ceres Seq. ID no. 13500184
US-11-096-568A-27391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature

LOCATION: (1)..(71)

MOTHER INFORMATION: Ceres Seq. ID no. 5677704

US-11-096-568A-27354
US-11-096-568A-27354
; Sequence 27354, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
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Sequence 95. Application US/11121612
Sequence 95. Application US/11121612
Publication No. US2006002533941
GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: The Stock Robert J
APPLICANT: Mazur, Wieslaw Application Title OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
FILE REFERENCE: 8847MD
CURRENT APPLICATION NUMBER: US/11/121,612
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: US 60/349,117
PRIOR PLING DATE: 2002-01-16
PRIOR FILING DATE: 2002-01-16
PRIOR FILING DATE: 2002-04-29
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Pred. No. 96;
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Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
ITILE OF INVENTION: Genes and Uses for Plant Improvement;
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 6642
           APPLICANT: TATALCLARY, ASSISTANCE, APPLICANT: SEKI, NACHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OSHIKAWA, TSUTOMU
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: NAGHARI, KENJI
CURRENT PREBRENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR PILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PARCENTIN VERSER: JP 2001-379298
PRIOR PILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PARCENTIN VERSER: JP 2001-379298
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.0%;
100.0%;
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         TAMECHIKA, ICHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
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ORGANISM: Guillardia theta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Homo sapiens
US-11-072-512-3867
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Best Local Similarity
Matches 6; Conserv
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US-11-121-612-95
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Sequence 27390, Application US/11096568A
Sequence 27390, Application US/11096568A
Publication No. US20060048240A1
GENERAL INPORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: 176-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 27390
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides TITLE OF INVENTION: Therby
FILE REFERENCE: 2.75-0-1592PUS CURRENT APPLICATION NUMBER: US.11/096,568A
CURRENT APPLICATION NUMBER: US.11/096,568A
SEQ ID NOS: 34471
SEQ ID NO 27353
LENGTH: 85
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Pred. No. 5.1;
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: LOCATION: (1) .. (85)

: DOTER INORWATION: Ceres Seq. ID no. 13500183

US-11-096-568A-27390
                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc feature
NOCATION: (1) - (65)
OTHER INFORMATION: Ceres Seq. ID no. 5677703
US-11-096-568A-27353
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APPLICANT: SUGIXAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
                                                                                                                                                                              TYPE: PRT
ORGANISM: Arabidopsis thaliana
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87.5%;
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ISONO, YUUKO
HIO, YURI
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Best Local Similarity 87.5
Best Local 7; Conservative
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NAGAI, KEIICHI
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PRIOR FILING DATE: 2004-07-15
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APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
FILE REFERENCE: 09531-12801
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT APPLICATION NUMBER: US/11/093/31318
PRIOR FILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-10-01
NUMBER OF SEQ ID NOS: 11433
SOFTWARE FREESE FREESEQ for Windows Version 4.0
SEQ ID NO 10163
LENGTH: 202
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: Chemically synthesized peptide sequence
                                                                                                                                                                                                                                                                                                                                                            Score 30; DB 7; Length 41;
Pred. No. 14;
1; Mismatches 1; Indels
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PRIOR APPLICATION NUMBER: US 60/388,895
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/411,988
PRIOR FILING DATE: 2002-09-19
PRIOR PLILING DATE: 2002-12-11
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 531
SOTTWARE: Patentin version 3.3
SEQ ID NO 95
LENGTH: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-11-098-686-10163
US-11-098-686-10163, Application US/11098686
; Sequence 10163, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10163
                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 87.5%;
Matches 7; Conservative
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; LOCATION: (41)
; OTHER INFORMATION: AMIDATION
US-11-121-612-95
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US-11-096-568A-6331

Sequence 6331, Application US/11096568A

Sequence 6331, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F

TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

SEQ ID NOS: 34471

ENGTH: 68
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                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:/note = OTHER INFORMATION: Synthetic Construct
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Publication No. US20060021075A1

GENERAL INFORMATION:

APPLICANT: WANG, CHYUNG-RU

TITLE OF INVENTION: USES

FILE REFERENCE: 2117.0001U2

CURRENT APPLICATION NUMBER: US/11/181,234

CURRENT FILING DATE: 2005-07-14

PRIOR APPLICATION NUMBER: 60/588,192

PRIOR APPLICATION NUMBER: 60/588,192

PRIOR RILING DATE: 2004-07-15

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FBELSEQ for Windows Version 4.0

SEQ ID NO 7
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                                                                                                                                                                                                                                                                         75.0%; Score 30; DB 7; Length 333; 75.0%; Pred. No. 1.2e+02; tive 1; Mismatches 1; Indels
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 333
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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ORGANISM: Glycine max
FEATURE:
NAME/KEY: misc feature
LOCATION: (1). (68)
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; OTHER INFORMATION: Ceres Seq. ID no. 14314773
US-11-096-568A-6331
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		Gaps
		0
	Length 68;	0; Indels
	Query Match 72.5%; Score 29; DB 7; Length 68; Best Local Similarity 85.7%; Pred. No. 36;	1; Mismatches
	72.5%;	vative
1	Similaritv	5; Conser
	Query Match Best Local	Matches

<sup>1</sup> SLLLPLQ 7 : |||||| 36 36 36 36 දු පු

Search completed: March 11, 2006, 01:38:42 Job time : 9 secs



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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-905-083A-80	30 1 GPLVCRGTL 9	BLOSUM62 Gapop 10.0 , Gapext 0.5	2443163 seqs, 439378781 residues	Total number of hits satisfying chosen parameters:
Title:	Sequence:	Scoring table: BLOSUM62 Gapop 10	Searched:	Total number of

ır of hits satisfying cl seq length: 0	Total number of hits satisfying chosen parameters: Minimum DB seq length: 0
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Post-processing:	Minimum	Match 0%		
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A Geneseq 21:*	1: geneseqp1980s:*	2: geneseqp1990s:*	••	••	5: geneseqp2002s:*	••	••	8: geneseqp2004s:*	
Database									

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Query e Match Length DB ID Description	AAE08285	Adr68841 Human	181 6 ADA05738 Ada05738 Human NOV	8 ADN62902 Human	Ada05736 Human	8 ADN62900 Adn62900 Human	6 ADA05744 Human	8 ADN62908 Human	9 ADV21100	THE COLOCAL PROPERTY OF THE PR
Query Match Ler	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
Score	50	20	20	20	20	20	20	20	20	(
Result No.	   	7	m	4	S	9	7	8	6	•

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uo	Human	Amino	Protein	Protein	Human																			
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& Query Match I	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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253 7 ADB80484 253 7 ADJ8803180 253 8 ADJ06515 253 8 ADRV4182 253 8 ADRV75880 253 9 ADRV75880 254 9 ABB4420 247 4 AAU123752 250 5 ABB64969 250 6 ADRV5540 250 6 ADRV5540 250 6 ADRV5540 250 8 ADVS3877 251 4 AAU16971	Adb80484 Ovarian c Adj68833 Human hea Adn39180 Cancerfan Adl06515 Human tum Adn04182 Antipsori Adr72880 Human ova Ady67588 Human kal Aec00353 Human kal Aeb21326 Human HSC Abb84420 Porcine S Aau86677 Novel hum Aau23752 Novel hum Aau23752 Novel hum Aau13752 Novel hum Aau17043 Human nov Adb60011 Connectiv Aab21298 Human Kik Abb64969 Human Kik Abb64969 Human Kik	
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## ALIGNMENTS

Human stratum corneum chymotrypsin enzyme peptide #50 (residues 207-215). Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia. AAE08285 standard; peptide; 9 AA. 01-NOV-2001 (first entry) AAE08285; RESULT 1 

WO200159158-A1. Homo sapiens. 16-AUG-2001. 07-FEB-2001; 2001WO-US003977.

11-FEB-2000; 2000US-00502600. (UYAR-) UNIV ARKANSAS.

O'brien TJ;

WPI; 2001-514676/56.

Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.

Claim 25; Page 113; 127pp; English.

The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide

Sequence 9 AA;

antidiabetic; anorectic; antibacterial; virucide;

(first entry)

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immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilpaemic; gene therapy; human disease;
metabolic disorder; diabetes; obseity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
                                                                                                                                                                                                                                                                                         immune disorder; haematopoietic disorder; dyslipidaemia
    ADA05738 standard; protein; 181 AA
                                                                                                                                      Human NOV18d protein SEQ ID NO:98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-OCT-2002; 2002WO-US031373
                                                                                                                                                                                                                                                                                                                                                                              WO2003029424-A2.
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09-OCT-2001;
12-OCT-2001;
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22-OCT-2001;
24-OCT-2001;
24-OCT-2001;
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01-NOV-2001;
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17-OCT-2001;
                                                                                                                                                                               human; NOVX;
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05-OCT-2001;
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17-MAY-2002;
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                                                                                          06-NOV-2003
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                                               ADA05738;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel method for vaccinating an individual against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating an individual with a SCCE peptide, which elicite an immune response in the individual with a SCCE peptide, which elicite an immune response in the individual. A peptide of the invention acts as a stratum corneum chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or at risk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligonucleotide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or paptides are also useful in the monitoring and development of immunotherapies for ovarian and other malignancies. The present sequence the prepresents a peptide fragment of serine protease SCCE (stratum corneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
                                                                                                                                                                                                                                                                                                                                                                                Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:80.
                                                  Gaps
                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                    serine protease; stratum corneum chymotrytic enzyme; SCCE; immune response; ovarian cancer; lung cancer; prostate cancer; pancreatic cancer; colon cancer.
    100.0%; Score 50; DB 4; Length 9; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 50; DB 8; Length 9; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; SEQ ID NO 80; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Santin A;
                                                                                                                                                                                                                                              ADR68841 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                  (first entry)
                                               9; Conservative
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O'brien TJ, Cannon MJ,
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                                                                                          GPLVCRGTL 9
                                                                                                                   ||||||||||||||| 9
GPLVCRGTL 9
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-SEP-2004.
                                                                                                                                                                                                                                                                                            ADR68841;
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                                               Matches
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11D ADR68841

11D ADR6841

XX AC ADR6

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2001US-0327917P. 2001US-0328029P. 2001US-0328044P. 2001US-0328056P.

2001US-0328849P 2001US-0329414P 2001US-0330142P

2001US-0330309P. 2001US-0341058P. 2001US-0339266P. 2001US-0343629P.

2001US-0349575P 2001US-0346357P 2002US-0373260P

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A, Shenoy SG;
Berghs C, Dipippo VA;
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                                                                                                                                                                                                            Catterton E;
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                                                                                                                                                                                                                                                                                                                                                                                                                    New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing
                                                                                                                                                      theon G, Millet I, Peyman JA, Kekuda R, Ju J, Li turajan M, Spytek KA, Edinger SR, Ellerman K, Mall T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Miller CE, Rastelli L, Stone DJ, Pena CEA, Sh M, Miller RA, Rothenberg ME, Leach MD, Agee ML, Berghlen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 171; 586pp; English
2002US-0383831P
2002US-0391335P
                                                      01-OCT-2002; 2002US-00262511
                                                                                                          (CURA-) CURAGEN CORP.
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N-PSDB; ADA05737.
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Patturajan M,
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1 GPLVCRGTL 9

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GPLVCRGTL

RESULT 3 ADA05738

2002US-0373884P. 2002US-0374977P. 2002US-0381037P.

2002US-0381042P. 2002US-0381642P.

2002US-0383656P

2002US-0381038P

2002US-0373815P. 2002US-0373817P.

2002US-0373826P

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Isolated NOVX polypeptides and nucleic acids, useful for preventing,
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           The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOV1). Also described (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit comprising, in one or more
containers, the composition described above; (3) an isolated nucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
comprising the above vector; (6) an antibody that immunospecifically
binds to the polypeptide described above; (5) a cell
comprising the nucleic acid molecule above; (7) methods for determining the
presence or amount of the above polypeptide or nucleic acid molecule in a
ca disease associated with altered levels of expression of the above
polypeptide or nucleic acid molecule in a first mammalial subject; (9) a
method of identifying an agent that binds to the polypeptide described
above; (10) a method for identifying a potential therappeutic agent for
ca berrant physiological interactions of the polypeptide; (11) a method of
above; (10) a method for identifying a potential therappeutic agent for
aberrant physiological interactions of the polypeptide; (11) a method of
ca deminating a pathology associated with the polypeptide; (12) a method for modulator of
ca pathology associated with the polypeptide; (12) a method for modulating
cor preventing a pathology associated with the above polypeptide; Novy
sequences have antidabetic, anorectic, antibacterial, vircide,
immunomodulator, cytostatic, noorectic, antibacterial, vircide,
cor preventing a pathology associated with the above polypeptide or the nucleic
cor preventing a pathology associated with the above polypeptide or mediating
cor preventing or profestatic, anorectic, antibacterial, vircide,
and antilipaemic activities, and can be used in gene therapy. The
and antilipaemic activities, and can be used in gene therapy.
Cor propertied is useful in manufacturing a medicament for treating a
corid molecule may be used to diagnose, treat or prevent mecabolic
acid molecule may be used to diagnose; reat or prevent mecabolic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X; wasting disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
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05-OCT-2001; 2001US-0327435P.
05-OCT-2001; 2001US-0327449P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention.
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Dipippo VA;
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2001US-0328849P.
2001US-0329414P.
2001US-0330142P.
2001US-0330309P.
2001US-0341058P.
                                                                  2001US-0339266P.
2001US-0343629P.
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EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
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PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
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GANGOLLI E A.
RIEGER D K.
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ANDERSON D W.
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                                                                                                                                                                                                                                                                                                                                                                                                           PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                             MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIPIPPO V A.
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CATTERTON E.
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RASTELLI L.
                                                                                                                                                                                                                                                                                                               SMITHSON G.
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BERGHS C.
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12-OCT-2001; 2
15-OCT-2001; 2
17-OCT-2001; 2
22-OCT-2001; 2
24-OCT-2001; 2
24-OCT-2001; 2
                                                                                                        01-NOV-2001;
17-APR-2002;
19-APR-2002;
19-APR-2002;
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16-MAY-2002;
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(EISE/)
(GANG/)
(RIEG/)
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(RAST/)
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(SHEN/)
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The invention relates to isolated NOVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the abberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and activity of NOVX polypeptides and activity of NOVX by supplementing the patient our controlled with decreased expression or to rectify mutations. Conversely, antiense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX probables and complementary sequences may also be used as DNA probables in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of the production of antibodies and in assays to identify modulators captive of the expression and activity of NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX colypeptides and polypeptide antibodies may be used in this way to prevent, diagnose and treat: metabolic disorders, inmune disorders, disorders, and the various dyslipidaemia, metabolic disorders, inmune disorders, may also be used as disorders, and disorders, and the various dyslipidaemia metabolic captive disorders.
diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
                                                            Claim 1; SEQ ID NO 98; 395pp; English.
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100.0%; Score 50; DB 8; Length 181; 100.0%; Pred. No. 2; ive 0; Mismatches 0; Indels
              Local Similarity 100.
    Query Match
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ADA05736 standard; protein; 198 AA. 06-NOV-2003 (first entry) ADA05736; RESULT 5

human; NOVX; antidiabetic; anorectic; antibacterial; virucide; Human NOV18c protein SEQ ID NO:96.

immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.

02-OCT-2001; 2001US-0326483P. 05-OCT-2001; 2001US-0327435P. 05-OCT-2001; 2001US-0327917P. 02-OCT-2002; 2002WO-US031373 WO2003029424-A2 Ното варіепв 10-APR-2003 ADA05736

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20010S-0328449P. 20010S-0329414P. 20010S-033042P. 20010S-033039P. 20010S-0341058P. 20010S-0343629P. 20010S-0343629P. 2002US-0374977P. 2002US-0373260P 2002US-0373815P. 2002US-0373826P 2002US-0373884P 2002US-0381038P 002US-0381042P 2002US-0381642P 2002US-0383656P 2002US-0383831P 2002US-0391335P 2002US-00262511 18-OCT-2001; 22-OCT-2001; 24-OCT-2001; 2 17-OCT-2001; 24-OCT-2001; 15-OCT-2001; 29-OCT-2001; 01-NOV-2001; 19-APR-2002; 19-APR-2002; 16-MAY-2002; 16-MAY-2002; 16-MAY-2002; 17-MAY-2002; 19-APR-2002; 19-APR-2002; 17-APR-2002; 28-MAY-2002; 

(CURA-) CURAGEN CORP.

4, car. Shenoy SG; Catterton E; Guo X; Kekuda R, Ju J, Li L, Guo X SR, Ellerman K, Malyankar UM; Berghs C, Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li Patturajan M, Spytek KA, Edinger SR, Ellerman K, Mal. Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Bergh Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

WPI; 2003-381626/36. N-PSDB; ADA05735.

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obesity, ö New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing pharmacogenomics

Claim 1; Page 170; 586pp; English.

The present invention describes NoVX proteins, where X can be 1 to 55

(e.g. NOV1). Also described: (1) a composition comprising a polypeptide

codescribed above and a carrier; (2) a kit comprising a polypeptide

containers, the composition described above; (3) an isolated nucleic acid

containers, the nucleic acid molecule described above; (5) a cell

comprising the nucleic acid molecule described above; (6) a vector

comprising the above vector; (6) an antibody that immunospecifically

binds to the polypeptide described above; (7) methods for determining the

comprising the above vector; (6) an antibody that immunospecifically

binds to the polypeptide described above; (7) methods for determining the

comprising the above vector; (6) an antibody that immunospecifically

comprising the above vector; (6) an antibody that immunospecifically

considered with altered levels of expression of the above

confidentifying an adent that binds to the polypeptide described

above; (10) a method for identifying a potential therapeutic agent for

constant physiological interactions of the polypeptide; (11) a method of

constant physiological interactions of the polypeptide; (11) a method of

constant physiological interactions of the polypeptide; (11) a method of

constant physiological interactions of the polypeptide; (12) a method for modulating

constant physiological interactions of the polypeptide; (12) a method of

constant physiological interactions of the polypeptide; (12) a method of

constant physiological interactions of the polypeptide; (12) a method of

constant physiological interactions of the polypeptide; (13) method of

constant physiological interactions of the polypeptide; (12) a method of

constant physiological interactions of the polypeptide; (12) a method of

constant physiological interactions of the polypeptide; (13) method of

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Shimkets RA,
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                                                                                                                                                                                                                                                    human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopojetic disorder; dyslipidaemia; metabolic syndrome X;
disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NoVX from the present invention.
                                                                                                       Gaps
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                                                                                    h Score 50; DB 6; Length 198; Similarity 100.0%; Pred. No. 2.2; 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                 ADN62900 standard; protein; 198 AA.
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09-OCT-2001; 20010S-0328029P.
09-OCT-2001; 20010S-0328029P.
09-OCT-2001; 20010S-0328044P.
12-OCT-2001; 20010S-0328049P.
12-OCT-2001; 20010S-0329144P.
17-OCT-2001; 20010S-033044P.
18-OCT-2001; 20010S-033026P.
24-OCT-2001; 20010S-0341058P.
24-OCT-2001; 20010S-034957P.
17-APR-2002; 2002US-0373260P.
17-APR-2002; 2002US-0373826P.
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22-APR-2002; 2002US-0374977P.
16-MAY-2002; 2002US-0381037P.
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                                                                                                                                                                                                                   01-JUL-2004 (first entry)
                                                                                                                                       152 GPLVCRGTL 160
                                                                                                                       1 GPLVCRGTL 9
                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                        US2004038223-A1.
                                                                     Sequence 198 AA;
                                                                                                                                                                                                                                                                                        wasting disorder
                                                                                                                                                                                                                                                                                                                                                                                           05-OCT-2001;
09-OCT-2001;
                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                    Human NOV18c
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The invention relates to isolated NOVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and activity of NOVX by supplementing the patient our polynucleotides may be used to treat disorders associated with decreased expression or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX colymelection of complementary sequences may also be used as DNA probbes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of constructive therapy. NOVX polypeptides may also be used as antigons in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. The used to modulate NOVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX colypeptides may be used in this way to prevent. Citagnose and treat: metabolic disorders, inthis way to prevent. Citagnose and treat: metabolic disorders, obesity, infectious disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative dissorders, immune disorders, immune disorders, immune disorders, immune disorders, immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TT, Gorman C., Rastella C., il W, Miller CE, Rastella E, inhimkets RA, Rothenberg ME, I'sen A, Gangolli EA, Rieger
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Patturajan M, Spytek KA,
Ort T, Gorman L, Zerhuse
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RASTELLI L.
STONE D J.
PENA C B A.
SHENOY S G.
SHINGERS R A.
ROTHENBERG M E
LEACH M D.
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GANGOLLI E A.
RIEGER D K.
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MALYANKAR U M.
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ANDERSON D W.
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PEYMAN J A.
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CATTERTON E.
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BERGHS C.
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SMITHSON
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haematopoietic disorders, and the various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
                                                                                                                                                                                                                                            human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkineonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alahaeimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
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                                                                      100.0%; Score 50; DB 8; Length 198; 100.0%; Pred. No. 2.2;
                                                                                        0; Indels
                                                                                         0; Mismatches
                                                                                                                                                                                                                             Human NOV18g protein SEQ ID NO:104.
                                                                                                                                                                       ADA05744 standard; protein; 224 AA
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; 2001US-0327435P.
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2001US-0330309P.
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2001US-0345875P.
2001US-0346375P.
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01-OCT-2002; 2002US-00262511.
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                                                                                        9; Conservative
                                                                                                                     152 GPLVCRGTL 160
                                                                                                          1 GPLVCRGTL 9
                                                                       Query Match
Best Local Similarity
                                                     Sequence 198 AA;
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09-0CT-2001; 2
15-0CT-2001; 2
117-0CT-2001; 2
18-0CT-2001; 2
24-0CT-2001; 2
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29-OCT-2001;
01-NOV-2001;
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ADA05744
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The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell of presence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) and sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above copypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for a berrant physiological interactions of the polypeptide; (11) a method of a pathology that is related to an aberrant expression or comparation and alternation and above; (11) a method of a pathology associated with the polypeptide; (12) a method of modulation to a pathology associated with the polypeptide; (12) a method of modulation to the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide or the nucleic and antilipaemic activities, and can be used in gene therapy. The copypeptide is useful in manufacturing a medicament for treating a pathology associated with a human disease. The polypeptide or the nucleic syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic acid molecule may be used to diagnose. The polypeptide or parent metabolic disorders such as diabetes such as diabetes or obesity, infections, cancer; or probes, in chromosome mapping, itsue
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                                                                                                                               1, Shenoy SG;
Bergha C, Dipippo VA;
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             Guo X;
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo >
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM,
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Cattertor
Ji W, Miller CE, Raetelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipi
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
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Pred. No. 2.4;
; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 9; Conservative
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                         EISEN A.
GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
                 DIPIPPO V A.
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(EISE/) H
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               human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; manorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
                                                                                                                                                            09-0CT-2001; 2001US-03279179.

09-0CT-2001; 2001US-0328029P.

09-0CT-2001; 2001US-0328049P.

12-0CT-2001; 2001US-0328049P.

15-0CT-2001; 2001US-0328049P.

17-0CT-2001; 2001US-03301042P.

18-0CT-2001; 2001US-0330309P.

24-0CT-2001; 2001US-0339266P.

24-0CT-2001; 2001US-0349575P.

10-NOV-2001; 2001US-0349575P.

17-APR-2002; 2001US-0373810P.

19-APR-2002; 2002US-0373817P.

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16-MAY-2002; 2002US-0381038P.

16-MAY-2002; 2002US-0381642P.

17-MAY-2002; 2002US-0381642P.

28-MAY-2002; 2002US-0383656P.

29-MAY-2002; 2002US-038331P.

25-UUN-2002; 2002US-0393331P.
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SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
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PATTURAJAN M.
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CATTERTON E.
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EDINGER S R.
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PEYMAN J A.
KEKUDA R.
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RASTELLI L.
STONE D J.
                                                                                                                                                                                                                                                                                                                                                                                                   SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELLERMAN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GORMAN L.
                                                 wasting disorder
                                                                                   US2004038223-A1
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1.3
                                                                                                                                                      05-OCT-2001;
Human NOV18g
                                                                   Homo sapiens
                                                                                                    26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                          (MILL/)
(PEYM/)
(KEKU/)
(JUJJ/)
(LILL/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SPYT/)
(EDIN/)
                                                                                                                                                                                                                                                                                                                                                                                                  SMIT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELLE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GUOX/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MILL/
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The invention relates to isolated NOVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides and cativity of NOVX polypeptides and cativity of NOVX polypeptides and complementations. Conversely, antisense NA molecules expression or activity of NOVX by supplementing the patient our crediffy mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX colymuclocides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators capcustive therapy. NOVX polypeptides may also be used as antigens in the production of antibodies, agonists and antagonists of the expression and activity of NOVX. The arti-NOVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX colypeptides and polymucleotides may be used in this way to prevent, diagnose and treat: metabolic disorders, inmune disorders, disorders, allowed cachexia, neurodegenerative disorders, and the various dyslipidaemias, metabolic disorders, and the various dyslipidaemias, metabolic manner and the various diseases and various cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                   Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indel's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human stratum corneum chymotrypsin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 104; 395pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADV21100 standard; protein; 224 AA.
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 GPLVCRGTL 201
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WPI; 2004-213931/20.
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                                                N-PSDB; ADN62907.
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Domain Domain Domain

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The present invention relates to human tumour antigen-derived gene 15 (TADG-15) protein and coding sequence (see AAH23601 and AAB98600). TADG-15 is an extracellular serine protease. It was found that TADG-15 is over-expressed in ovarian tumours. TADG-15 protein or its fragments of 9-20 residues that lack TADG-15 protease activity are useful for vaccinating an individual against TADG-15, having, suspected of having or at risk of getting cancer. Furthermore, the TADG-15 gene can be used as a diagnostic or therapeutic target in cancer. The present sequence was used in a sequence homology alignment with the catalytic domain of TADG-15
                                                                                                                                                                                                                                                                                                                                                                                         Novel extracellular serine protease, termed tumor antigen-derived gene 1
protein overexpressed in carcinomas and DNA encoding it, for diagnosis,
treatment, prevention of cancer, particularly breast, ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obseity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antidiabetic; anorectic; antibacterial; virucide;
Human, TADG-15; cytostatic; vaccine; ovarian tumour; cancer; tumour antigen-derived gene 15; serine protease; Stratum Corneum Chymotryptic Enzyme; SCCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50; DB 4
Pred. No. 2.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA05742 standard; protein; 247 AA.
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                                                                                                                                                                                              20-OCT-2000; 2000WO-US029095
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                                                                                                                                                                                                                                                                                                                  Tanimoto H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 GPLVCRGTL 187
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Best Local Similarity

9, Conserve
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                                                                                                                   WO200129056-A1
                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                              O'brien TJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polypeptides, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining predisposition to diseases or conditions of the prostate such as prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protease family and its corresponding nucleic acid sequence. PS133 polypeptide is useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to diseases or conditions of the prostate such as prostatic cancer. The present sequence is the human stratum corneum chymotrypsin protein. This sequence is used to align with PS133 consensus protein.
Protein purification; PS133 protein; serine protease; prostate disease; andrology; genitourinary disease; prostatic cancer; cytostatic; protein therapy; chymotrypsin; enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to PS133 protein, a member of the human serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 100.0%; Score 50; DB 9; Length 224; Similarity 100.0%; Pred. No. 2.4; 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                     26. .42
/note = Catalytically functional motif
83. .97
/note = Catalytically functional motif
174. .179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Granados E,
                                                                                                                                                                                                                                     /note = Catalytically functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 33; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Friedman PN,
Stroupe SD;
                                                                                                                   cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB98502 standard; protein; 225 AA.
                                                                                                                                                                                                                                                                                                                                                       20-FEB-2001; 2001US-00789210
                                                                                                                                                                                                                                                                                                                                                                                             97US-00944483
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10,
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                                                                                                                                                                                                                                                                                                                                                                                                                                COHEN M.
COLPITTS T L.
FRIEDMAN P N.
GRANADOS E.
KLASS M R.
KLASS M R.
STEWART K D.
STROUPE S D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPLVCRGTL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 224 AA;
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                                                                                                                                                                                                                                                                           US2004241646-A1
                                                                                                                                                                                                                                                                                                                                                                                             06-OCT-1997;
                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Russell JC,
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Cohen M,

(KLAS/) (RUSS/) (STEW/) (STRO/)

GRAN/

COHE/) FRIE/) 178

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Query Match

AAB98502;

RESULT 10
AAB98502
ID AAB9
XX
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DT 03-A
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Gape

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0; Indels 4; Length

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05-OCT-2001; 2001US-0327435P.
05-OCT-2001; 2001US-0327449P.
09-OCT-2001; 2001US-0328054P.
09-OCT-2001; 2001US-0328054P.
12-OCT-2001; 2001US-0328054P.
12-OCT-2001; 2001US-0328056P.
13-OCT-2001; 2001US-0328056P.
15-OCT-2001; 2001US-0339166P.
24-OCT-2001; 2001US-0339166P.
24-OCT-2001; 2001US-034957P.
17-APR-2002; 2001US-034957P.
17-APR-2002; 2001US-034957P.
19-APR-2002; 2001US-0349162P.
19-APR-2002; 2002US-0373810P.
19-APR-2002; 2002US-0373810P.
19-APR-2002; 2002US-0373810P.
19-APR-2002; 2002US-0373810P.
19-APR-2002; 2002US-0373810P.
16-MAY-2002; 2002US-0381038P.
16-MAY-2002; 2002US-0381038P.
17-MAY-2002; 2002US-0381038P.
18-MAY-2002; 2002US-0381038P.
25-JUNN-2002; 2002US-0381038P.
                                                                                                                                                                                                                   01-OCT-2002; 2002US-00262511
                                                                                                                                                                                                                                  (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                   WPI; 2003-381626/36.
N-PSDB; ADA05741.
                                                                                                                                                                                                                                                                                                                                                  pharmacogenomics.
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Dipippo VA; Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B; Ji M, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or

Claim 1; Page 172; 586pp; English.

The present invention describes NoVX proteins, where X can be 1 to 55

(e.g. NOVI). Also described: (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit comprising, in one or more
containers, the composition described above; (3) an isolated nucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
comprising the nucleic acid molecule described above; (5) a cell
comprising the above vector; (6) an antibody that immunospecifically
binds to the polypeptide described above; (7) methods for determining the
presence or amount of the above polypeptide or nucleic acid molecule in a
sample; (8) methods for determining the presence of or predisposition to
a disease associated with altered levels of expression of the above
comprising a pathology that is frem ammalian subject; (9) a
method of identifying an agent that binds to the polypeptide described
above; (10) a method for identifying a potential therapeutic agent for
ca berrant physiological interactions of the polypeptide; (11) a method of
correct the activity of the polypeptide described above; (12) a method of
correcting for a modulator of activity or of latency or predisposition to
correct the activity of the polypeptide described above; (13) methods of traating
corrected have antidiabetic, anotectic, antibacterial, virucide,
corrected have antidiabetic, noncopic, antibacterial, virucide,
corrected have antidiabetic, noncopic, antibacterial, retrapary. The
corrective and antilipaemic activities, and can be used in gene therapy. The

2002US-0383656P

28-MAY-2002;

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                                                                                                                                                                                                                                                                                                                                                                                                                                        human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; meurodegenerative disorder; Altheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
                nucleic
polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to disquose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
                                                                                                                                                                                                        Gaps
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                                                                                                                                                                              100.0%; Score 50; DB 6; Length 247; 100.0%; Pred. No. 2.7; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                              ADN62906 standard; protein; 247 AA.
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2001US-0328056P.
2001US-0328849P.
2001US-0329414P.
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2001US-0330309P.
2001US-0341058P.
2001US-0339266P.
2001US-0343529P.
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2002US-0373815P.
2002US-0373817P.
2002US-0373826P.
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2001US-0327917P.
2001US-0328029P.
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                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                             193 GPLVCRGTL 201
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                                                                                                                                                                                                                                   1 GPLVCRGTL
                                                                                                                           present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wasting disorder.
                                                                                                                                                    Sequence 247 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2004038223-A1
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12-0CT-2001; 2
15-0CT-2001; 2
17-0CT-2001; 2
22-0CT-2001; 2
24-0CT-2001; 2
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29-OCT-2001; 2
01-NOV-2001; 3
                                                                                                                                                                                                                                                                                                                                                                                                                Human NOV18f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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09-OCT-2001;
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19-APR-2002;
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obesity, infectious

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diagnose and treat: metabolic disorders, diabetes,
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                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                Sequence 247 AA;
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15-OCT-2001;
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19-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated NOVX polypeptides and polynucleotides. NOVX polypeptides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and polynucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polymucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (agonists and antagonists) of the expression and activity of NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polypurclectide expression and activity of NOVX polypeptides. The anti-NOVX polypeptide antibodies may also be used alagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polynuclecting the presence of NOVX in samples. NOVX polypeptides and polynuclectides may be used in this way to prevent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
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29-MAY-2002; 2002US-0383831P.
25-JUN-2002; 2002US-0391335P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RASTELLI L.
STONE D J.
FENA C E A.
SHENOY S G.
SHENOY S G.
SHEKOY E A.
COTHENBERG M E.
LEACH M D.
BERGHS C.
DIPIPPO V A.
                                                                                                                                                                                                                PATTURAJAN M.
SPYTEK K A.
EDINGER S R.
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MALYANKAR U M.
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GANGOLLI E A.
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SPADERNA S K.
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ANDERSON D W.
                                                                                   MILLET I.
PEYMAN J A.
KEKUDA R.
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CATTERTON E.
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                                                                 SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MILLER C E.
                                                                                                                                                                                                                                                                                                                                                   GORMAN L.
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(AGEE/)
(BERG/)
                                                               (SMIT/)
(MILL/)
(PEYM/)
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(GANG/)
(RIEG/)
(SPAD/)
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(RAST/)
(STON/)
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(EDIN/)
(ELLE/)
(MALY/)
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                                                                                                                                                                         (LILL/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (JIMM/
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disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, haematopoietic disorders, and the various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obseity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                              human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                                                                                                             100.0%; Score 50; DB 8; Length 247; 100.0%; Pred. No. 2.7; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                            ADA05732 standard; protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                  Human NOV18a protein SEQ ID NO:92
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2001US-0327917P.
2001US-0328029P.
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                                                                                                                                                                                                                                                                                                                                                                    06-NOV-2003 (first entry)
                                                                                                                                                                               9; Conservative
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2002US-0383831P

29-MAY-2002;

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The present invention describes NoVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising on or more containers, the composition described above; (3) an isolated nucleic acid molecule described above; (5) a coll comprising the nucleic acid molecule described above; (5) a cell composition the nucleic acid molecule above; (5) a cell comprising the nucleic acid molecule above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a disease associated with altered levels of expression of the above corrected acid molecule in a first mammalian subject; (9) a method for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for a bove; (10) a method for identifying a potential therapeutic gent for other above; (10) a method of cartivity of the polypeptide above; (12) a method of correctivity of the polypeptide described above; (13) methods for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology that is related to an aberrant expression or aptropendic and untilipaemic activities, and can be used in gene therapy. The collypeptide is useful in manifectual a medicament for treating a pathology associated with the above polypeptide in and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manifectual a medicament for treating and antilipaemic activities, and can be used in gene therapy. The cold molecule may be used to observe, infercion, cachexia, cachexia and activity of disease, immune disease or besity, infection, cachexia, cachexia, immune disease and a shitchmark and a poly
                                                                                                                  Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 169-170; 586pp; English.
25-JUN-2002; 2002US-0391335P
01-OCT-2002; 2002US-00262511
                                                                          (CURA-) CURAGEN CORP.
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SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
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ANDERSON D W.
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CATTERTON E.
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PEYMAN J ;
KEKUDA R.
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RASTELLI
wasting disorder.
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                                         US2004038223-A1
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                      Homo sapiens.
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15-OCT-2001;
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(MALY/)
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Matches 9; Conservative
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ADN62896;

RESULT 14
ADN62896
ID ADN62
XX
AC ADN62

Query Match

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human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
                                                                                                                                                                2001US - 0327435P

2001US - 0327449P

2001US - 0328029P

2001US - 0328044P

2001US - 0328044P

2001US - 0328044P

2001US - 0328049P

2001US - 0329414P

2001US - 03394105P

2001US - 03341058P

2001US - 0349575P

2002US - 0373806P

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2002US-0374977P.
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2002US-0381042P.
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25-JUN-2002; 2002US-0391335P.
                                                                                                                                         01-OCT-2002; 2002US-00262511
        (first entry)
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PENA C E A.
SHENOY S G.
                        Human NOV18a.
       01-JUL-2004
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(PENA/)
(SHEN/)
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Human NOV18b protein SEQ ID NO:94.

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Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Bisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                 The invention relates to isolated NOVX polypeptides and polynucleotides.
                                                                                                                                                                                                  Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                     Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X
M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
                                                                                                                                                                                                                              Claim 1; SEQ ID NO 92; 395pp; English.
SHIMKETS R A. ROTHENBERG M E.
                                                       EISEN A.
GANGOLLI E A.
                           AGEE M L.
BERGHS C.
DIPIPPO V A.
                                                                         RIEGER D K.
SPADERNA S K.
                                                                                                                                                                       2004-213931/20.
                   LEACH M D.
                                                                                                                                                                                N-PSDB; ADN62895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 250 AA;
                                                                                                                Patturajan M,
                                                                                                      Smithson G,
(SHIM/)
(ROTH/)
(LEAC/)
(AGEE/)
(BERG/)
                                              (DIPI/)
(EISE/)
(GANG/)
(RIEG/)
(SPAD/)
```

The invention relates to isolates and your perpetuses and polymention relates to the invention relates to isolates are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NovX polypeptides and complements. For example, NovX polypeptides and polymucleotides may be used to treat disorders associated with decreased complementary sequences associated with decreased expression or activity of NoVX by supplementing the patient our complementary sequences may also be used as DNA binding with the cells own genes and preventing their expression. NoVX polymetic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of complementary sequences may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NoVX. The anti-NoVX polypeptide antibodies may also be used as disorders. Althormer's and polypeptides antibodies may also be used as disorders, cancer, cancer, cancer-associated cachexia, neurodegenerative disorders, and the various dyslipidaemias, metabolic disorders, and the various dyslipidaemias, metabolic calenter and paralled services and various disorders associated with obesity, the metabolic syndrome X and complements and the various displaces and error and the various dyslipidaemias, metabolic cachers. The present of th present sequence They may also be used as antibacterial agents. The present represents the amino acid sequence of a human NOVX protein. 100.0%; Score 50; DB 8; Length 250; 100.0%; Pred. No. 2.7; Query Match Best Local Similarity

Mismatches ; 9; Conservative 204 GPLVCRGTL 212 GPLVCRGTL 9 Matches ò 셤

ADA05734 standard; protein; 252 AA. ADA05734; RESULT 15 ADA05734 SXXXE

06-NOV-2003 (first entry)

human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia. 2001US-0328044P. 2001US-0328056P. 2001US-0328849P. 2002US-0373826P. 2002US-0373884P. 2002US-0374977P. 2001US-0327435P. 2001US-0327449P. 2001US-0327917P. 2001US-0346357P. 2002US-0373260P. 02-OCT-2002; 2002WO-US031373 2001US-0328029P 2001US-0329414P 2001US-0330142P 2001US-0330309P 2001US-0341058P 2001US-0339266P 2001US-0343629P 2001US-0349575P 2002US-0373815P 2002US-0373817P 002US-0381037P 002US-0381038P 2002US-0381642P 2002US-0383656P 2002US-0383831P 2002US-0391335P 2002US-00262511 WO2003029424-A2. 18-OCT-2001; 22-OCT-2001; 24-OCT-2001; Homo sapiens. 09-OCT-2001; 12-OCT-2001; 15-OCT-2001; 17-OCT-2001; 02-OCT-2001; 05-OCT-2001; 05-OCT-2001; 24-OCT-2001; 29-OCT-2001; 01-NOV-2001; 17-APR-2002; 19-APR-2002; 19-APR-2002; 19-APR-2002; 22-APR-2002; 16-MAY-2002; 16-MAY-2002; 19-APR-2002; 17-MAY-2002; 10-APR-2003 25-JUN-2002  $egin{array}{c} egin{array}{c} \egin{array}{c} \egin{array}{c} \egin{array}{c} \egin{array}{c} \egin{array}{c} \egin{array}$ 

A, Shenoy SG; Berghs C, Dipippo VA; Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UW; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

(CURA-) CURAGEN CORP.

WPI; 2003-381626/36. N-PSDB; ADA05733

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Gaps

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obesity, New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing pharmacogenomics.

Claim 1; Page 170; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector

comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aborrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide, (12) a method for modulating the activity or the polypeptide described above; (13) methods of treating or pathology associated with the above polypeptide. Novx equences have antidiabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, noctropic, neuroprotective, antiparkinsonian corrections associated with a human disease. The polypeptide or the nucleic syndrome associated with a human disease. The polypeptide or prevent metabolic corrections, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's cidisease immune disorders, haematopoletic disorders and various corrections, inchromosome mapphing, tissue typing, preventive medicine and cypoletic acids can also be used as hybridisation corrections, themselves and cold sorders and antipartice. The present sequence represents a human NoVX from the consent inchromes and acids can also be used to be properticed as the propertice. present invention 8899999999999999999999999999

Sequence 252 AA;

Gарв ; 0 100.0%; Score 50; DB 6; Length 252; 100.0%; Pred. No. 2.7; o; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 9; Conservative

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1 GPLVCRGTL 9

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206 GPLVCRGTL 214

Search completed: March 11, 2006, 00:24:16 Job time : 86.6667 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March 11, 2006, 00:24:40; Search time 14.1111 Seconds (without alignments) 61.367 Million cell updates/sec Run on:

US-09-905-083A-80 50 1 GPLVCRGTL 9 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\*
1: pir1:\*
3: pir2:\*
5: pir3:\*
7: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S	Description	serine proteinase	semenogelase (BC 3	tissue kallikrein	probable aminoglyc	hypothetical prote	tissue kallikrein		semenogelase (EC 3	glandular kallikre	tissue kallikrein			tissue kallikrein	probable serine pr	111	ည <u>ှ</u>	trypsin (EC 3.4.21		kallikrein, glandu	chymotrypsin-like	~	_		tissue kallikrein	neuropsin - mouse	tissue kallikrein	7S nerve growth fa	tissue kallikrein	tissue kallikrein
SUMMARIES	ΙD	A53968	A32297	A29586	T35999	G72548	KQRTP	DBHO	835711	I49416	A05308	S15395	B23863	B32340	845356	A27207	S39047	S39048	A44284	S15685	835585	156220	KORTTN	A29746	D23863	156559	KQMS1	NGMSG	TRMSM5	S45303
	DB	2	-	~	7	~	-	Н	-	~	~	~	~	~	~	7	ď	7	~	N	~	N	7	~	~	N	-	-	Н	7
	Query Match Length	253	261	261	262	155	265	246	261	46	96	104	156	188	225	239	240	241	244	250	254	258	259	259	259	260	261	261	261	261
	Query Match	100.0	80.0	80.0	80.0	78.0	78.0	76.0	76.0	74.0	•	74.0	74.0	•	74.0	٠	74.0	74.0	74.0	74.0	74.0	74.0		74.0	•	•			74.0	74.0
	Score	50	40	40	40	39	39	38	38	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37
	Regult No.		8	m	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

gamma-renin (EC 3.	tissue kallikrein	granzyme 3 (EC 3.4	riboflavin biosynt	kallikrein - mouse	elastase (EC 3.4.2	tissue kallikrein	duodenase - bovine	EC 3	trypsin (EC 3.4.21	EC 3	snake venom factor				
A28062	A25606	S01971	A29745	A34079	S15686	865663	T12994	152972	S44462	KOMSM	869370	TRDFS	TRPGTR	S31778	A32121
~	~	ď	~	~	~	7	~	~	~	7	~	-	-	~	-
261	261	261	261	261	263	264	599	99	73	149	226	229	231	231	236
74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	72.0	72.0	72.0	72.0	72.0	72.0	72.0	72.0
37	37	37	37	37	37	37	37	36	36	36	36	36	36	36	36
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1
A53968
serine proteinase SCCE precursor - human
N;Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C,Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53968
R; Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A,Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A; Reference number: A53968; MUID: 94308225; PMID: 8034709
A;Accession: A53968
A;Status: preliminary
A, Molecule type: mRNA
A;Residues: 1-253 <han></han>
A; Cross-references: UNIPROT: P49862; UNIPARC: UP10000001BC4; GB:L33404; NID: 9521214; PIDN: P
C, Genetics:
A;Gene: GDB:PRSS6; SCCE
A;Cross-references: GDB:377730
A;Map position: 7g35-7g35
C; Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology <try></try>
Query Match 100.0%; Score 50; DB 2; Length 253;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPLVCRGTL 9
Db 207 GPLVCRGTL 215
RESULT 2

Alternate names: gamma-seminoprotein; P-30 antigated] - human
N;Alternate names: gamma-seminoprotein; P-30 antigan; prostate-specific antigen; prostate
C;Species: Homo sapalens (man)
C;Date: 19-May-2000 #sequence revision 19-May-2000 #text change 09-Jul-2004
C;Accession: A32297; A32423; \$03604; \$05468; \$05467; A32546; \$02239; A26757; C31567; A315
R;Riegman, P.H.J; Vlatestrar, R.J.; van der Korput, J.A.G.M.; Romijn, J.C.; Trapman, J.
B;Ochem. B;Ophys. Res. Commun. 159; 95-102, 1989
A;Title: Characterization of the prostate-specific antigen gene: a novel human kallikreir
A;Reference number: A32297; MUID:89165891; PMID:2466464
A;Residues: preliminary
A;Residues: 1-261 < RIS
A;Residues: 1-261 < RIS
A;Coss-references: UNIPROT:P07288; UNIPARC:UPI0000001C9E; GB:M24543
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B;Coss-references: UNIPROT:P07288; UNIPARC:UPI000001C9E; GB:M24543
A;Reference mumber: A32423; MUID:89302090; PMID:2472789

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Rjwatt, K.W.K.; Lee, P.J.; M'Timkulu, T.; Chan, W.P.; Loor, R.
Proc. Natl. Acad. Sci. U.S.A. 83, 3166-3170, 1986
A,Title: Human prostate-specific antigen: structural and functional similarity with serir
A,Reference number: A23937; MUID:86205857; PMID:2422647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: G01551
A;Status: translated from GB/EMBL/DDBJ
A;Oblocule type: mRNA
A;Nolcule type: mRNA
A;Residues: 1-261 <MOR>
A;Residues: 1-261 <MOR>
A;Cross-references: UNIPARC:UPI000001C9E; EMBL:U17040; NID:g595945; PIDN:AAA56764.1; PII
R;Monne, M.; Croce, C.M.; Yu, H.; Diamandis, B.P.
Cancer Res. 54, 6344-6347, 1994
A;Title: Molecular characterization of prostate-specific antigen messenger RNA expressed
A;Reference number: 152712; MUID:95079406; PMID:7527295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: mRNA
A;Readidus: 'PGATHIFBESCUT',1-176 <RES>
A;Cross-references: UNIPARC:UP1000016B467; GB:S75755; NID:g861469; PIDN:AAD14185.1; PID:g
R;Christensson, A.; Lilja, H.
Bur. J. Blochen. 220, 45-53, 1994
A;Title: Complex formation between protein C inhibitor and prostate-specific antigen in NA;Reference number: 841212; MUID:94164172; PMID:7509746
A;Title: Isolation, characterization and amino-acid sequence of gamma-seminoprotein, A;Reference number: S00232; MUID:88082806; PMID:3691515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A23937
A;Molecule type: protein
A;Residues: 25-99.'T', 95-164,'HL',166,'YDQM',169-174,'Q',176-261 <WAT>
A;Cross-references: UNIPARC:UP10000172AC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: protein
A,Residues: 25-30,'X',32-49 <CHR>
A;Cross-references: UNIPARC:UPI0000172AC7
C;Comment: This enzyme preferentially cleaves after tyrosine residues.
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A/Cross-references: GDB:119695; OMIM:176820
A/Cross-references: GDB:119695; OMIM:176820
A/AND POSITION: 19413.3-19413.3-1943.3
A/Introns: 16/1; 69/2; 165/1; 210/3
C/Superfamily: trypsin; trypsin; homology
C/Superfamily: trypsin; trypsin; homology
C/Superfamily: trypsin; hydrolase; prostate; serine proteinase
F;1-17/Domain: signal sequence #status predicted <SIG>F;18-24/Domain: propeptide #status predicted <PRO>
F;25-261/Product: semenogelase #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.0%; Score 40; DB 1; Length 261; 77.8%; Pred. No. 6.2; 2; Indels ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;25-253/Domain: trypsin_homology <TRY>
F;65,120,213/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Moreno, J.M. submitted to the EMBL Data Library, November 1994
                                                                                                                            A;Molecule type: protein
A;Residues: 25-261 <SC2>
A;Cross-references: UNIPARC:UPI0000347FB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 GPĽVČNGVĽ 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: G07735
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                                                                                                 A; Accession: S00232
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R; Henttu, P.; Vihko, P.
B; Henttu, P.; State, P.; MID:89246551; PMID:2470373
B; Reference number: A32546
B; Molecule type: mRNA
B; Residues: 1-72, T', 74-85, I', 87-174, P', 176-183, Q', 185-259, D', 261 < HEN>
B; Cross-references: UNIPARC: HEID1000172AC4; GB:M2663
B; Schulz, P.; Stucka, R.; Feldmann, H.; Combriato, G.; Klobeck, H.G.; Fittler, F.
Nucleic Acids Res. 16, 6226, 1988
B; MUD:88289366; PMID:2456523
B; Accession: S02239; MUD:88289366; PMID:2456523
                                                                                                                            A;Residues: 1-261 <LUN>
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A;Cross-references: UNIPARC:UPI000001C9E; GB:M27274; NID:g190552; PIDN:AAA60192.1; PID:
B;Cligby, M.; Zhang, X.Y.; Richards, R.I.
Nucleic Res. 17, 77, 1989
A;Title: Human prostate specific antigen (PSA) gene: structure and linkage to the kallik
A;Reference number: S03604; MUID:89183632; PMID:2467258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPARC:UPI000001C9E; EMBL:X14810; NID:g35732; PIDN:CAA32915.1; PID R;Klobeck, H.G.; Combriato, G.; Schulz, P.; Arbusow, V.; Fittler, F. Wucleic Acids Res. 17, 3981, 1989
A;Title: Genomic sequence of human prostate specific antigen (PSA).
A;Reference number: S05467; MUID:89282407; PMID:2471958
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A,Residues: 5-261 <RI2>
A,Crose-references: UNIPARC:UPI000000448; GB:M21895; NID:g189523; PIDN:AAAS9995.1; PID:
A,Note: the authors translated the codon GGC for residue 28 as Arg and TGG for residue 2
A,Accession: A31567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: mRNA
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A,Residues: 5-164, 'CTBGPDGAAGSPDAWV' <R14>
A,Cross-references: UNIPARC:UP1000006F4E5; GB:M21897; NID:g189529; PIDN:AAAS9997.1; PID.
A,Note: the authors translated the codon GGC for residue 28 as Arg, TGG for residue 29 s.
R,Schaller, J.; Akiyama, K.; Tsuda, R.; Hara, M.; Marti, T.; Rickli, E.E.
Eur. J. Blochem. 170, 111-120, 1987
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*Residues: 5-10; WVILITELTMPA',223,'PWVLHGSLV',233,'WRGGV' <R13>
A; Cross-references: UNIPARC:UP1000006EF4F; GB:M21896; NID:g189525; PIDN:AAA59996.1; PID
A; Note: the authors translated the codon GGC for residue 28 as Arg and TGG for residue
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R;Riegman, P.H.J.; Klaassen, P.; van der Korput, J.A.G.M.; Romijn, J.C.; Trapman, Biochem. Biophys. Res. Commun. 155, 181-188, 1988
AjTitle: Molecular cloning and characterization of novel prostate antigen cDNA's. A;Reference number: A90144; MUID:88326297; PMID:2458104
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A; Residues: 17-63, Tr, 65-135, M', 137-261 <SCH>
A; Cross-references: UNIPARC: UP10000172AC5, EMBL: X07730
A; Lundwall, A.; Lilja, H.
FEBS Lett. 214, 317-322, 1987
A; Title: Molecular cloning of human prostate specific antigen cDNA.
A; Reference number: A26757; MUD: 87190978; PMID: 2436946
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-261 <DIG>
A; Residues: 1-261 <DIG>
A; Crosa-references: UNIPARC: UPI0000001C9E; EMBL: X13940
B; Klobeck, H.G.; Combriato, G.; Schulz, P.; Arbusow, V.; Fittler, submitted to the EMBL Data Library, May 1989
A; Reference number: 805468
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A; Residues: 5-261 <LU2>
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A; Residues: 1-29 <KL2>
                                                     A;Status: preliminary
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.Kato, H.; Nakanishi, E.; Enjyoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
Blochka. 102, 1389-1404, 1387
Title: Characterization of serine proteinases isolated from rat submaxillary gland: wit
Reference number: A41429; MUID:88198057; PMID:3482210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerald, W.L.; Chao, J.; Chao, L.
occhim. Biophys. Acta 866, 1-14, 1986
Title: Immunological identification of rat tissue kallikrein cDNA and characterization
Reference number: A25137, MID:86131678; PMID:3004582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inoue, H.; Fukui, K.; Miyake, Y.
Blochem. 105, 834-840, 1989
Title: Identification and structure of the rat true tissue kallikrein gene expressed ir
Reference number: JX0073; MUID:89327211; PMID:2753879
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Experimental source: kidney
Ashley, P.L.; MacDonald, R.J.
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;Molecule type: mRNA;
;Mosidues: 1.265 <ASH>;
;Crossinces: 1.265 <ASH>;
;Crossinces: 1.265 <ASH>;
;Crossinces: UNIPARC:UDI0000167958; GB:M11563; NID:g205029; PIDN:AAA41464.1; PID:ç
;Experimental source: submaxillary gland;
;Mines, D.R.; Brady, J.M.; Pritchett, D.B.; Roberts, J.L.; MacDonald, R.J.
;Mines, D.R.; Brady, J.M.; Pritchett, D.B.; Roberts, J.L.; MacDonald, R.J.
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A, Residues: 5-265 cWIN>
A, Cross-references: UNIPARC:UPI000012DEE1; GB:M23874; GB:J04701; GB:M23875; GB:M23876; NJ
C, Comment: The kallikreins liberate lysyl-bradykinin, a vasoactive decapeptide, from kinj
C, Comment: The protein presumably assumes the two-chain form by cleavage between residues
C; Comment: The protein cleave Met-Lys and Arg-Ser bonds in kininogen to release l}
                                                                                                                                                                                                                                  Visite kallikrein (EC 3.4.21.35) precursor - rat
NyAlternate names: glandular kallikrein; kininogenin; true tissue kallikrein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Apr-1983 #sequence revision 05-Apr-1983 #text change 09-Jul-2004
C;Accession: A00944; A41429; A25137; JX0073; A23863; A33359
C;Accession: A00944; A41429; A25137; JX0073; A23863; A33359
Broc. Natl. Acad. Sci. U.S.A. 79, 7263-7267, 1982
A;Title: Rat pancreatic kallikrein mRNA: nuclectide sequence and amino acid sequence of A;Reference number: A00944; MUID:83117659; PMID:6961406
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Title: Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of
Reference number: A23863, MUID:86051477, PMID:2998455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Experimental source: pancreatic
Kato, H.; Nakanishi, E.; Enjyoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga,
Biochem. 102, 1389-1404, 1987
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C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; serine proteinase; zymogen
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Residues: 1-265 <SWI>.
Cross-references: UNIPROT:P00758; UNIPARC:UPI0000167958
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Kolecule type: protein
Residues: 29-53,7x,55-87 <KAT>
Cross-references: UNIPARC:UP10000172ABF
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Residues: 115-265 <GER>
Cross-references: UNIPARC:UP10000172AC0
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23 GPLITRGTL 31
          1 GPLVCRGTL
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Residues: 1-265 <INO>
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C;Date: 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G72549
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawarabayasi, S.; Jill, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: A29586
A;Molecule type: DNA
A;Residues: 1-261 <SCH>
A;Cross-references: UNIPROT:P20151; UNIPARC:UPI000004CA0C; GB:M18157; NID:9186640; PIDN:
A;Note: the authors translated the codon TAC for residue 43 as Trp
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Experimental source: strain A3(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable aminoglycoside acetyltransferase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T35999
R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
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Superfamily: Escherichia coli aminoglycoside N3'-acetyltransferase
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0
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Pred, No. 6;
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                                                                                              A;Cross-references: UNIPROT:P20151; UNIPARC:UPIUUUU4cAuu; A;Oross-references: translated the codon TAC for residue 4:CGenetics:
A;Nutcons: 16/1; 69/2; 165/1; 210/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;25-253/Domain: trypsin homology <TRY>
F;65-120,213/Active site: His, Asp, Ser #status predicted
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Pred. No. 6.3;
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0; Mismatches
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Best Local Similarity 77.8%;
Matches 7; Conservative 1
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nes 7; Conservative
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A;Accession: T35999
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Best Local Similarity
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NyAlternate names gamma-seminoprotein; Pisous macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Species: Macaca mulatta (rhesus macaque)
C;Species: Macaca mulatta (rhesus macaque)
C;Species: May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: S35711; S34239
R;Gauthier, E.R.; Chapdelaine, P.; Tremblay, R.R.; Dube, J.Y.
B;Cothim. Biophys. Acta 1174, 207-210, 1993
A;Ritle: Characterization of rhesus monkey prostate specific antigen cDNA.
A;Reference number: S35711
A;Nolecule type: mRNA
A;Residues: 1-261 <GAU>A;Cossion: S35711
A;MulD:93363642; PMID:7689340
A;Accession: S35711
A;Residues: 1-261 <GAU>A;Cossion: S35711
A;Residues: 1-261 <GAU>A;Cossion: This enzyme preferentially cleaves after tyrosine residues.
C;Comment: This enzyme preferentially cleaves after tyrosine residues.
C;Comment: This enzyme preferentially cleaves after tyrosine residues.
C;Superfamily: trypsin; trypsin homology
C;Reywords: glycoprotein; hydrolase; prostate; serine proteinase
F;1-17/Domain: signal sequence #status predicted <RIO>F;Reywords: Glycoprotein; hydrolase; prostate; serine proteinase
F;1-17/Domain: signal sequence #status predicted <AIO>F;25-261/Product: semenogelase #status predicted <MAT>F;25-251/Product: semenogelase #status predicted <MAT>F;65,120,213/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glandular kallikrein - western wild mouse (fragment)
C;Species: Mus spretus (western wild mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49416
R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H. Mamm. Genome 5, 349-355, 1994
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A;Reference number: I48934; MUID:94319082; PMID:8043949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:062540; UNIPARC:UPI00000E8743; EMBL:U05716; NID:g497047; PIDR C;Superfamily: trypsin; trypsin homology
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N;Alternate names: glandular kallikrein
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 22-Jun-1999
C;Accession: A05308
R;Mason, A.J.; Evans, B.A.; Cox, D.R.; Shine, J.; Richards, R.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 4.6;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                           semenogelase (EC 3.4.21.77) precursor - rhesus macaque
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Conservative
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Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                203 ĠPĽVĊGĠVĽ 211
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Matches 7; Conserv
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A; Residues: 19-44, 'G', 46-51, 'Q', 53-75, 'TH', 78, 'P', 80-83, 'XXXITIE', 90-172, 86-91, 185-235,'
A; Residues: 19-44, 'G', 46-51, 'Q', 53-75, 'TH', 78, 'P', 80-83, 'XXXITIE', 90-172, 86-91, 185-235,'
A; Cross-references: UNIPARC: UPI0000172AE5
A; Note: a few residues were assigned from the previously published sequence of Reid et a
R; Miyata, T; Oda, O; Inagi, R; Sugiyama, S; Miyama, A; Maeda, K; Nakashima, I; Ya
A): Inagi, R; Sugiyama, S; Miyama, A; Maeda, R; Nakashima, I; Ya
A; Title: Molecular and functional identification and purification of complement component
A; Reference number: A60571; MUID: 90370044; PMID: 2395435
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A; Regidues: 19-20,'XX',23-27,'XX',30-31,'XX',34,'X',36-40 <MIY>
A; Regidues: 19-20,'XX',23-27,'XX',30-31,'XX',34,'X',36-40 <MIY>
A; Cross-references: UNIPARC:UPI0000122ABG
R; Balke, N.; Holtkamp, U.; Hoerl, W.H.; Tschesche, H.
FEBS Lett. 371, 300-302, 1995
A; Title: Inhibition of degranulation of human polymorphonuclear leukocytes by complement
A; Reference number: 866645; MUID:96013156; PMID:7556615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement factor D (EC 3.4.21.46) precursor [validated] - human (fragment)
NyAlternate names: adipsin; C3 convertase activator
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A40197, A00936, A60511; 866645
R;White, R.T.; Damm, D.; Hancock, N.; Rosen, B.S.; Lowell, B.B.; Usher, P.; Flier, J.S.; A;White: Human adipsin is identical to complement factor D and is expressed at high leve
A;Reference number: A40197; WUID:92250520; PMID:1374388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 19-44,'C',46-48 <BAL>
A;Cross-raferences: UNIPARC:UPI0000172AE7
C;Comment: Factor D cleaves factor B when the latter is complexed with factor C3b, activ
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C; Superfamily: trypsin; trypsin homology
C; Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase
P;1-18/Domain: signal sequence #status predicted <SIG>
F;19-246/Product: complement factor D (fragment) #status experimental <MAT>
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A;Reference number: A00936; MUID:85000441; PMID:6383466
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-28/Domain: activation peptide #status predicted <APT>
F;29-265/Product: tissue kallikrein, pancreatic #status predicted <MPT>
F;29-257/Domain: trypsin homology <IRY>
F;35-177,54-70,156-223,188-202,213-238/Disulfide bonds: #status predicted
F;59,124,217/Active site: His, Asp, Ser #status predicted
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A;Residues: 1-246 <WHI>
A;Cross-references: UNIPROT:P00746; UNIPARC:UPI0000172AE4; GB:M84526
R;Niemann, M.A.; Bhown, A.S.; Bennett, J.C.; Volanakis, J.E.
Biochemistry 23, 2482-2486, 1984
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;44-60,141-207,172-188,197-222/Disulfide bonds: #status predicted
;59,105,201/Active site: His, Asp, Ser #status predicted
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Pred. No. 14;
                                                                                                                                                                                                                                                                Score 39; DB 1; Length 265;
Pred. No. 9.7;
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A;Cross-references: GDB:132645; OMIM:134350
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66.7%;
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Local Similarity 77.8%;
hes 7; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-148/Domain: trypsin homology (fragment) <TRY>
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66.7%;
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Best Local Similarity 66.7
Matches 6; Conservative
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Matches 6; Conserv
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A; Residues: 1-188 <SHA>
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B21863
Itistace kallikrein (EC 3.4.21.35) S1, submaxillary - rat (fragment)
N.Alternate names: glandular kallikrein; kininogenin
C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus
C.Socossion: B23863
R;Ashley, P.L.; MacDonald, R.J.
Biochemietry 24, 4512-4520, 1988
A;Accession: Ralikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of A;Reference number: A23863; MUID:86051477; PMID:2998455
A;Accession: B23863
A;Molecule type: mRNA
A;Neletrences: UNIPROF:P15950; UNIPARC:UPI00001709DD; GB:M11564; NID:g205031; PIDN:
                                                                             A, Accession: A05308
A, Molecule type: DNA
A, Rolecule type: DNA
A, Ross-references: UNIPARC:UPI000011E01B; GB:V00829; NID:g52775; PIDN:CAA24212.1; PID:g
A, Experimental source: Quakenbush inbred strain
A, Experimental source: Quakenbush inbred strain
C;Comment: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to releas
C;Genetics:
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A;Molecule type: protein
A;Residues: 1-23;24-51;52-104 cgUT>
A;Cross-references: UNIPARC:UPI0000175BEB; UNIPARC:UPI0000175BEB; UNIPARC:UPI0000175BEB
A;Experimental source: submaxillary gland
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-104/Domain: trypsin homology (fragments) <TRY>
F;1-104/Domain: trypsin homology (fragments) <TRY>
F;1-104/Domain: trypsin homology (fragment) #status exp
F;2-23/Product: tissue kallikrein-related protein kl0 heavy chain (fragment) #status exp
F;52-104/Product: tissue kallikrein-related protein kl0 heavy chain (fragment) #status exp
F;52-104/Product: tissue kallikrein-related protein kl0 heavy chain (fragment) #status exp
Nature 303, 300-307, 1983
A;Title: Structure of mouse kallikrein gene family suggests a role in specific processin
A;Reference number: A00941; MUID:83219214; PMID:6602295
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C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; saliva; serine proteinase; submandibular gland
F;1-88/Domain: trypsin homology (fragment) <TRY>
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Cissos
Ratlikrein-related proteinase (EC 3.4.21.-) kl0 - rat (fragments)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: 18-Feb-1994 #sequence_revision 19-Jul-1996 #text_change 17-Oct-1997
Cispecession: 51395; S15448
Riduman, N.; Elmoujahed, A.; Brillard, M.; Monegier du Sorbier, B.; Gauthier, F. Bur. J. Biochem. 197, 425-429, 1991
A; Fitle: Miscohetersogeneity of rat submaxillary gland kallikrein kl0, a member of tA; Reference number: S15395; MUID:91224135; PMID:2026164
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C.Species: Nature norvegicus (Norway rat)
C.Date: 22-Nov-1989 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C.Date: 22-Nov-1989 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C.Accession: B32340
R.Shai, S.Y.; Woodley-Miller, C.; Chao, J.; Chao, L.
Biocohemistry 28, 5334-5343, 1989
A,Title: Characterization of genes encoding rat tonin and a kallikrein-like serine protes
A,Reference number: A32340; MUID:89375248; PMID:2550051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P15950; UNIPARC:UP10000170B08; GB:M26534; NID:g206773; PIDN:
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A;Cross-references: UNIPARC:UPI000016AFB3; EMBL:X75363; NID:g407137; PIDN:CAA53145.1; PII
A;Experimental source: Alzheimer's disease patient brain cortex
C;Genetics:
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C;Species: Homo sapiens (man)
C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 19-May-2000
C;Accession: S45356
R;Dihanich, M.; Spiess, M.
Biochim. Biophys. Acta 12.18, 225-228, 1994
A;Title: A novel serine proteinase-like sequence from human brain.
A;Reference number: S45356; MUID:94289486; PMID:8018728
A;Accession: S45356
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Pred. No. 17;
                                                                 Indels
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C;Keywords: hydrolase; serine proteinase
F;1-180/Domain: trypsin homology (fragment) <TRY>
Score 37; DB 2
Pred. No. 14;
1; Mismatches
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tissue kallikrein (EC 3.4.21.35), prostatic - guinea pig
NyAlternate names: glandular kallikrein
C;Species: Cavia porcellula (guinea pig)
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 09-Jul-2004
C;Accession: A27207
R;Dunbar, J.C.; Baradshaw, R.A.
Biochemistry 26, 3471-3478, 1987
A;Title: Amino acid sequence of guinea pig prostate kallikrein.
A;Reference number: A27207; MUID:88000549; PMID:3307909
A;Accession: A27207
A;Residues: 1-239 *CUNA
A;Cross-references: UNIPROT:P12323; UNIPARC:UPI000012DEE2
A;Cross-references: UNIPROT:P12323; UNIPARC:UPI000012DEE2
A;Note: 50-Trp was also found
C;Superfamily: trypsin; trypsin; homology
C;Keywords: hydrolase; serine proteinase
F;1-231/Domain: trypsin; homology 

C;Superfamily: trypsin; homology 

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Search completed: March 11, 2006, 00:40:51 Job time : 14.1111 secs

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Q63z11 xenopus lae
Q90q3 homo sapien
Q9q78 mus musculu
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Q94311 bifidobacte
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Q9f83 micromonosp
Q9f83 anopheles g
Q8nos sapien
Q6qyj5 struthio ca
C6myj5 struthio ca
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Q7q23 anopheles g
Q61d83 homo sapien
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09CYM3 MOUSE
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08G311 B1FLO
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262 2 Q9XAC9 STRCO 619 2 Q8KEH3_CHLJE 1155 2 Q9YBC2_ABRPE 1161 2 Q5YBC2_ABRPE 1176 2 Q5ZQ15_9PBRC 214 2 Q4SSW0_TETNG 247 2 Q9WTQ5_PAROL 249 2 Q5W9T9_TRNTR 249 2 Q5W9T9_TRNTR 249 2 Q5W9T8_XENTR 250 2 Q5W9T8_XENTR 251 2 Q5W9T8_XENTR 252 2 Q5W9T8_XENTR 253 2 Q5W9T8_XENTR 254 2 Q5W9T8_XENTR 255 2 Q5W9T8_XENTR 256 1 KIKL RAT 257 2 Q5W9T8_XENTR 257 2 Q5W9T8_XENTR	GNWEN  ( ) 1  ( ) 1  ( ) ( ) ( ) ( ) ( ) ( ) ( ) ( ) ( ) (	ilarity 100.0%; Score 50; DB 2; Len Conservative 0; Mismatches 0; I IVCRGTL 9  [LVCRGTL 9]  [
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MEDLINE-2238825; PubMede-12477932; DOI=10.1073/pnas.242603899; MEDLINE-2238825; PubMede-12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Stuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Astachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Astachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L., Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M.J., Uddin T.B., Toshiyuki S., Abramson R.D., Mullahy S.J., Brands S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., M. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Metterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., M. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones B., Jones C., Mander B., Jones C., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones B., Jones C., Mander B., Jones C., Jones C., Jones C., Jones C., Jones C., Sherrard, M., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones B., Jones C., Sherrard, M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones C., Jon
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic enzyme is a new member of the human kallikrein gene family - genomic characterization, mapping, tissue expression and hormonal
                                                                                                                   23-53
                                                                                                                                                                                                   Hansson L., Stroemgvist M., Baeckman A., Wallbrandt P., Carlstein A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22623266; PubMed=12738725;
Dong Y., Kaushal A., Brattsand M., Nicklin J., Clements J.A.;
"Differential splicing of KLKs and KLK7 in epithelial ovarian cancer
produces novel variants with potential as cancer biomarkers.";
Clin. Cancer Res. 9:1710-1720(2003).
                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hansson L., Baeckman A., Ny A., Edlund M., Edholm E., Tornell J., Wallbrandt P., Egelrud T., Eglund M., Edholm E., Tornell J., "Epidermal overagression of Exratum corneum chymotryptic enzyme in mice; a model for chronic thchy dermatitis."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [5]
NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION,
AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
Moss P., Paeper B., Wang K.;
                                                                                                                NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region."; Gene 257:119-130(2000).
                                                                                                                                                                                                                              Egelrud T.; "Cloning, expression, and characterization of stratum corneum "Cloning, expression, a skin-specific human serine proteinase."; J. Biol. Chem. 269:19420-19426(1994).
                                                                                                                                                                                                                                                                                                                                                                                                    TISSUB=Keratinocyte;
PubMed=10974542; DOI=10.1016/S0378-1119(00)00280-8;
Yousef G.M., Scorilas A., Magklara A., Soosaipillai A.,
Diamandis B.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [GENOMIC DNA]
                                                                                                                                                                      MEDLINE=94308225; PubMed=8034709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Ovarian carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 254:119-128(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [7]
CHARACTERIZATION
                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regulation.";
                                                                                                                                              rissum=Skin;
Berrar be
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                                                              Isolde-19862-2; Sequence=vSP_013581;
TISSUE SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermis. Also expressed in the brain, mammary gland, cerebellum, spinal cord and kidney. Lower levels in salivary glands, uterus, thymus, thyroid, placenta, trachea and testis. Up-regulated in ovarian carcinoma, especially late-stage serous carcinoma, compared with normal ovaries and benign adenomas (at the protein level).

INDUCTION: By estrogens and glucocorticoids in a breast carcinoma
          Skytt A., Stroemgvist M., Egelrud T., "Primary substrate specificity of recombinant human stratum corneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
similarity).
similarity).
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp. SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
Alternative splicing; Direct protein sequencing; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the peptidase SI family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0008236; F:serine-type peptidase activity; TAS. GO; GO:0008544; P:epidermis development; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease; Signal; Zymogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Activation peptide.
Kallikrein 7.
Peptidase Si.
Charge relay system (i
                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing, Named isoforms=2;
Name=1; Synonyms=Long;
IsoId=P49862-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 peptidase S1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0008544; P:epidermis development; TAS.
InterPro; IPR001254; Peptidase S1_S6.
InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AF166330, AAD49718.1; -; Genomic_DNA.
EMBL, AF243527; AAG3360.1; -; Genomic_DNA.
EMBL, AF31254; AAK69624.1; -; Genomic_DNA.
EMBL, AF411214; AAN03662.1; -; mRNA.
EMBL, BC032005; AAH32005.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; S01.300; -.
Ensembl; ENSG00000169035; Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L33404; AAC37551.1; -; mRNA.
MEDLINE=95314630; PubMed=7794273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=2; Synonyme=Short;
                                                                                                                                                                                                                                                                                                                                                    invasive front.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H-InvDB; HIX0015373; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGNC; HGNC:6368; KLK7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A53968; A53968.
HSSP; P00760; 1EZX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell line.
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ACT SITE
ACT SITE
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us-09-905-083a-80.rup

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DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                        removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yousef G.M., Diamandis E.P.;
"The expanded human Kallikrein gene family: locus characterization and molecular cloning of a new member, KLK-L3.";
Genomics 65:184-194(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pubmed=15057824; DOI=10.1038/nature02399;
Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J., Gordon L.A., Olsen A.S., Terry A., Schmutz J., Gordon L.A., Ashwartan D., Couronne O., Tran-Gyamfi M., Aerts A., Altherr M., Ashwarth L., Bajorek E., Black S., Branscomb E., Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M., Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Detter J.C., Georgescu A.M., Flowers D., Fotopulos D., Garcia C., Georgescu A.M., Glavina T., Gomez M., Gorzales E., Groza M., Hammon N., Hawkins T., Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H., Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S., Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J., Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M., Popkie A.P., Predki P., Rash S., Retterer J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last amoutation update)
Kallikrein 9 precursor (EC 3.4.21.-) (Kallikrein-like protein 3) (KLK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20118156; PubMed=10652563;
Yousef G.M., Luo L.-Y., Diamandis E.P.;
"Identification of novel human kallikrein-like genes on chromosome
  .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6; Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J. Moss P., Paeper B., Wang K.; Squencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";
                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20247258; PubMed=10783266; DOI=10.1006/geno.2000.6159;
              By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
Missing (in isoform 2).
FIId=VSP 013881.
C -> W (in Ref. 6; AAH32005).
W; 2D68B6B15A76A668 CRC64;
                                                                                                                                                                                                                                           100.0%; Score 50; DB 1; Length 253, 100.0%; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                   0; Indels
N-linked (GlcNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [4]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 AA.
                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19q13.3-q13.4.";
Anticancer Res. 19:2843-2852(1999)
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NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                     27525 MW;
                                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 257:119-130(2000).
  246
137
71
211
211
226
239
72
                                                                                                                                                                                                                                                                                                                                                      207 GPLVCRGTL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                           1 GPLVCRGTL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                     253 AA;
                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLK9 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=KLK9;
                DISULPID
DISULPID
DISULPID
                                                                                                DISULFID
DISULFID
VARSPLIC
                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                           Query Match
CARBOHYD
                                                                             DISULFID
                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gauk<u>ō</u>9;
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
KLK9_HUMAN
                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HERE REARES REPORTED TO THE PROPERTY OF THE PR
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Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D., Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A., Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I., Verrey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E., Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M., Rubin E.M., Lucas S.M., "The DNA sequence and biology of human chromosome 19.";

"The DNA sequence and biology of human chromosome 19.";

"INSUER AIS:529-535(2004).

-! SUBCELLULAR LOCATION: Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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(By similarity).
(By similarity).
) (Potential).
) (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00089; Trypain; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
MARRY; SM0020; Tryp SPc; 1.
PROSITE; PS50240; TryPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
Glycoprotein; Hydrolase; Protease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
InterPro; IPR001254; Peptidase 31 S6.
InterPro; IPR001314; Peptidase $\frac{1}{2}\frac\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2
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Charge relay system (I
Charge relay system (I
Charge relay system (I
N-linked (GlCNAC...
N-linked (GlCNAC...
N-linked (GlCNAC...
By similarity.
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OSDBOB MOUSE PRELIMINARY, PRT; 251 AA.
OSDBOB;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 1 peptidase S1 domain.
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Pred. No. 2.5;
0; Mismatches
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EMBL, AF24527; AAG33362.1; -; Genomic_DNA.
EMBL, AC011473; AAG23255.1; -; Genomic_DNA.
HSSP; P00746; 1FDP.
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Kallikrein 9.
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Ensembl; ENSG00000129455; Homo sapiens.
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Best Local Similarity
Matches 8; Conserv
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/3505500;

A RATAWA J., Shihadawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsud H.A., Ashburner M., Batalov G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fullita M., Mariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nacholia K., Vang K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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A Shibate K. Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Abibate K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Anibate K., Itoh M., Hazawa K., Nagaoka S., Sasaki N., Carninci P., A Ronno H., Akipama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishli Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., A Pujwake S., Inoue K., Izawa M., Ohara B., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RIGA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Lung;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
Hanalysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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MEDILINE=20499314; PUNed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M.,

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes.";

Genome Res. 10:1617-1630(2000).
Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200016C12 product:similar to KALLIKREIN 9 (EC 3.4.21.-) (KALLIKREIN-LIKE PROTEIN 3) (KIK- L3).
                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUB=Lung;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 409:685-690(2001).
                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                            [1] -
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
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NUCLEOTIDE SEQUENCE
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                                                                                                                   Name=1200016C12R1k;
                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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CTRAIN-CSTBL/GST. TISSUE=Lung;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatau N., Hiramoto K., Hiraoka T., Hori F.,
M. Managaki T., Hara Y., Kono M., Koya S., Kurihara C.,
M. Kayai J., Kojima Y., Konono H., Kouda M., Koya S., Kurihara C.,
M. Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata K., Shinagawa A., Shiraki T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
M. Tojam Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
M. Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

R. EMBL, AKO04607; BAB23579-1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Eye,
MEDLINE=22380E57; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gарв
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Skaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinee; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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88.9%; Pred. No. 2.5;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERMY, PRO0089; TYPBAIN; 1.
PRINTS, PR00722; CHYMOTRYPSIN.
SMART; SM0020; TYPPSFC; 1.
PROSITE; PS00134; TRYPSIN DM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
SEQUENCE 251 AA; 28155 MW; F4D667F8C80C4A23 CRC64;
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Last annotation update)
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Ensembl; ENSMUSGO000047884; Mus musculus.
MGI; MGI:1921082; 12000166712Rik.
GO:0005615; C:extracellular space; TAS.
InterPro; IPR001254; Peptidase_S1_S6.
InterPro; IPR001314; Peptidase_S1&6.
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Matches 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 ĠPĽVĊEĠŤĽ 214
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Name=LOC494802;
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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"Molecular characterization, mapping, and tissue expression of KLKL6,
a hormonally regulated kallikrein-like gene.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
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10-MAY-2005 (Rel. 47, Last annotation update)
Kallikrein 14 precursor (BC 3.4.21.-) (Kallikrein-like protein 6)
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MEDLINE=21250997; PubMed=11352573; DOI=10.1006/geno.2000.6490;
Hooper J.D., Bui L.T., Rae F.K., Harvey T.J., Myers S.A.,
Ashworth L.K., Clements J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                             NUCLECTIDE SEQUENCE.

TISSUE=Eye;

A Lieln S., Gerhard D.S.;

A Lieln S., Gerhard D.S.;

A Lieln S., Gerhard D.S.;

R Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0008233; Fichymotrypsin activity; IEA.

GO; GO:0008233; Fichypsin activity; IEA.

GO; GO:0008233; Fichypsin activity; IEA.

GO; GO:0008233; Fichypsin activity; IEA.

R GO; GO:0008235; Firrypsin activity; IEA.

R InterPro; IPR00134; Peptidase_S1_S6.

InterPro; IPR00134; Peptidase_S1_S6.

R From; PR00029; Trypsin; 1.

R SMART; SM0020; Tryp SPC; 1.

R RSMART; SM0020; Tryp SPC; 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN SEX; UNKNOWN 1.

Hydrolase; Protesse; Serine protesse.

Q SEQUENCE 210 AA; 22897 WW; 7543224C2227DA35 CRC64;
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Pred. No. 3.2;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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16-OCT-2001 (Rel. 40, Last seqn
10-MAY-2005 (Rel. 47, Last anno
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Best Local Similarity 88.9%;
Matches 8; Conservative (
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AC 09P0G3;
DT 16-OCT-2001 (R
DT 16-OCT-2001 (R
DT 10-MAY-2005 (R
DE Kallikrein 14
DE Kallikrein 15
DE MOOS OS HOMO Sapiens (CO Sukaryota; Met OC HOMO.
OX NOBI_TAXID=960
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RA HOOPET J.D., E
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

Pubmed=15057824; DOI=10.1038/nature02399;

A Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,

Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,

A erts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,

Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M.,

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Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,

Robkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,

Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,

Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,

No N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,

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Punic D. M., Parkin D., Rubbs L., Rokhsar D.S., Myers R.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clements J.A.;
"Tissue-specific expression patterns and fine mapping of the human
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J. Biol. Chem. 275:37397-37406(2000).
-!- SUBCELLULAR LOCATION: Secreted (Probable).
-!- TISSUB SPECITOTY: High expression in brain, bone marrow and fetal liver. Also expressed in liver, pancreas, fetal spleen, prostate and skeletal muscle.
-!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
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R GO; GO: 0005526; F: serine-type endopeptidase activity; NAS.

R GO; GO: 0006528; P: proteolysis and peptidolysis; NAS.

R GO: GO: 0006589; P: proteolysis and peptidolysis; NAS.

InterPro; IPR001254; Peptidase_SIĀ.

R InterPro; IPR001314; Peptidase_SIĀ.

R PÉan; PF00089; Trypsin; 1.

R RNOTTS; PR00722; CHYMOTRYPSIN.

R RNOSITE; PS50240; TRYPSIN DOM; 1.

R RNOSITE; PS00134; TRYPSIN LIS; 1.

R RNOSITE; PS00135; TRYPSIN LIS; 1.

R RNOSITE; PS00135; TRYPSIN LIS; 1.

R ROSITE; PS00135; TRYPSIN SEN; 1.

R ROSITE; PS00135; TRYPSIN SEN; 1.

R PROFITE; PS00135; TRYPSIN SEN; 1.
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MEDLINE=20545474; PubMed=10969073; DOI=10.1074/jbc.M004525200;
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    -!- SIMILARITY: Contains 1 peptidase S1 domain.

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EMBL; AF283669; AAK4823.1; -; Genomic_DNA.
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Genomic_DNA.
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Ensembl; ENSG00000129437; Homo sapiens.
HGNC; HGNC:6362; KLK14.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Pred. No. 3.9;
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Wy 9087953BAFA7ED25 CRC64;
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Director MGC Project;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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   68 BY
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                                                                                                                                                                                                      88.04;
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NIH MGC Project;
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KX MEDLINE=21085660; PubMed=1127851; DOI=10.1038/35055500;

RX Awai J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

KAwai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara M., Pukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Azawa T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

M. Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havashizaki V.,

Havashizaki V.,

Havashizaki V.,
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MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
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01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Mus musculus adult male tongue cDNA, RIKEN full-length enriched
library, clone:2310081E03 product:protease, serine, 20, full insert
sequence (Mus musculus adult male tongue cDNA, RIKEN full-length
enriched library, clone:2310021N04 product:protease, serine, 20, full
insert sequence) (Fragment).
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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Pred. No. 3.9;
0; Mismatches 1; Indels
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM0020; TYP, SPC; 1.
PROSITE; PS0040; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00405; TRYPSIN SER; 1.
PROCIDE SECOND SEC
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Q9CQ78;
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Matches 8; Conservative
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Name=2310015108Rik;
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Baidarelli R., Hill D. P., Bult C., Hume D.A., Onackenbush J.,
Bandarelli R., Kannpin A., Marsdal H., Marsdal J.,
Balk G. A., Beard C. P., Epico. Chorhia C., Coother L.B., Constill L.B.,
Balk G. A., Brand C. P., Epico. Chorhia C., Coother L.B., Constill S.,
Balk G. A., Brand C., Brand C., Chorhia C., Coother L.B., Couls S.,
Balk G. Coother L.B., Coother C., Coother L.B., Couls S.,
Balk G., Coother L.B., Coother C., Coother L.B., Coother C., Cooth
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Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejama Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AKO19102; BAB31548.1; -; mRNA.
HSSP: P00760; 1EZX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Brain;
MEDLINE-2055460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
MEDLINE-2055460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
MILSUI S., Okui A., Kominami K., Uemura H., Yamagushi N.;
"CDNA cloning and tissue-specific splicing variants of mouse hippostasin/TLSP (PRSS20).";
hippostasin/TLSP (PRSS20).";
Biochim. Biophys. Acta 1494:206-210(2000).
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO16226; BAA88825.1; -; mRNA.
HSSP; P00760; 1EZX.
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PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp SPC; 1.

PROSITE; PS00134; TRYPSIN DM; 1.

PROSITE; PS00134; TRYPSIN TR; UNKNOWN 1.

PROSITE; PS00135; TRYPSIN SRE; 1.

Hydrolase; Protease; Serine protease.

SEQUENCE 249 AA; 27604 MW; F9FF9CB457D727D5 CRC64;
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87 AA; 9549 MW; B988D0CD62926EAA CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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Pred. No. 5;
1; Mismatches
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GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR001254; Peptidase_S1_S6.
InterPro; IPR001314; Peptidase_S1Ā.
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GO; GO:0005615; C:extracellular space;
InterPro; IPR001254; Peptidase_S1_S6.
Pfam; PF00089; Trypsin; 1.
SWART; SM00020; Tryp SPC; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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77.8%;
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Best Local Similarity 77.8:
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QQQYN4;
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42 GPLVCNGSL 50
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Mus musculus (Mouse)
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SEQUENCE
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NCBI_TaxID=10090;
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A Campbell C.L., Vandyke K.A., Letchworth G.J., Drolet B.S., Hanekamp T., Wilson W.C.;

Hanekamp T., Wilson W.C.;

Midgut and salivary gland transcriptomes of the arbovirus vector culcoides sonorensis (Diptera: Ceratopogonidae).";

R. Insect Mol. Biol. 14:121-136(2005).

R. BMB.; AY752846; AAV84259.1, -; MRNA.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0004295; P:regative regulation of blood coagulation; IEA.

BR GO; GO:0006089; P:procteolysis and peptidolysis; IEA.

BR CO: GO:00060819; P:procteolysis and peptidolysis; IEA.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 29, Last sequence update)
01-FBB-2005 (TrEMBLrel. 29, Last annotation update)
Hippostasin prostate type (Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310015108 product:protease, serine, 20, full insert sequence) (Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310040F07
product:protease, serine, 20, full insert sequence).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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Neoptera; Endopterygota; Diptera; Nematocera; Chironomoidea;
Ceratopogonidae; Ceratopogoninae; Culicoides; Monoculicoides.
    DB 2; Length 249;
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                                                1; Indels
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                                                                                                                                                                                                                                                                                         01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
                                                                                                                                                                                                                                                  253 AA
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                                                1; Mismatches
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp_SPC; I.
PROSITE; PS00240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
    Score 41;
Pred. No.
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    82.0%;
77.8%;
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QSQBGS;
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Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                            1 GPLVCRGTL 9
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NUCLEOTIDE SEQUENCE.
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2907N3 MOUSE
0907N3 MOUSE
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AC 0907N3 MO
DT 01-MAY-20
DT 01-MAY-2
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Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Anagaki T., Hara A., Hayatsu N., Hiramoko K., Hiranka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Hori F.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Kawai J., Kojima Y., Nohio M., Koya S., Kurihara C.,
Antsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata Y., Shibata Y., Shinagawa A., Sakai K.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tajima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramateu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, AR009360; BAB26461.2; -; mRNA.
BMBL, AK009360; BAB26461.2; -; mRNA.
BRBL, MC00930; BAB26461.2; -; mRNA.
BRBL, MC009517; 2310015108Rik.
AGO; GO:0005615; cextracellular space; TAS.
RICEPPC; IPR001334; Peptidase_S1A.
RITEFPC; IPR001334; Peptidase_S1A.
RITEFPC; IPR001334; Peptidase_S1A.
RIMER PROCONSIA PEPTIGASE S1A.
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Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Tongue;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsunnoto H., Sakaguchi S., Ikegami T., Rashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
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SWART; SM0020; TryP_SPC; 1.
PROSITE; PS0040; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN SEX; 1.
PROSITE; PS00135; TRYPSIN SEX; 1.
PROSITE; PS004080; SEXIN DOM; 90BDC03ABAB178D6 CRC64; SEQUENCE 276 AA; 30754 MW; 90BDC03ABAB178D6 CRC64;
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Matches 7; Conservative
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MEDLINE=20231737; PubMed=10767533; DOI=10.1016/S0378-1119(00)00060-3; Suwa M., Sugino H., Sasaoka A., Mori E., Fujii S., Shinkawa H., Nimi O., Kinashi H.; "Identification of two polyketide synthase gene clusters on the linear plasmid pSiA2-L in Streptomyces rochei."; Gene 246:123-131(2000).
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MEDLINE=20408175; PubMed=10954087;
Hiratou K., Mochizuki S., Kinashi H.;
Hiratou K., Mochizuki S., Kinashi H.;
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Mol. Gen. Genet. 263:1015-1021(2000).
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"Physical mapping of the linear plasmid pSLA2-L and localization of the eryAl and actI homologs ";
Biosci. Biotechnol. Biochem. 62:1892-1897 (1998).
EMBL; AB088224; BAC75588.1; -; Genomic_DNA.
Hypothetical protein; Plasmid.
SEQUENCE 612 AA; 66525 MW; 9BF0EIEE8D3110FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The large linear plasmid pSLA2-L of Streptomyces rochei has an unusually condensed gene organization for secondary metabolism."; Mol. Microbiol. 48:1501-1510(2003).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Probable long-chain-fatty-acid
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22676866; PubMed=12791134;
DOI=10.1046/j.1365-2958.2003.03523.x;
Mochizuki S., Hiratsu K., Suwa M., Ishii T., Sugino F., Yamada
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Bifidobacterium longum.
Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
NCBI_TaxID=216816;
                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Streptomyces rochei (Streptomyces parvullus).
Plasmid pSLA2-L.
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Q8G3L1;
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Best Local Similarity 77.8'
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DT 01-MAR-2(
DF Probable
DB Syntheta(
DR Name=fadi
OS Bifidoba(
OC Bacteria
OC Bacteria
OC CRIGODA
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RESULT 12 Q83WX7\_STRRO

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Pfam; PF00698; Acyl_transf_1; 2.
Pfam; PF00106; adh_abort; 2.
Pfam; PF00109; ketoacyl-synt. 2.
Pfam; PF00130; Ketoacyl-synt.C; 2.
Pfam; PF00550; PP-binding; 2.
Pfam; PF00575; Thioseterase; 1.
PROSITE; PS00015; APOSPHOPNITETHENE; 2.
PROSITE; PS00012; PHOSPHOPNITETHENE; 2.
PROSITE; PS00626; RCC1_2; UNKNOWN 1.
SEQUENCE 3201 AA; 334783 MW; 44BDA30E146
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MEDLINE=20430101; PubMed=10972798;
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Q9F830 9ACTO PRELIMINARY;
Q9F830;
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Best Local Similarity 77...
Fig. 1. Conservative
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                                     STRAINSINCE 2705;
MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
Schell M.A., Karmirantzou M., Shel B., Vilanova D., Berger B.,
Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
Pridmore R.D., Arigoni F.; Bork P., Delley M.,
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to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Volchegursky Y., Hu Z., Katz L., McDaniel R.;
"Biospyrtheis of the anti-parasitic agent megalomicin: transformation
of erythromycin to megalomicin in Saccharopolyspora erythraea.";
Mol. Microbiol. 37:752-762(2000).
EMBL. AP263245; AAG13919.1; -; Genomic_DNA.
HSSP; Q07833; 1M02.
SWR; Q9F828; 2932-3198.
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100.0%; Pred. No. 37;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                       EMBL; AE014295; AAN25531.1; -; Genomic_DNA.
HSSP; P08659; 1LCI.
GO; GO:00168014; F:1igase activity; IEA.
GO; GO:000152; P:metabolism; IEA.
InterPro; IPR002086; Aldehyd dehydrog.
InterPro; IPR008073; AMP-bind.
InterPro; IPR006073; AMP-binding; I.
PRINTS; PR00501; AMP-binding; I.
PRINTS; PR00501; AMP-binding; I.
PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
PROSITE; PS00455; AMP_BINDING.
COMPJETE proteome; Ligase.
SEQUENCE 621 AA; 67948 MW; SECDDB4B5BF3083A CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Megalomicin 6-deoxyerythronolide B synthase 3.
      [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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MEDLINE=20430101; PubMed=10972798;
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Q9F828;
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Best Local Similarity 100..
7, Conservative
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"Biosynthesis of the anti-parasitic agent megalomicin: transformation of erythromycin to megalomicin in Saccharopolyspora erythraea.";

MOI. Microbiol. 37:755-762 (2000).

EMBL; AF263245; AAG13917.1; -; Genomic_DNA.

HSSP; P72391; INNA.

GO; GO:00146491; F:oxidoreductase activity; IEA.

GO; GO:001177; F:phosphopantetheine binding; IEA.

GO; GO:0016491; F:phosphopantetheine binding; IEA.

GO; GO:0001631; F:fatty acid biosynthesis; IEA.

GO; GO:000152; P:metaboliem; IEA.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micromonosporineae; Micromonosporaceae; Micromonospora.
                                                                                                   82.0%; Score 41; DB 2; Length 3201; 77.8%; Pred. No. 2e+02; rative 1; Mismatches 1; Indels
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3201 AA; 334783 MW; 44BDA30E14855650 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Megalomicin 6-deoxyerythronolide B synthase 1.
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InterPro; IPR00127; AC Transferase.
InterPro; IPR001298; ADH short.
InterPro; IPR00198; ADH short.
InterPro; IPR002198; ADH short.
InterPro; IPR002198; Lipocalin.
InterPro; IPR006163; Phappanteth_bind.
InterPro; IPR006162; Ppantne_S.
Pfam; PF00106; adh_short; Z.
Pfam; PF00109; ketoacyl-synt; Z.
Pfam; PF002801; Ketoacyl-synt; Z.
Pfam; PF002801; Ketoacyl-synt; Z.
Pfam; PF002801; Retoacyl-synt; Z.
Pfam; PF002801; Retoacyl-synt; Z.
Pfam; PF002801; Retoacyl-synt; Z.
PROSITE; PS000013; ALPOCALIN; UNRNOWN Z.
PROSITE; PS00012; PHOSPHORMITETHEINE; Z.
PROSITE; PS00012; PHOSPHORMITETHEINE; Z.
PROSITE; PS00012; PHOSPHORMITETHEINE; Z.
PROSITE; PS00012; PHOSPHORMITETHEINE; Z.
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Search completed: March 11, 2006, 00:38:52 Job time : 97.3333 secs

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Sequence 7, A Sequence 12, Sequence 37, Sequence 38,

Sequence 3 Sequence 3 Sequence 3

Sequence Sequence Sequence

Sequence 1, Al Sequence 3, Al Sequence 12,

Sequence 7, 1 Sequence 8, 1 Sequence 1, 1 Sequence 2, Sequence 1,

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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Patent No. 629434
GENERAL INFORMATION:
Factor No. 629434
GENERAL INFORMATION:
TITLE OF INVENTION:
Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION:
COMPOSITION:
TITLE OF INVENTION:
O'BATION:
CURRENT FILING DATE:
CURRENT APPLICATION NUMBER: US/09/502,600A
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 80
FEATURE OF SEQ ID NOS: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 80, Application US/09918243

Sequence 80, Application US/09918243

GENERAL INFORMATION:

APPLICANT: Cannon, Martin J.

CURRENT PLICATION NUMBER: US/09/918,243

CURRENT FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NOS 0

IENGTH: 9

TYPE: PRT

CURRENT: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 50; DB 2; Length 9; 100.0%; Pred. No. 4.6e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: Residues 207-215 of the SCCE protein
                      US-08-767-820A-1
US-08-767-820A-1
US-08-767-820A-1
US-08-622-046B-1
US-08-622-046B-1
US-08-944-483-37
US-08-944-483-38
US-09-100-264-1
US-09-100-264-1
US-09-100-264-1
US-09-100-264-1
US-09-100-264-1
US-09-100-264-1
                                                                                                                                                                          US-08-843-076D-1
US-08-843-076D-7
                                                                                                                                                                                                   US-08-843-076D-8
US-09-303-208-1
                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 9, Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GPLVCRGTL 9
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RESULT 2
US-09-918-243-80
                                                                                                                                                                                                                                                                                                        US-09-502-600-80
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 LENGTH: 9
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Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 7716, Appli
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Appl
Appl
Appl
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Sequence 80, Appl
Sequence 33, Appl
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                                                                                   March 11, 2006, 00:41:16 ; Search time 21.2222 Seconds (without alignments) 35.061 Million cell updates/sec
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Sequence 10,
Sequence 11,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13,
Sequence 19,
Sequence 19,
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Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
           GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                   Issued Patents AA:*
: /cgn2 6/ptodata1/iaa/5_COMB.pep:*
: /cgn2 6/ptodata1/iaa/6_COMB.pep:*
: /cgn2 6/ptodata1/iaa/H_COMB.pep:*
: /cgn2 6/ptodata1/iaa/H_COMB.pep:*
: /cgn2 6/ptodata1/iaa/RECOMB.pep:*
: /cgn2 6/ptodata1/iaa/RECOMB.pep:*
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US-09-918-243-80
US-08-544-483-33
US-08-557-146-12
US-09-0154-344-12
US-09-154-44-600-4
US-09-654-600A-4
US-09-654-600A-4
US-09-154-344-2
US-09-154-344-2
US-09-154-344-2
US-09-154-344-2
US-09-154-344-2
US-09-154-344-2
US-09-154-344-2
US-09-154-344-2
US-09-154-344-2
US-09-154-341-3
US-09-164-13
US-09-679-279-15
US-09-679-279-15
US-09-679-279-15
US-09-146-831-19
US-08-096-946-11
US-08-096-946-11
US-08-146-831-2
US-08-146-831-2
US-08-146-831-3
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                                                                                                                                                                                                                            572060 segs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                US-09-905-083A-80
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Maximum DB seq length: 2000000000
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178 GPLVCRGTL 186
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nes 9; Conserv
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                                                     RESULT 4
US-08-557-146-12
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                                                                                                                                                                                                                                                                                                                                                     APPLICANT: COLENT, MAURICE
APPLICANT: COLENT, TRACEY L.
APPLICANT: COLENT, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: STEWART, KENT D.
APPLICANT: STEWART, KENT D.
APPLICANT: STROWER, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
CORRESPONDENCES: 76
CORRESPONDENCE ADDRESS:
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                                                                                             Query Match 100.0%; Score 50; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 9; Conservative 0; Mismatches 0; Indels
                               ; OTHER INFORMATION: Residues 207-215 of the SCCE protein US-09-918-243-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6183.US.01
                                                                                                                                                                                                                                                                             RESULT 3
US-08-944-483-33
; Sequence 33, Application US/08944483
; Patent No. 6223456
; Patent No. 623456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Abbott Laboratories
100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BECKET, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183
TELECHONICATION INFORMATION:
TELECHONE: 847/938-1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFOAMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: No. 6232456e
                                                                                                                                                                               1 GPLVCRGTL 9
                                                                                                                                                                                                      Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                  NAME/KEY: CHAIN
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STREET: 10
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APPLICANT: O'Brian, Timothy J.
APPLICANT: O'Brian, Hirotoshi
TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REFERENCE: D6064
CURRENT APPLICATION NUMBER: US/09/027,337B
CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 4
LIBRORY 225
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SCRANISM: Unknown
FEATURE:
OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                      GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Banseon, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 225;
                                                                                                                                                                                                                                                                      STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/557,146
FILING DATE: 14-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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100.0%; Pred. No.
Sequence 12, Application US/08557146 Patent No. 5834290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09027337B Patent No. 5972616 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION: TELEPHONE: (212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELBEAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: polypeptide US-08-557-146-12
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amino acids
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Tanimoto, Hirotoshi
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1998-02-20
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 4
LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: SCCE US-09-654-600A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 GPLVCRGTL 187
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                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GPLVCRGTL 9
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                                                                                                                                                                                                                                                                                                                                                                               Recombinant Stratum Corneum Chymotryptic Enzyme (SCCE)
                                                             Query Match 100.0%; Score 50; DB 1; Length 225; Best Local Similarity 100.0%; Pred. No. 0.21; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 50; DB 1; Length 225; Best Local Similarity 100.0%; Pred. No. 0.21; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/154,344
FILING DATE: 16-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: White & Case, Patent Department
; OTHER INFORMATION: similar domain in TADG-15 US-09-027-337-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1155 Avenue of the America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                          Sequence 12, Application US/09154344
Patent No. 5981256
GENERAL INPORMATION:
APPLICANT: Bgelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Str
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09644600; Patent No. 6451500
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                               179 GPLVCRGTL 187
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                                                                                                                                           1 GPLVCRGTL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
                                                                                                                                                                                                                                         RESULT 6
US-09-154-344-12
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US-09-644-600-4
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PATEUR NO. 3924200.

PATEUR NO. 3924200.

APPLICANT: Egelrud, Torbjorn
APPLICANT: Hanson, Lennart
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: 17
CORRESPONDENCE ADDRESS: 3
ADDRESSEE: White & Case, Patent Department
STRET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.
ZIP: 1036-2787
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBMP Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURSIT APPLICATION DATA:
PRILNG DATE: 16-SEP-1998
CLASSIFICATION DATA:
PRILNG DATE: 14-DEC-1995
FILING DATE: 14-DEC-1995
CLASSIFICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION NUMBER: US 08/557,146
FILING DATE: TAPODAMPTON.
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                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 50; DB 1; Length 253; 100.0%; Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Patent No. 5981256
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REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION: (212) 819-8783
                                                                                          LENGTH: 253 amino acide
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 253 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-154-344-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 10v...
Best Local Similarity 10v...
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acid
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 GPLVCRGTL 215
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                                                                                                                                                                                                                                                                                                                        US-08-824-874-3
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US-09-154-344-2
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                                                                                                                            COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 50; DB 1; Length 253; Best Local Similarity 100.0%; Pred. No. 0.24; Matches 9; Conservative 0; Mismatches 0; Indels
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COUNTY.

COUNTY.

STATE: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, Lucy J.
NAME: BILLINGS, Lucy J.
NAME: BILLINGS, Lucy J.
NAME: BILLINGS, Lucy J.
NAME: BILLINGS.
NAME: NUMBER: PF-0252 US
ADDRESSEE: White & Cage, Patent Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08824874

Sequence 3, Application US/08824874

Patent No. 5963300

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

STREET: 11, Preset Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

STATE: CA
                                 1155 Avenue of the America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 GPLVCRGTL 215
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                                                                                                 New York
: U.S.A.
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIFICATION CURKNOWN>
PRIOR APPLICATION ATA:
APPLICATION NUMBER: 09/210,084
FILING DATE: UNKNOWN:
ATTORNEY/AGRNT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
RECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09764762
; Sequence 3, Application US/09764762
; Patent No. 6472195
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; STREET: 3174 Porter Drive
; STREET: 3174 Porter Drive
; STATE: CA
; COUNTRY: Palo Alto
; COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 97.49
REFERENCE/DOCKET NUMBER: 96,749
REFERENCE/DATION INFORMATION:
TELEPHONE: 415-85-055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE: 532504
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US-09-764-762-3
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                                                                                           Sequence 2. Application US/08930188

Patent No. 6093337

GENERAL INFORMATION:

APPLICANT: Dixon, Eric P.

APPLICANT: Little, Sheila P.

ITILE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: RELATED NUCLEIC ACIDS

NUMBER OF SEQUENCES: 3

CORRESPONDENCE S: 3

CORRESPONDENCE BILLILLY COMPANY

STREET: Lilly Corporate Center

CITY: Indianapolis

STREET: United States of America

COUNTRY: United States of America

STREE: ADDRESSE:

COMPUTER: EADABLE FORM:

MEDIUM TYPE: Flopy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/930,188

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 50; DB 2; Length 253; Best Local Similarity 100.0%; Pred. No. 0.24; Matches 9; Conservative 0; Mismatches 0; Indels
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; Sequence 3, Application US/09210084
; Patent No. 6197511
; GENERAL INFORMATION:
    APPLICANT: Hillman, Jennifer L.
    APPLICANT: Lal, Preeti
    TITLE OF INVENTION: NOVEL KALLIKKEIN
    NUMBER OF SEQUENCES: 5
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Incyte Pharmaceuticals, Inc.
    STREET: 3174 Porter Drive
    CITY: Palo Alto
    STATE: CA
COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
RPELOTATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
TELEFAX: 317-277-1090
TELEFAX: 317-277-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 GPLVCRGTL 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 94304
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US-09-210-084-3
                                                                                      US-08-930-188-2
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100.0%; Score 50; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 50; DB 2; Length 253; Best Local Similarity 100.0%; Pred. No. 0.24; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indianapolis
COMPUTR: Indianapolis
COMPUTR: Eloppy disk
COMPUTER READABLE FORM:
MEDIUM TYBE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04294
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION NUMBER: 38,082
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
FILING DATE: 01-APR-1995
ATTORNEY/AGENT INFORMATION:
FILING DATE: 01-000
FILING DATE: 01-000
FILING APPLICATION NUMBER: 38,082
FILING APPLICATION NUMBER: 317-277-1090
FILING DATE: 01-000
FILING APPLICATION NUMBER: 38,082
FILING APPLICATION NUMBER: 38,082
FILING DATE: 01-000

FILING DATE: 01-000
FILING DATE: 01-0000
FILING DATE: 01-0000
FILING DATE: 01-
                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3
                                                                                                   LENGTH: 253 amino acide
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
INMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 GPLVCRGTL 215
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1 GPLVCRGTL 9

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Db 207 GPLVCRGTL 215
Search completed: March 11, 2006, 01:24:27
Job time : 21.2222 secs
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Sequence 68, Appl Sequence 67, Appl Sequence 4, Appli Sequence 5, Appli Sequence 182803,

3, Appli 212, App 46, App 27, Appl 20, Appl 210636, 410636, 6, Appl 348061,

Sequence Seguence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

OM protein

Run on:

Sequence:

Minimum DB Maximum DB

Searched:

Database :

Result

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Sequence 80, Application US/09918243

Sequence 80, Application US/09918243

Batent No. US20020142317A1

GENERAL INFORMATION:

APPLICANT: O'Brien, Martin J.

APPLICANT: Cannon, Martin J.

APPLICANT: Cannon, Methods for the early diagnosis of ovarian cancer;

TITLE OF INVENTION WHERE US/09/918,243

CURRENT FILING DATE: 2001-07-30

PRIOR PPLICATION NUMBER: US

CURRENT PILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-33

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 80

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 80, Application US/09905083
; Sequence 80, Application US/09905083
; Ratent No. US2002046708A1
; GRNERAL INFORMATION:
; APPLICANT: O'BIGH, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REPERBNCE: D6223GIP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; RROW FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 207-215 of the SCCE protein
US-09-918-243-80
                              US-10-492-740-3
US-09-764-898-212
US-10-071-214-46
US-10-344-394-27
US-10-480-988-20
US-10-424-599-210636
US-10-450-459-210636
US-10-071-214-6
US-10-071-214-6
                                                                                                                                                                               US-09-860-739-5
US-10-437-963-182803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 50; DB 3; 1
100.0%; Pred. No. 1.7e+06;
iive 0; Mismatches 0;
                                                                                                                                             US-10-055-569A-68
US-10-055-569A-67
US-11-055-989-4
                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 9, Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
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US-09-918-243-80
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 TYPE: PRT
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Sequence 80, Appl
Sequence 98, Appl
Sequence 96, Appl
Sequence 13, Appl
Sequence 104, Appl
Sequence 4, Appl
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48, Appl
639, App
95, Appl
95, Appl
1, Appli
38, Appl
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92, Appl
94, Appl
98, Appl
3, Appli
2, Appli
48, Appl
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                                                                        March 11, 2006, 01:24:47; Search time 69.444 Seconds (without alignments) 54.151 Million cell updates/sec
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Sequence
Sequence
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(cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/USO3_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
          GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-905-083-80
US-10-8372-521-80
US-10-825-511-96
US-10-262-511-96
US-10-262-511-104
US-10-262-511-104
US-10-262-511-104
US-10-262-511-104
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US-10-262-511-94
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US-10-262-511-94
US-10-262-511-94
US-10-262-511-94
US-10-263-99-48
US-10-264-283-99-48
US-10-408-7654-639
US-10-948-518-95
US-10-948-518-95
US-10-948-518-95
US-10-948-518-95
US-10-948-518-95
US-10-144-17
                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                     1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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50
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seq length: 2000000000
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Match Length DB
                                                                                                                                             1 GPLVCRGTL 9
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1000.0
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Gaps

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Length 9; 0; Indels ō

Pred. No. 1.7e+06;

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100.08;
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Catterton, Elina
  Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                      Ju, Jingfang
Li, Li
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ORGANISM: Homo sapiens
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; Sequence 80, Application US/2030223973A1
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: Cannon, Martin J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer; FILE REPRENCE: DE232CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/110/372,521
; CURRENT PILING DATE: 2003-02-21
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-831-075-80

| US-10-831-075-80
| Sequence 80, Application US/10831075
| Publication No. US20040224891A1
| GENERAL INFORMATION:
| APPLICANT: Cannon, Martin J.
| APPLICANT: Cannon, Martin J.
| APPLICANT: Santin, Alesandro
| TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
| FILE REFERENCE: D6223CIP/C/D/CIP3
| CURRENT PELLION NUMBER: US/10/831,075
| PRIOR APPLICATION NUMBER: US 10/372,521
| PRIOR APPLICATION NUMBER: US 10/372,521
| NUMBER OF SEQ ID NOS: 140
| SEQ ID NO 80
| LENGTH: 9
                                                                                                                                                                             Gaps
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                                                                                                                                Query Match 100.0%; Score 50; DB 3; Length 9; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 9; Conservative 0; Mismatches 0; Indels
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                           ; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 207-215 of the SCCE protein
US-09-905-083-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 207-215 of the SCCE protein
US-10-372-521-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 207-215 of the SCCE protein
US-10-831-075-80
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Best Local Similarity 100.
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
                                                                                                                                                                                                                      1 GPLVCRGTL 9
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GPL/CRCII 9

1 GPL/
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APPLICANT: COHEN, MAUKICE
OLDITITS, TRACET L.
FRIEDMAN, PAULA N.
GRANADOS, EDWARD N.
KLASS, MICHAEL R.
RUSSELL, JOHN C.
STEWART, KENT D.
STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
AND METHODS. USEFUL FOR DETECTING AND TREATING DISEASES
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                    100.0%; Score 50; DB 4; Length 198; 100.0%; Pred. No. 1.1;
                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FEASED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/789,210
FILING DATE: 20-Feb-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: 08/944,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: BECKET, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-789-210-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33, Application US/09789210
Publication No. US20040241646A1
GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 224 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 847/938-2623
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       9; Conservative
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                                                                                                                                                                                                                                                                        152 GPLVCRGTL 160
     ; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-96
                                                                                                                                                                                                                                          1 GPLVCRGTL 9
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                                                                                                                                 Query Match
Best Local Similarity
Matches 9; Conserv
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERENCE: 21402-462C
CURRENT APPLICATION NUMBER: 60/236,483
FRICA PAPLICATION NUMBER: 60/373,815
PRIOR PELICATION NUMBER: 60/373,815
PRIOR PELICATION NUMBER: 60/373,815
PRIOR PELICATION NUMBER: 60/377,917
PRIOR PELICATION NUMBER: 60/327,917
PRIOR PELICATION NUMBER: 60/327,917
PRIOR PELICATION NUMBER: 60/327,917
PRIOR PELICATION NUMBER: 60/327,917
PRIOR PELICATION NUMBER: 60/328,029
PRIOR PELICATION NUMBER: 60/328,029
PRIOR PELICATION NUMBER: 60/328,026
PRIOR FILING DATE: 2002-10-09
PRIOR FILING DATE: 2002-05-17
PRIOR PELICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2001-10-09
PRIOR PELICATION NUMBER: 60/373,260
PRIOR PELICATION NUMBER: 60/373,260
PRIOR PELICATION NUMBER: 60/373,260
PRIOR PELING DATE: 2001-10-09
PRIOR PELING DATE: 2001-10-09
PRIOR PELING DATE: 2001-10-05
                                                                                                           Gaps
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                                                   100.0%; Score 50; DB 4; Length 181; 100.0%; Pred. No. 1; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                      ; Sequence 96, Application US/10262511; Publication No. US20040038223A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guo, Xiaojia (Sasha)
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Ort, Tatiana
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                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kewda, Ramesh
APPLICANT: Li, Jingfang
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Leach, Martin D.
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Anderson, David W.
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Rastelli, Luca
Stone, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhong, Mei
Catterton, Elina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agee, Michele L.
                                                Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gorman, Linda
                                                                                                                                                                                                  133 GPLVCRGTL 141
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                                                                                                                                                         1 GPLVCRGTL 9
US-10-262-511-98
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Matches
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APPLICANT: AGGE, MIGHER L.
APPLICANT: AGGE, MIGHER L.
APPLICANT: BERGE, MIGHER L.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT FILING DATE: 2003-05-28
FRIOR PELICATION NUMBER: 60/373,815
FRIOR APPLICATION NUMBER: 60/373,915
FRIOR APPLICATION NUMBER: 60/373,917
FRIOR PILING DATE: 2002-04-19
FRIOR PILING DATE: 2002-05-17
FRIOR PILING DATE: 2002-05-17
FRIOR APPLICATION NUMBER: 60/328,029
FRIOR FILING DATE: 2002-05-16
FRIOR APPLICATION NUMBER: 60/328,056
FRIOR PILING DATE: 2002-05-16
FRIOR PILING DATE: 2002-04-17
FRIOR APPLICATION NUMBER: 60/323,260
FRIOR PILING DATE: 2002-04-17
FRIOR APPLICATION NUMBER: 60/373,260
FRIOR PILING DATE: 2002-04-17
FRIOR PILING DATE: 2003-04-17
FRIOR PILING DAT
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                                                                                                                                                                              Sequence 104, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miller, Charles B.
Rastelli, Luca
Stone, David J.
Pena, Carol B. A.
Shenoy, Suresh G.
Shimkets, Richard A.
Rothenberg, Mark B.
Leach, Martin D.
Agee, Michele L.
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Malyankar, Uriel M.
Ort, Tatiana
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Zerhusen, Bryan D.
Anderson, David W.
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Li, Li
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178 GPLVCRGTL 186
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ORGANISM: Homo sapiens
US-10-262-511-104
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Best Local Similarity
                                                                                                                                                           US-10-262-511-104
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LENGTH: 224
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APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
TITLE OF INVENTION: Overexpressed in Carcinomas
TITLE OF INVENTION: Overexpressed in Carcinomas
FILE REFERENCE: D6064CIP/D
CURRENT FILING DATE: 2003-06-20
FRIOR APPLICATION NUMBER: US/10/660,187
CURRENT FILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
PRIOR FILING DATE: 1999-10-20
SPRIOR FILING DATE: 1999-10-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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Malyankar, Uriel M.
Ort, Tatiana
Gorman, Linda
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Catterton, Elina
Ji, Weizhen
Miller, Charles E.
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Anderson, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
  9; Conservative
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Li, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: SCCE
US-10-600-187-4
                                                                                                         193 GPLVCRGTL 201
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ORGANISM: Homo sapiens
                                                      1 GPLVCRGTL 9
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APPLICANT: Rothenberg, Martin D.
APPLICANT: Rethenberg, Martin D.
APPLICANT: Rechenberg, Martin D.
APPLICANT: Rechenberg, Martin D.
APPLICANT: Agee, Michaele L.
APPLICANT: Agee, Michaele L.
APPLICANT: Bergin, Constance
CURRENT Agee, Michaele L.
APPLICANT: Bergin, Constance
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
FILE REFERENCE: 2001-10-02
FRIOR APPLICATION NUMBER: 60/326,483
FRIOR PELING DATE: 2001-10-03
FRIOR PELING DATE: 2001-10-09
FRIOR PELING DATE: 2002-05-17
FRIOR APPLICATION NUMBER: 60/327,917
FRIOR APPLICATION NUMBER: 60/328,029
FRIOR FILING DATE: 2002-05-17
FRIOR APPLICATION NUMBER: 60/373,260
FRIOR FILING DATE: 2002-05-16
FRIOR PELING DATE: 2002-05-16
FRIOR PELING DATE: 2002-05-16
FRIOR PELING DATE: 2002-05-17
FRIOR PELING DATE: 2002-05-16
FRIOR PELING DATE: 2002-05-17
FRIOR PELING DATE: 2002-05-17
FRIOR PELING DATE: 2002-05-16
FRIOR PELING DATE: 2002-05-17
FRIOR PELING DATE: 2002-05-16
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FRIOR PELING DATE: 2002-05-16
FRIOR PELING DATE: 2002-05-17
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FRIOR PELING DATE: 2002-05-16
FRIOR PELING DATE: 2002-05-17
FRIOR PELING DATE: 2002-05-16
FRIOR PELING DATE: 2002-05-17
FRIOR PELING DATE: 2002-05-16
FRIOR PELING DATE: 2002-05-1
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US-10-26-511-94
Sequence 94, Application US/10262511
GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
RAPLICANT: Rekuda, Ramesh
RAPPLICANT: Rekuda, Ramesh
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Li, Li
Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Bdinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
Ort, Tatiana
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Zerhusen, Bryan D.
Anderson, David W.
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Catterton, Elina
Ji, Weizhen
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Best Local Similarity 100.
Matches 9; Conservative
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APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: BERGH, Contended
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPRENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
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100.0%; Score 50; DB 4; Length 247;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                               CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR PILING DATE: 2001-0-02
PRIOR PILING DATE: 2001-0-02
PRIOR FILING DATE: 2001-0-03
PRIOR PILING DATE: 2001-0-09
PRIOR PILING DATE: 2001-0-09
PRIOR PILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/321,039
PRIOR PILING DATE: 2002-05-10
PRIOR PILING DATE: 2002-0-09
PRIOR FILING DATE: 2002-0-09
PRIOR FILING DATE: 2002-0-09
PRIOR PILING DATE: 2002-0-09
PRIOR PILING DATE: 2002-0-09
PRIOR PILING DATE: 2001-0-09
PRIOR PILING DATE: 2001-0-09
PRIOR PILING DATE: 2002-04-17
PRIOR PILING DATE: 2001-0-05
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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Ji, Weizhen
Miller, Charles E.
Rastelli, Luca
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Malyankar, Uriel M.
Ort, Tatiana
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Zerhusen, Bryan D.
Anderson, David W.
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; ORGANISM: Homo sapiens
US-10-262-511-102
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US-10-262-511-92
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LENGTH: 247
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Gaps ö DB 3; Length 253;

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Query Match 100.0%; Score 50; DB 3
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches
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  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-98
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Best Local Similarity
Matches 9; Conserv
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APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: APPLICANT: Berge, Michele L.
APPLICANT: Berge, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TITLE OF INVENTION NUMBER: 60/373,815
PRIOR PILING DATE: 2001-10-03
PRIOR PILING DATE: 2001-10-03
PRIOR PILING DATE: 2002-05-17
PRIOR PILING DATE: 2002-05-17
PRIOR PILING DATE: 2002-05-17
PRIOR PILING DATE: 2002-05-17
PRIOR PILING DATE: 2002-05-16
PRIOR PILING DATE: 2002-05-16
PRIOR PILING DATE: 2002-05-16
PRIOR PILING DATE: 2002-05-17
PRIOR PELING DATE: 2002-05-16
PRIOR PILING DATE: 2002-05-17
PRIOR PILING DATE: 2002-04-17
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SOFTWARE: CuraSeqList version 0.1
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Sequence 99. Application US/0988615

Patent No. US20020064856A1

GENERAL INFORMATION:

APPLICANT: PLOWMAN, GREGORY

APPLICANT: CARNEDEL, SEAN

APPLICANT: CARNEDEL, SEAN

APPLICANT: CARNEDEL, SEAN

APPLICANT: CHRYDCZAK, GLEN

APPLICANT: CARNEDEL, SEAN

APPLICANT: CARNEDEL, SEAN

APPLICANT: MANNING, GERARD

APPLICANT: MANNING, GERARD

TITLE OF INVENTION: NOVEL PROTEASES

ITLE REPERBNCE: 038602/1214

CURRENT FILING DATE: 2001-06-26

FRIOR PELING DATE: 2000-06-26

NUMBER OF SEQ ID NOS: 150

SOPTWARE: Patentin Ver. 2.1

SERO ID NO 98

LENGTH: 253
                          Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
Shimkets, Richard A.
Miller, Charles E.
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Best Local Similarity 100.
Matches 9; Conservative
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US-10-262-511-94
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                                                                                                                              US-09-764-762-3

Sequence 3, Application US/09764762

Sequence 3, Application US/09764762

Sequence 3, Application US/09764762

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

TITLE OF INVENTION: NOVEL KALLIKREIN

NUMBER OF SEQUENCES: 5

CORRESPONDENCE SED

STREET: 3174 Porter Drive

CITT: Palo Alto

STATE: CA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/210,084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-10-071-214-2
Sequence 2, Application US/10071214
; Publication No. US20030066099A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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GENERAL INFORMATION:

APPLICANT: HANSSON, Lennart

APPLICANT: BGELEAUD, Torbjorn

TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN

TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN

TITLE OF INVENTION: AUGUST: 1000-11

PRIOR PEPLICATION NUMBER: US 60/267,422

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

NUMBER OF SEQ ID NOS: 50

SOCTWARE: PATENTING THE SOUTH OF SEQ ID NOS: 50

LENGTHARE: PATENT

TYPE: PRT

CRENGTH: 253

TYPE: PRT

CRENGTH: 253

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100.0%; Score 50; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels
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Job time : 70.4444 secs
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207 GPLVCRGTL 215
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US-10-412-748-11

Sequence 11, Application US/10412748

Publication No. US20060035219A1

GENERAL INFORMATION:

APPLICANT: Queensland University of Technology

APPLICANT: Clements, Judith A

TITLE OF INVENTION: Aberrant Kallikrein Expression

FILE REFERENCE: DAVILT-2.003A08

CURRENT APPLICATION NUMBER: US/10/412,748

CURRENT FILING DATE: 2003-04-09

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin version 3.2

SEQ ID NO 11

LENGTH: 20

LENGTH: 20

TYPE: PRI
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Best Local Similarity
Matches 9; Conserv
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Sequence 11, Appl
Sequence 17, Appl
Sequence 552, Appl
Sequence 552, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 1, Appl
Sequence 5, Appli
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Sequence 396, App
Sequence 7, Appli
Sequence 3, Appli
Sequence 10, Appli
Sequence 3, Appli
                                                                         March 11, 2006, 01:27:17 ; Search time 8 Seconds
    (without alignments)
    31.314 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USOB NEW PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USOF NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USOF NEW PUB.pep:*
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8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW PUB.pep:*
          GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-412-748-11

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US-10-412-748-17

US-10-995-561-552

US-10-995-561-553

US-10-995-561-553

US-10-401-386B-12

US-10-401-386B-24

US-11-138-242A-8

US-11-138-242A-8

US-11-138-242A-8

US-11-138-242A-8

US-11-138-242A-5

US-10-401-386B-2

US-10-401-386B-6

US-10-401-386B-6

US-11-138-242A-5

US-10-401-386B-6

US-11-138-242A-5

US-11-150-066-5

US-11-150-066-5

US-11-150-066-5

US-10-121-236-0
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US-11-138-242A-10
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                                                                                                                                                                                                     161667 segs, 27834885 residues
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Sequence 7, Appli
Sequence 11986, App
Sequence 11986, App
Sequence 61, Appl
Sequence 172, Appl
Sequence 172, Appl
Sequence 176, Appl
Sequence 523, Appl
Sequence 525, Appl
Sequence 617, Appl
Sequence 617, Appl
Sequence 617, Appl
Sequence 11, Appl
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Sequence 1
Sequence 4
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Sequence 19, Application US/10412748
Sequence 19, Application US/10412748
Publication No. US20060035219A1
GENERAL INFORMATION: US20060035219A1
APPLICANT: Queensland University of Technology
TILE OF INVENTION: Aberrant Kallikrein Expression
FILE REFERENCE: DAVI172.003AUS
CURRENT FILIG DATE: 2003-04-09
PRIOR APPLICATION NUMBER: 3003-04-09
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
SEQ ID NO 19
LENGTH: 181
TYPE: PRI
TYPE: PRI
US-10-412-748-19
          US-10-131-826A-456
US-10-412-748-2
US-10-412-748-2
US-10-973-115B-456
US-11-087-099-11986
US-11-234-786-512
US-11-234-786-172
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US-11-087-099-1581
US-10-718-264-8
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135 GPLVCRGTL 143
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RESULT 6
US-10-995-561-552
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100.0%; Score 50; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                               RESULT 3
US-10-412-748-14

Sequence 14, Application US/10412748

Publication No. US20060035219A1

GENERAL INFORMATION:
APPLICANT: Clements, University of Technology
APPLICANT: Clements, University of Technology
PILE OF INVENTION: Aberrant Kallikrein Expression
FILE OF INVENTION: Aberrant Kallikrein Expression
FILE OF INVENTION: Aberrant Kallikrein Expression
FILE OF INVENTION: Aberrant CALLIA CONTRAIN
FRIENT APPLICATION NUMBER: US/10/412,748
CURRENT FILING DATE: 2003-04-09

PRIOR PILING DATE: 2002-04-09

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin version 3.2

LENGTH: 253
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US-10-412-748-17

Sequence 17, Application US/10412748

Publication Wo. US20060035219A1

GENERAL INFORMATION:

APPLICANT: Queeneland University of Technology

APPLICANT: Clements, Judith A

TITLE OF INVENTION: Aberrant Kallikrein Expression

PILE REFERENCE: DAVIAT2.003408

CURRENT APPLICATION NUMBER: US/10/412,748

CURRENT FILING DATE: 2003-04-09

PRIOR APPLICATION NUMBER: AU PS1616/02

PRIOR APPLICATION NUMBER: AU PS1616/02

PRIOR PILING DATE: 2002-04-09

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn version 3.2

LENGTH: 253
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Best Local Similarity 100.0
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Best Local Similarity 100.
Matches 9; Conservative
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; ORGANISM: Human
US-10-412-748-11
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US-10-412-748-17
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TITLE OF INVENTION: CARDIOLANGE DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 552
LENGTH: 267
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GENETIC POLYMORPHISMS ASSOCIATED WITH
CENDIOVASCULAR DISCORDERS AND DRUG RESPONSE, METHODS OF
DETECTION AND USES THEREOF
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Sequence 98, Application US/11037243
| Publication No. US20050287546A1
| Publication No. US20050287546A1
| GENERAL INPORMATION:
| APPLICANT: PLOWMAN, GREGORY
| APPLICANT: GENERALE, SEAN
| APPLICANT: GENERALE, SEAN
| APPLICANT: GENERALE, GENERALE
| APPLICANT: GENERALE, GENERALE
| APPLICANT: GENERALE
| APPLICANT: GENERALE
| APPLICANT: MANNING, GERARD
| APPLICANT: ON WUBBER: US/11/037,243
| CURRENT APPLICATION NUMBER: US/09/88,615
| PRIOR FILING DATE: 2000-06-26
| PRIOR FILING DATE: 2000-06-26
| PRIOR FILING DATE: 2000-06-26
| NUMBER OF SEQ ID NOS: 150
| SOFTWARE: PREDETTING US: 150
| LENGTH: 253
| TYPE: PRT
| TYPE: PRT
| TYPE: PRT
| US-11-037-243-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPH
; TITLE OF INVENTION: CARDIOVASCULAR D
; TITLE OF INVENTION: DETECTION AND US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 552, Application US/10995561; Publication No. US20050272054A1; GENERAL INFORMATION:
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Best Local Similarity 100.
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Best Local Similarity 88.9
Matches 8; Conservative
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; ORGANISM: Homo sapiens
US-10-995-561-552
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Gaps .; 0

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US-11-150-066-8

Sequence 8, Application US/11150066

Sequence 8, Application US/11150066

Publication No. US20050276758A1

Sequence 8, Application No. US20050276758A1

SEQUENCE STATE OF TRANSMATION:

APPLICANT: Marchall, Deborah J.

APPLICANT: Marchall, Deborah J.

TITLE OF INVENTION: Method for Screening Agents Against Human Prostate Disease

TITLE OF INVENTION: WHOMER: US/11/150,066

CURRENT FILING DATE: 2005-06-09

PRIOR APPLICATION NUMBER: 60/579,871

PRIOR PILING DATE: 2004-06-15

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin version 3.2

SEQ ID NO 8

TYPE: PRT
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Pred. No. 2.4;
0; Mismatches 2; Indels
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Publication No. US20050266530A1
REDIGART: Narshall, Deborah J.
APPLICANT: Snyder, Linda A.
TITLE OF INVENTION: Cynomolgus Prostate Specific Antigen
FILE REPERBUCE: CEN5056 USA NP
CURRENT APPLICATION NUMBER: US/11/138,242A
PRIOR APPLICATION NUMBER: 60/575,079
PRIOR FILING DATE: 2004-05-27
  PRIOR APPLICATION NUMBER: 10/247,203
PRIOR FILING DATE: 2002-09-19
PRIOR PILING DATE: 2001-09-19
PRIOR PILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PREKSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 237
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SOFWARE: Patentin version 3.2
SEQ ID NO 8
LENGTH: 261
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Best Local Similarity 77.8%;
Matches 7; Conservative
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                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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US-11-150-066-8
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US-11-138-242A-8
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; Sequence 12, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: Stephen G McCarthy
; APPLICANT: Stephen G McCarthy
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; TITLE OF INVENTION: For Use
; TITLE OF INVENTION: for Use
; TITLE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR FILING DATE: 2002-09-19
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SEQ ID NOS: 81
; SEQ ID NOS: 81
; SEQ ID NOS: 81
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APPLICANT: Theresa J Goletz
APPLICANT: Theresa J Goletz
APPLICANT: Stephen G McCarthy
APPLICANT: Stephen G McCarthy
APPLICANT: Bernard J Scallon
APPLICANT: Linda A Snyder
TITLE OF INVENTION: Nucleic Acid Compositions and Methods
TITLE OF INVENTION: Lor Use
FILE REFERENCE: CEN 310CIP
CURRENT APPLICATION NUMBER: US/10/401,386B
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Pred. No. 0.49;
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; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 553
; TYPE: PRT
; TYPE: PRT
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US-10-401-386B-24
; Sequence 24, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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US-10-401-386B-12
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US-10-401-386B-12
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US-10-401-386B-2
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Publication No. US20060008468A1

GENERAL INFORMATION:
APPLICANT: Chiang, Chih-Shang
APPLICANT: Chiang, Chih-Shang
APPLICANT: Simard, John J.L.
TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
TITLE OF INVENTION: WANNK. 050A
TITLE OF INVENTION: WANNK. 050A
TITLE OF INVENTION: WANNK. 050A
CURRENT PELING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: 60/580, 969
PRIOR FILING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 40
SEQ ID NOS: 40
SEQ ID NO 10
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                        Sequence 358, Application US/11033039
| Publication No. US2006002947A1
| GENERAL INFORMATION:
| APPLICANT: HUMPRINGS, ROBERT
| APPLICANT: HUMPRINGS, ROBERT
| APPLICANT: HUMPRINGS, ROBERT
| TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
| TITLE REFERENCE: REH-2017US01
| CURRENT APPLICATION NUMBER: US/11/033,039
| CURRENT PILING DATE: 2002-09-17
| PRIOR PEPLICATION NUMBER: 10/197,000
| PRIOR FILING DATE: 2002-09-17
| PRIOR APPLICATION NUMBER: 09/396,813
| PRIOR FILING DATE: 2002-07-17
| PRIOR FILING DATE: 10/197,000
| PRIOR FILING DATE: 2002-07-17
| PRIOR APPLICATION NUMBER: 09/396,813
| PRIOR FILING DATE: 10/197,000
| PRIOR FILING DATE: 2002-07-17
| PRIOR APPLICATION NUMBER: 09/396,813
| PRIOR FILING DATE: 2002-07-17
| PRIOR APPLICATION NUMBER: 09/396,813
| PRIOR FILING DATE: 2002-07-17
| PRIOR APPLICATION NUMBER: 09/396,813
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                      2; Indels
  Pred. No. 2.6;
0; Mismatches
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  77.8%;
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Best Local Similarity 77.8.
Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                         215 ĠPĽVĆNĠVĽ 223
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ORGANISM: Homo sapiens
                                                                1 GPLVCRGTL 9
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US-11-033-039-358
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US-11-155-288-10
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US-10-81-234-1274

US-10-81-234-1274

Sequence 1274, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REPERENCE: 82.1A

CURRENT FILING DATE: 2004-04-07

PRIOR FILING DATE: 2003-04-07

PRIOR FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: pt SEQ_genes Version 1.0

SEQ ID NO 1274

LENDET 1236

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Sequence 2, Application US/10401386B

Sequence 2, Application US/10401386B

Publication No. US20050261213A1

GENERAL INFORMATION:

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TITLE OF INVENTION: Nucleic Acid Compositions and Methods

TITLE OF INVENTION: Nucleic Acid Compositions and Methods

TITLE OF INVENTION: Nucleic Acid Compositions and Methods

TITLE OF INVENTION: 100C1P

CURRENT APPLICATION NUMBER: US/10/401,386B

CURRENT APPLICATION NUMBER: 10/247,203

PRIOR APPLICATION NUMBER: 60/328,371

PRIOR PILING DATE: 2002-09-19

PRIOR FILING DATE: 2001-10-10

NUMBER OF SEQ ID NOS: 81

SEQ ID NOS: 81

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Pred. No. 2.7;
0; Mismatches 2; Indels
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Best Local Similarity 77.8%;
Matches 7; Conservative (
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March 11, 2006, 00:10:50; Search time 86.6667 Seconds (without alignments) 45.628 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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(first entry)

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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in
                                                                               Novel human diagnostic protein #23369.
 ABG23378 standard; protein; 136 AA
                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                            WO200175067-A2
                                                                                                                                                  Homo sapiens.
                                                     18-FEB-2002
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                          ABG23378;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel method for vaccinating an individual against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating an individual with a SCCE peptide, which elicits an immune response in the individual with a SCCE peptide, which elicits an immune response in chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or at risk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligonucleotide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or pancreatic cancer, and other cancers in which SCCE is overexpressed. The peptides are also useful in the monitoring and development of immunotherapies for ovarian and other malignancies. The present sequence represents a peptide fragment of serine protease SCCE (stratum corneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
                                                                                                                                                                                                                                 Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:86.
                            Gaps
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                                                                                                                                                                                                                                                         serine protease; stratum corneum chymotrytic enzyme; SCCE; immune response; ovarian cancer; lung cancer; prostate cancer; pancreatic cancer; colon cancer.
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100.0%; Score 41; DB 4; Length 9; 100.0%; Pred. No. 2e+06; cive 0; Mismatches 0; Indels
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Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Tang YT;

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed consists of (II) are useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a cupylypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders cipylypeptide and polymucleotide sequences have applications in colypeptide and polymucleotide sequences have applications in diagnostics, forgenetic disorders or other trails to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in celectronic format directly from WIPO at
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diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                Claim 20; SEQ ID NO 53737; 103pp; English.
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                                                                               biodiversity.
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RESULT 3 ABG23378

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ADA05736;

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New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                            human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinnonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                Human NOV18c protein SEQ ID NO:96.
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                                                                                                                                                                                                                                                                                                                                                02-OCT-2001; 2001US-0326483P.
05-OCT-2001; 2001US-0327435P.
09-OCT-2001; 2001US-03279179P.
09-OCT-2001; 2001US-0328029P.
09-OCT-2001; 2001US-0328029P.
09-OCT-2001; 2001US-0328044P.
12-OCT-2001; 2001US-0328044P.
12-OCT-2001; 2001US-0328044P.
17-OCT-2001; 2001US-0328044P.
17-OCT-2001; 2001US-0328044P.
17-OCT-2001; 2001US-0328049P.
18-OCT-2001; 2001US-034058P.
24-OCT-2001; 2001US-034058P.
24-OCT-2001; 2001US-034058P.
24-OCT-2001; 2001US-034058P.
24-OCT-2001; 2001US-034058P.
24-OCT-2001; 2001US-034058P.
24-OCT-2001; 2001US-034058P.
25-OCT-2002S-03010S-034058P.
19-APR-2002; 2002US-0373814P.
19-APR-2002; 2002US-0373814P.
19-APR-2002; 2002US-0373817P.
16-MAY-2002; 2002US-0381038P.
16-MAY-2002; 2002US-0381038P.
16-MAY-2002; 2002US-0381038P.
16-MAY-2002; 2002US-0381038P.
17-MAY-2002; 2002US-0381038P.
17-MAY-2002; 2002US-0381038P.
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                                 06-NOV-2003 (first entry)
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N-PSDB; ADA05735
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                                                                                                                                                                                                                     Homo sapiens
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Dipippo VA;

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comparished above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid containers, the composition described above; (3) an isolated nucleic acid containers the nucleic and molecule described above; (5) a cell comprising the nucleic add molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically bresence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above or polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeut agent for use in treating a pathology that is related to an aberrant expression or above; (10) a method for identifying a potential therapeut agent for use in treating a pathology that is related to an aberrant expression or above; (10) a method for identifying a potential therapeut agent for a medulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating or pathology associated with the above polypeptide; NovX sequences have antidabetic, anoretic, antibatetrial, viruide, and antilipaemic activities, and can be used in gene therapy. The copulation activities, and can be used in gene therapy. The and antilipaemic activities, and can be used in gene therapy. The copulationers is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic and disease, immune disorders such as diabetes such as diabetes such as diabetes or obesity, infections, cachexia, cachexia, cachexia, reserved and pathology associated with a numbic acid cachexial and various disease, immune disorders, haematopoletic disorders su
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human, NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopojetic disorder; dyslipidaemia; metabolic syndrome X;
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2001US-0327435P.
2001US-0327449P.
2001US-0327917P.
2001US-0328029P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention.
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05-OCT-2001; 2
09-OCT-2001; 2
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The invention relates to isolated NOVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX by supplementing the patient our polymucleotides may be used to treat disorders associated with decreased complements of NOVX polypeptides and preventing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of probes in diagnostic assays to detect and quantitate the presence of complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of caponists and antagonists of the expression and activity of NOVX. The carti-NOVX polypeptides and plandices and in assays to identify modulators canti-NOVX polypeptide antibodies and antagonists may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX colypeptides and polymucleotide expression and activity of NOVX colypeptides and polymucleotide may be used in this way to prevent, colypeptides and polymucleotides may be used in this way to prevent, colarges and treat: metabolic disorders, diabetes, beauty, neurodegenerative dissorders, allowed to mocavia, cancer, cancer-associated cachexia, neurodegenerative dissorders, and various dyslipidaemas, may also be used as antibacterial agents. The present sequence colarunce of a human NOVX protein.
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                                                                                                                                                                                                                                                                                                                                                                                                      They may also be used as antibacterial agents. The represents the amino acid sequence of a human NOVX
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 Claim 1; SEQ ID NO 96; 395pp; English.
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Best Local Similarity 100.
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N-PSDB; AAQ81203.
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09-AUG-1995
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SR, Ellerman K, Malyankar UM;
derson DW, Zhong W, Catterton E;
ne DJ, Penne CEA, Shenoy SG;
MD, Agee ML, Berghs C, Dipippo VA;
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tek KA, Edinger SR, Ellerman K,
Zerhusen BD, Anderson DW, Zhor
Rastelli L, Stone DJ, Pena CEP
nenberg ME, Leach MD, Agee ML,
EA, Rieger DK, Spaderna SK;
09-OCT-2001; 2001US-0328044P.

12-OCT-2001; 2001US-0328056P.

15-OCT-2001; 2001US-0328414P.

17-OCT-2001; 2001US-0329414P.

18-OCT-2001; 2001US-0330142P.

18-OCT-2001; 2001US-033926P.

24-OCT-2001; 2001US-0349559P.

24-OCT-2001; 2001US-0349559P.

29-OCT-2001; 2001US-0349575P.
                                                                                                                                                                                                                             22-APR-2002; 2002US-0374977P.
16-MAY-2002; 2002US-0381037P.
16-MAY-2002; 2002US-0381038P.
16-MAY-2002; 2002US-0381042P.
17-MAY-2002; 2002US-0381642P.
28-MAY-2002; 2002US-0383656P.
29-MAY-2002; 2002US-0383656P.
                                                                                                                            2001US - 0349575P.
2001US - 034637P.
2002US - 0373860P.
2002US - 0373815P.
2002US - 0373817P.
2002US - 0373864P.
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Ji W, Miller CE, Rastelli L
Shimkets RA, Rothenberg ME,
Eisen A, Gangolli EA, Riege
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25-JUN-2002; 2002US-0391335P
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Patturajan M, Spytek KA,
Ort T, Gorman L, Zerhuse
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STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E.
LEACH M D.
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GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
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SPYTEK K A.
EDINGER S R.
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MALYANKAR U M.
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BERGHS C.
DIPIPPO V A.
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ANDERSON D W.
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PEYMAN J A.
KEKUDA R.
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N-PSDB; ADN62899.
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(KEKU/)
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(GANG/)
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(SPAD/)
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Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and related vectors, transformed cells and polypeptides, useful for treating skin disorders, e.g. acne or psoriasis, and for identification of
                                                                                                                                                                                                              The enzyme encoded by this sequence is used in pharmaceutical, cosmetic and skin care products, especially to treat and prevent acne, xeroderma, or other hyperkeratotic conditions (e.g. callosities or keratosis pilaris), ichthyoses, psoriasis, eczema, etc. It is produced recombinantly following mammal, insect, plant, or microorganism transformation with plasmid pS507. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                        Disclosure; Page 97; 137pp; English.
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                                                                                            specific inhibitors.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 253 AA;
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Human amyloid precursor protein protease (AAW05383) is involved in the processing or clearance of amyloid precursor protein to form beta-amyloid peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783) obtd. from a human lung library. Recombinant protease can be produced in transformed or transfected prokaryotic (partic. E. coli) or eukaryotic and testing of cods. useful for treating or preventing conditions associated with beta-amyloid peptide, esp. Alzheimer's disease

Sequence 253 AA;

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This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide equence comprising at least a significant part of a nucleotide sequence condinging of least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, or stratum corneum chymotryptic enzyme (SCCE) or its variant, or promoter that drives expression of heterologous scce or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development of a diagnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal hyperkeracosis, ecompound or composition or treatment of an anodel for further studies of tich mechanisms and the testing of potential compounds and compositions for relieve of various skin diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           potential compounds and compositions for relieve of various skin diseases where itch is a component. This sequence represents the N-terminal fragment of the human stratum corneum chymotryptic enzyme, SCCE synonymous with human kallikrein 7 (KLK7), used in the development of the transgenic mammals described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
                                                                                 Gaps
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100.0%; Score 41; DB 2; Length 253; ilarity 100.0%; Pred. No. 4.3; Conservative 0; Mismar-L
                                                                                                                                                                                                                                                                                                                                                                                                                          Human SCCE protein N-terminal fragment SEQ ID 48.
                                                                                                                                                                                                                                                                                    ABB84421 standard; peptide; 253 AA.
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09-FEB-2001; 2001DK-00000218.
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                                                                                                                        1 MARSLLLPL
                                                       Similarity
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Length 253; Indels

DB 5;

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with human kallikrein 7 (KLK7) and is used in the development of the transgenic mammals described in the invention
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Best Local Similarity
                                                                                                           Sequence 253 AA;
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                                                                       100.0%; Score 41; DB 5; Length 253; 100.0%; Pred. No. 4.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB84406 standard; protein; 253 AA.
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09-FEB-2001; 2001DK-00000218.
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1 MARSLLLPL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human SCCE protein.
                                                                                                        Local Similarity
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(HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABQ76226.
          Sequence 253 AA;
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                                                                           Query Match
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ABB84406
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The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breaat, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. restenosis and coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. restenosis and coronary thrombosis), pain, sexual dysfunction, mood disorders (e.g. relations diseases, migraines, pain, sexual dysfunction, mood disorders, attention disorders, capation disorders, hypotension, psychotic disorders, neurological disorders (e.g. Albaimer's disease, Parkinson's disease) and dyskinesias. The nucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. c. human proteases of the invention
                                                                                                                                                   Human; protease; cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder; hypertension; psychotic disorder; neurological disorder; disorder; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sudarsanam S, Manning G, Caenepeel S;
                                                                                                                  Amino acid sequence of novel human protease #39.
AAU82740 standard; protein; 253 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Fig 2N; 313pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-2001; 2001WO-US020171.
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                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABK31782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Charydczak G;
                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                             23-APR-2002
                                                                                                                                                                                                                                                                                                                                                                              03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plowman G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders.
                                       AAU82740;
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The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves determining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer. Of target genes which are differentially-regulated in prostate cancer. (I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells, which involves contacting a polypeptide differentially-regulated contextions in prostate cancer cells with a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, charactering a prediaposition to diseases and conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer cells, in tissue sections, in biopsy sample, in total RNA, in lymph, in blood etc. (I) is useful for assessing cancer e.g., to determine the type of cancer, its stage of development, the nature of genetic detect, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.
                                                                                      Gaps
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                                           100.0%; Score 41; DB 5; Length 253; 100.0%; Pred. No. 4.3;
                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Protein differentially regulated in prostate cancer #43.
                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                 ABU07440 standard; protein; 253 AA
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                                        Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Sequence 253 AA;
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The polypeptide encoded by (I) can be used as target for therapy or drug discovery. (I) can also be used for expressing the polypeptide and thus for searching specific binding partners of the polypeptide and thus in therapeutic applications to treat prostate cancer. The identification of specific genes, and groups of genes, expressed in pathways physiologically relevant to prostate cancer permits the definition of functional and disease pathways and the delineation of targets in these applications. This is the amino acid sequence of a protein differentially regulated in prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves determining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer. Preferably, the expression levels of at least 10 genes are determined. (I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells, which involves contacting a polypeptide differentially-regulated
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prostate cancer; gene expression; differential regulation;
molecular marker; drug target; cancer detection; cancer diagnosis;
cancer staging; cancer grading; cancer assessing; cancer monitoring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for diagnosing prostate cancer in prostate tissue sample and assess therapeutic or preventive intervention in prostate cancer patients.
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                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 41; DB 6; Length 253; Best Local Similarity 100.0%; Pred. No. 4.3; Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                             Sequence 253 AA;
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Sequence 253 AA;

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The processor can call which a cast again united controlled. The processor can be called a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, diagnosing, grading, assessing, monitoring, prognosticating, preventing or treating, determining predisposition to diseases and conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer. (Conditions assessing to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer. (Conditions, in biopsy sample, in total RNA, in lymph, in blood etc. (I) is useful for assessing cancer og., to determine the type of cancer, its stage of development, the nature of genetic defect, etc. (The polypeptide encoded by (I) can be used as target for therapy or drug discovery. (I) can also be used for expressing the polypeptide and thus for searching specific binding partners of the polypeptide and thus for searching specific binding partners of the polypeptide. (I) is useful of specific genes, and groups of genes, expressed in pathways of genes, cancer permits the definition of functional and disease pathways and the delineation of targets in these pathways which are useful in diagnostic, therapeutic, and clinical applications. This is the amino acid sequence of a protein differentially regulated in prostate cancer.
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prostate cancer cells with a test agent under conditions effective for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human stratum corneum chymotryptic enzyme - ovarian cancer clone 01676P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-OCT-2001; 2001US-0327135P. 30-MAY-2002; 2002US-0384531P.
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Best Local Similarity luv.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 253 AA;
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polymucleotides of the invention have cytostatic activity, and may have a use in gene therapy, and in a vaccine. The composition and methods are useful in diagnosing and/or treating cancer, particularly ovarian cancer. The composition may also be used as a vaccine to prevent cancer. The present sequence is used in the exemplification of the invention

The invention relates to a novel isolated polynucleotide. The

Claim 2; Page 157-158; 169pp; English

New polynucleotide and polypeptide useful for diagnosing and/or treating cancer, particularly ovarian cancer, and as a vaccine.

WPI; 2003-372001/35.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method of detecting an ovarian cancer-
associated transcript in a cell from a patient, by contacting
biological sample from the patient with a polynucleotide that selectively
hybridizes to a sequence at least 80% identical to any of one of 80
nucleic acid sequences given in the specification. The method is useful
in diagnosing ovarian cancer and in identifying and using agents and/or
targets that inhibit ovarian cancer. The nucleic acid molecule,
polypeptide and the antibody may also be used in detecting ovarian
cancers, monitoring and early detection of relapse following treatment,
monitoring response to therapy, selecting patients for post-operative
chemotherapy or radiation therapy, in selecting mode of therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              determining tumour prognosis, early detection of pre-cancerous lesions, and as vaccines. This sequence corresponds to one of the proteins used
                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection.
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               6; Length 253;
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                                                0; Indels
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                 Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                      Ovarian cancer-associated protein #24.
                                                                                                                                                                                                   ADB80484 standard; protein; 253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; Page 291; 332pp; English.
               100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUN-2001; 2001US-0299234P.
27-AUG-2001; 2001US-0315287P.
05-SEP-2001; 2001US-031544P.
13-NOV-2001; 2001US-0350666P.
12-APR-2002; 2002US-0372246P.
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Query Match
Best Local Similarity 100...
9; Conservative
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Best Local Similarity
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                                                                                                     1 MARSLLLPL
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                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial concephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRP) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, antidiabetic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huntington's disease; osteoarthritis;
Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalogathy lactic acidosis and stroke; MELAS;
mycolonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; noctropic; antidiabetic; anticonvulsant; antiarthritic;
osteopathic; ophthalmological; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human heat mitochondrial protein as a therapeutic target SeqID639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mitochondrial; human; screening assay; diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gibson BW, Taylor SW,
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                                                                                                                                                                                                                                                  ADJ68833 standard; protein; 253 AA.
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17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
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(BUCK-) BUCK INST AGE RES.
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   MARSLLLPL
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Warnock DE;
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Glenn GM;

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Query Match

100.0%; Score 41; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels

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Search completed: March 11, 2006, 00:24:18 Job time : 88.6667 secs
 1 MARSLLLPL 9
                1 MARSLLLPL
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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protein search, using sw model OM protein - Run on:

March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds (without alignments) 61.367 Million cell updates/sec

US-09-905-083A-86 Title: Perfect score:

1 MARSLLLPL 9 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\*
1: pir1:\*
2: pir2:\*
1: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

-	Description	serine proteinase	suppressor protein		hypothetical prote	matrix metalloprot	matrix metalloprot	hypothetical prote	DNA-binding protei	hypothetical prote	conserved membrane	ionotropic glutama	probable ligand-ga	hypothetical prote	sodium channel alp	hetical p	c	cell division inhi	hypothetical prote	lydro	probable transamin	probable transamin	ដ	m		cytolysin B transp		poly	corazonin precurso	hypothetical prote
SUMMARIES	8	A53968	A46394	B87343	E96550	I48673	I84471	B97856	C82169	A83060	B87102	T51136	F84732	T38055	I48107	828698	AB0627	B29016	B86450	T11364	C71917	H64597	A83734	JC6197	831330	T43109	B25019	T17464	JC2384	T17834
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d	Query Match	100.0	82.9	80.5	80.5		80.5		78.0	78.0	78.0	78.0	78.0	78.0	75.6	75.6	75.6	75.6	75.6	75.6	75.6	75.6	75.6	75.6	75.6	75.6	75.6	75.6	73.2	73.2
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histone-like DNA-b DRE/CRT-binding pr	transcription fact hypothetical prote	hypothetical prote transcription acti	transcription acti probable transcrip	probable transcrip	probable transcrip	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	transmembrane glyc
S43476 JE0297	T51830 D82132	T17832 D85294	T05799	B86025	A91179	T25122	A97482	A12699	G87494	A48931
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170	216	299	314	323	323	325	325	325	331	354
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30 31	33.2	3.4 3.5	36	38	3 9 0 0	4.1	42	43	44	45

## ALIGNMENTS

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Cispeciaes: Homo sapiens (man)
Cipate: 07-Unl-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
R.Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Bgelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A;Reference number: A53968
A;Reference number: A53968
A;Residues: 1-253 cHAN>
A;Gene: GDB:PRSS6; SCCE
A;Gene: GDB:PRSS6; SCCE
A;Gene: GDB:PRSS6; SCCE
A;Gene: GDB:PRSS6; CCE
A;G
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serine proteinase SCCE precursor - human
N;Alternate names: stratum corneum chymotryptic enzyme
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Matches 9; Conserv
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RESULT 2

mutation, is essential for transla NyAlternate names: protein L1531; protein YLR005w Cispecies: Saccharomyces cerevisiae Cispecies: Saccharomyces cerevisiae Cipate: 18-May-1994 #eequence\_revision 19-Jul-1996 #text\_change 31-Dec-2004 Cipate: 18-May-1994 #equence\_revision 19-Jul-1996 #text\_change 31-Dec-2004 Cipate: 18-May-1994 #equence\_revision 19-Jul-1996 #text\_change 31-Dec-2004 Cipate: 18-May-1994 #equence\_revision 19-Jul-1996 #text\_change 31-Dec-2004 Cipate: 20-May-1994 #equence\_revision 19-Jul-1996 #text\_change 31-Dec-2004 Aritle: SSII, a suppressor of a HIS4 5'-UTR stem-loop mutation, is essentic Areference number: A46394; MUID:94040711; PMID:1340463

A;Accession: A46394 A;Status: preliminary A;Molecule type: DNA

A;Residues: 1-461 <YOO>
A;Residues: 1-461 <YOO>
A;Cross-references: UNIPROT:Q04673; UNIPARC:UPI0000053049; GB:Z17385; NID:g2695; PID:g2695; R;Vandenbol, M.; Portetelle, D.; Hilger, F.
B;Vandenbol, M.; Portein Sequence Database, May 1996
A;Reference number: S64742
A;Reference number: S64827

Mon Mar 13 12:28:02 2006

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80.5%;
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A, Gene: F11M15.13
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C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C; Ccession: E96550
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.H.; C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughee, B.; Huizar, L.
Nature 408, 816-820, 2000
A,Authors: Hunter, J.L.; Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C.C., Li, J.J., T.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A,Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A,Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A,Accession: E96550
                                                     A;Cross-references: UNIPARC:UPI0000053049; EMBL:Z73177; NID:g1360293; PID:g1360294; MIPS
A;Note: experimental source strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession B87343
C;Accession B87343
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. US.A. 98, 4136-4141, 201
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-397 <5TO>
A;Cross-references: UNIPROT:Q9AA49; UNIPARC:UPI00000C7168; GB:AE005673; NID:g13421992;
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein CC0757 [imported] - Caulobacter crescentus
                                                                                                                                                                                                   A,Map position: 12R
C,Suberfamily: TFIIH basal transcription factor complex, subunit SSL1
C,Keywords: transmembrane protein
F,356-372/Domain: transmembrane #status predicted <TMM>
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                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                        Score 34; DB 2;
Pred. No. 21;
1; Mismatches
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3; Mismatches
                                                                                                                                           A,Gene: SGD:SSL1
A,Cross-references: SGD:S0003995; MIPS:YLR005w
                                                                                                                                                                                                                                                                                                                                              82.9%;
77.8%;
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 77.0
Ear 7; Conservative
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Matches 6; Conservative
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285 LARALILPL 293
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A; Residues: 1-571 <STO>
                             A; Residues: 1-461 < VAN>
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C;Accession: 148673
R;Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, P. Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A;Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cellA;Reference number: 138046; MUID:95224014; PMID:7708715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-582 <RES>
A; Cross-references: UNIPARC: UP10000030971; EMBL: X83536; NID: 9804999; PIDN: CAA58520.1; PII
C; Superfamily: interstitial collagenase; hemoperain repeat homology; matrix metalloproteir C; Keywords: hydrolase; metalloproteinase; zinc; zymogen
F; 1-23/Domain: signal sequence #status predicted <SIG>
F; 24-97/Domain: activation peptide #status predicted <PRO>
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F;93,239,243,249/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status F;239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
F;240/Active site: Glu #status predicted
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N;Alternate names: membrane-type metalloproteinase
C;Species: Rattus norvegicus (Norway rat)
C;Dapei 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 184471; 161946
R;Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, P.
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A;ritle: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cell
A;Reference number: 138046; MUID:95224014; PMID:7708715
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A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Moolecule type: mRNA
A.Residues: 1-582 <RES>
A.Residues: 1-582 <RES>
A.Cross-references: UNIPROT:Q10739; UNIPARC:UP10000030970; EMBL:X83537; NID:g805012; PIDN-A.Accession: 161946
A.Accession: 161946
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-67, 'M', 69-254, 'A', 256-582 <RE2>
A.Cross-references: UNIPARC:UP100001679D1; EMBL:X91785; NID:g1001926; PIDN:CAA62897.1; Pl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999
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                                                                                         Gape
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Length 571;
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87.5%; Pred. No. 43;
1.ve 1; Mismatches 0; Indels
                                                                                    1; Indels
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(7)
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A,Molecule type: mRNA
                                                                                    Mismatches
    Score 33;
Pred. No.
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accesion: A83060
R;Stover, C.K.; Pham, X.Q.; Brwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Briadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A;Accession: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-432 cSTO-
A;Cross-references: UNIPROT:Q9HVB1; UNIPARC:UPI00000C5DC4; GB:AE004882; GB:AE004091; NID
A;Experimental source: strain PAO1
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C)Species: Mycobacterium leprae
C)Species: Mycobacterium leprae
C)Species: Mycobacterium leprae
C)Species: Mycobacterium leprae
C)Appr-2001 #text_change 09-Jul-2004
C)Accession: B87102
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, am. M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A,Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sqn A;Title: Massive gene decay in the leprosy bacillus.
A,Title: Massive gene decay in the leprosy bacillus.
A,Reference number: A86909; MUID:21128732; PMID:11234002
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-506 <STO>
A;Cross-references: UNIPROT:Q9Z513; UNIPARC:UPI0000D4376; GB:AL450380; NID:g13093364; P)
C;Genetics:
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C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004
C;Accession: T51136
R;Davenport, R.J; Kiegle, E.A.; Tester, M.
submitted to the EMBL Data library, December 1999
A;Description: GLR5, an ionotropic glutamate receptor ortholog from Arabidopsis. A;Reference number: 225309
                                                                            hypothetical protein PA4684 [imported] - Pseudomonas aeruginosa (strain PAO1)
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C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1782
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 61;
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Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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A; Gene: PA4684
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DNA-binding protein inhibitor Id-2-related protein VC1696 [imported] - Vibrio cholerae (Cispeciaes: Vibrio cholerae) (Cispec
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C;Genetics:
A;Gene: RC1250
F;61-284/Domain: matrix metalloproteinase homology <MMP>
F;313-508/Domain: hemopexin repeat homology <PXN>
F;33-539,243,249/Binding site: zinc, catalytic (Cys, His, His, His, His) (inhibited) #status F;239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
F;240/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B97856

Hypothetical protein RC1250 [imported] - Rickettsia conorii (strain Malish 7)

C,Species: Rickettsia conorii
C,Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C,Accession: B97856
R;Ogata, H.; Audic., S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
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                                                                                                                                                                                                              80.5%; Score 33; DB 2; Length 582;
87.5%; Pred. No. 43;
                                                                                                                                                                                                                                                                                          0; Indels
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Pred. No. 9.3;
2; Mismatches
                                                                                                                                                                                                                                                                               1; Mismatches
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Similarity 75.0%;
6; Conservative
                                                                                                                                                                                                              Query Match 80.5
Best Local Similarity 87.5
Matches 7; Conservative
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Matches 6; Conserv
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les 7; Conser
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A, Status: preliminary
A, Molecule type: DNA
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A, Map position: 1
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A;Molecule type: mRNA A;Residues: 1-921 <DAV>

1; Mismatches

7; Conservative

Matches

|||| |:|| 705 MARSRLVPL 713

1 MARSLLLPL 9

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78.0**%**; 77.8**%**;

Query Match Best Local Similarity

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-138 <RES>
A;Cross-references: UNIPROT:Q60463; UNIPARC:UPI00000E7D6C; GB:M87540; NID:g191067; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dispondentical protein 16 - Agrobacterium tumefaciens plasmid pri15955
C;Species: Agrobacterium tumefaciens
C;Accession: S28698
R;Barker, R.F.; Idler, K.B.; Thompson, D.V.; Kemp, J.D.
Plant Mol. Biol. 2, 335-350, 1983
A;Title: Nucleotide sequence of the T-DNA region from the Agrobacterium tumefaciens octog
A;Reference number: S28698
A;Reference number: S28698
A;Reference number: S28698
A;Reference under: Agrobacterium tumefaciens octog
A;Accession: S28698
A;Reference under: S28698
A;Refere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: 148107
R;Lalik, P.H.; Krafte, D.S.; Ciccarelli, R.B.
Am. J. Physiol. 264, 803-809, 1993
A;Title: Characterization of endogenous Sodium channel gene expressed in chinese hamster
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                                                                                                                                                                                                                                                                                                                                                                                                                   sodium channel alpha subunit - long-tailed hamster (fragment)
C;Species: Cricetulus longicaudatus (long-tailed hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 26;
2; Mismatches 0; Indels
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    100.0%; Fred. No. 2e+02;
tive 0; Mismatches 0;
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87.5%; Pred. No. 28;
ive 0; Mismatches
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C,Superfamily: sodium channel protein
C,Keywords: duplication
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Best Local Similarity 75.0%;
Matches 6; Conservative
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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A; Accession: 148107
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1 MARSVLVP 8
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                                                                                                                             3 RSLLLPL
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A;Residues: 1-923 <STO>
A;Cross-references: UNIPROT:Q9SDQ4; UNIPARC:UPI000017A6D8; GB:AE002093; NID:g3831456; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable ligand-gated ion channel subunit [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 0.2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C; Accession: F84732
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; euss, D.; Nicerman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vanter, J. Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
A; Titles: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID: 20083487; PMID: 10617197
                                                                         A;Cross-references: UNIPROT:09SDQ4; UNIPARC:UPI00000A3CD0; EMBL:AF210701; PIDN:AAF21042.
C;Genetics:
A;Gene: glr5
A;Gene: glr5
A;Map position: 2
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A;Reference number: Z2176
A;Reference number: Z21776
A;Accession: T38177
A;Accession: T38177
A;Residues: 8-1621 < LY2>
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                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 1.1e+02;
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Score 32; DB 2; 1 Pred. No. 1.1e+02;

78.0%; 77.8%;

Query Match
Best Local Similarity 77.8
Matches 7; Conservative

C;Genetics: A;Gene: At2g32400 A;Map position: 2

A; Status: preliminary

|||| |:|| 707 MARSRLVPL 715

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1 MARSLLLPL 9

1; Mismatches

78.0%; Score 32; DB 2; Length 1628;

A, Cross-references: UNIPARC: UPI000017B1DE; EMBL: Z54285; NID: 91008429; PIDN: CAA91079.2;

Genetics: Gene: SPACID4.14

A; Map position: Query Match

A;Reference number: 221765
A;Accession: T38055
A;Status: preliminary
A;Modecule type: DNA
A;Reaidues: 1-26 < LY1>

Search completed: March 11, 2006, 00:40:53 Job time : 16.1111 secs

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Q6dtyl homo sapien
Q5443 homo sapien
Q5443 homo sapien
Q5418 homo sapien
Q9nzll homo sapien
Q9nzll homo sapien
Q9nzl2 homo sapien
Q9y5z0 homo sapien
Q9y5z0 homo sapien
Q9y5z0 homo sapien
Q9xz5 neurospora
Q8ny89 arabidopsis
Q7nz54 neurospora
Q8n584 oryza sativ
Q6h537 saccharomyc
Q6ta5 candida gla
Q61237 saccharomyc
Q6sd7 triticum ae
Q61237 saccharomyc
Q6sd7 triticum ae
Q6124 arabidopsis
Q56y44 arabidopsis
Q56y4 arabidopsis
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Q56y2 oryza sativ
Q7p0i6 chromobacte
Q5v391 brachymonas
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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Q84W49 ARATH
Q95ATTO ARAZH
Q95ATTO ARAZH
Q97BAZ ANDUK
Q67D4 Z SNWT
Q67U4 Z SNWT
Q68237 YEAST
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Q68257 WHEAT
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Q68257 WHEAT
Q6825 ARATH
Q97NC4 ARATH
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Q97NC4 ARATH
Q98V25 GYENC
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Q85AT6 QRYSA
Q95V391 9BURK
Q85AT6 QRYSA
Q93AT6 GRYSA
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Q9SYC9 ARATH
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Maximum Match 100%
Listing first 45 summaries
                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
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MWP14_MOUSE MWP14_RAT Q8BYX2_MOUSE G6DFW5_MOUSE G6DFW5_MOUSE G6SS23_ENCCU G9BER4_CHICK G6SZ3_ENCCU G9SR4_CHICK G9SR4_CHICK G6SY67_RECN G9SR6_VIBCH G6SR6_VIBCH G6SR6_VIBCH	ALIGNMENTS	PRT; 66 AA. reated) ast sequence update ast annotation upda . Craniata; Vertebra oglires; Primates;	andis E.P.; EMBL/GenBank/DDBJ -; mRNA. 82E1C392BC822FDB	Score 41; DB 2; ; Pred. No. 0.99; 0; Mismatches 0;		T; 253 AAnce update) ation updat 1) (hK7) aniata; Ver ires; Prima CRM 1), AND kman A., Wa terization ific human
00000000000000		28, 28, 28, ant date	Diam the '.1; MW;	66		77, 77, 77, 77, 77, 77, 77, 77, 77, 77,
582 582 582 582 582 582 934 1048 1124 1124 1136 1149		MINARY;  Urel. 28, C  Urel. 28, L  Urel. 28,	717	larity 100 Conservative	on on	STANDARD; QBNEV7; 11. 34, Created) 11. 34, Last sequescent Last sequescent CS 3.40.  recursor (CS 3.40.  rayme) (hSCCE).  rayme) (hSCCE).  rayme) (hSCCE).  rayme) (hSCCE).  rayme) (hSCCE).  rayme (hSCEE).
888800.5 8800.5 8800.5 78800.5 78800.5 788000.5		TIT 1 QEDTY1 HUMAN PRELIMINARY; QEDTY1 HUMAN PRELIMINARY; QEDTY1 HUMAN PRELIMINARY; QEDTY1 25-OCT-2004 (TEMBLEE]. 26 25-OCT-2004 (TEMBLEE]. 26 25-OCT-2004 (TEMBLEE]. 26 Z5-OCT-2004 (TEMBLEE]. 26 Z5-OCT-2004 (TEMBLEE]. 26 MAILKEEIN 7 SPLICE VARIATION SULPARYOLE; HOMO SAPIENS (HUMAN). BUKATYOLE; HOMO. NCBI_TAXID=9606;	NUCLECATIDE SEQUENCE. TISSUE=Brain, Kishi T., Michael I.P., Dia Submitted (JUN-2004) to the EMBL; AY64152; AAT66047.1; SEQUENCE 66 AA; 7171 MW;	Similarity 9; Conser	MARSLLLPL          	LT 2 HUMAN  STANDARD; PR P49862; QBNSN9; QBNFV7; O1-OCT-1996 (Rel. 34, Created) O1-OCT-1996 (Rel. 34, Last seque L1-SEP-2005 (Rel. 34, Last seque STANDARD; SALlikrein 7 precursor (C 3.4.2 chymotryptic enzyme) (hSCCB; Name=KLK7; Synonyma=PRSS6, SCCE; HOMO sapiens (Human). Eukaryota; Metazoa; Chordata; Cr HOMO sapiens (Human) Eukaryota; Metazoa; Chordata; Cr HOMO. NCBI_TAXID=9606; IL) NUCLEOTIDE SEQUENCE [MENA] (ISOF TISSUE=SKin; MEDLINE=94308225; PubMed=8034709 HANDSON L., Stroemqviet M., Baec Egelrud T.; CLOning, expression, and charac chymotryptic enzyme. A skin-spec
		11 HUMAN QEDTY1 HUMAN PRE QEDTY1, HUMAN PRE QEDTY1, 25-OCT-2004 (TrE 25-OCT-2004 (TrE 25-OCT-2004 (TrE Mallikrein, 7 spl HOMO sapiens (Hu Bukaryota, Metaz Mammalia, Euther HOMO.	NUCLEOTIDE SE TISSUE=Brain; Kishi T., Mic Submitted (JU EMBL; AY64615 SEQUENCE 66	atch cal	1 1 M_M	HUMAN KLK7 HUMAN KLK7 HUMAN P4986.2, 0808N9; 01-0CT-1996 (Re 113-SEP-2005 (Re Kallikrein 7 pr. chymotryptic en Name-KLK7; Syno Homo sapiens (He Mammalia; Buthe Homo. NCBI_TaxID=9606 [1] NUCLEOTIDE SEQU TISSUE-SKin; MEDLINES-9430822 HANSSON L.; Str Egelrud T.; Str Egelrud T.; Egelru
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MEDLINE=228825; PubMed=12477932; DOI=10.1073/pnss.242603899; MEDLINE=228825; PubMed=12477932; DOI=10.1073/pnss.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Villalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A., Faby J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Youchan J.W., Shevchenko Y., Bouffard G.G., A Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C., A Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C., A Butterfield Y.S.N., Krzywinski W.I., Skalska U., Smailus D.E., Rechertical M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Touchman J.W., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones C. Handley R.W., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones R.M., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones R.M., J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M.,
                                                                                                                                                                   Yousef G.M., Scorilas A., Magklara A., Soosaipillai A., Diamandis B.P.,
"The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic enzyme is a new member of the human kallikrein gene family - genomic characterization, mapping, tissue expression and hormonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chymotryptic enzyme.";
Biochem. Biophys. Res. Commun. 211:586-589(1995).

-I- FUNCTION: May catalyze the degradation of intercellular cohesive structures in the cornified layer of the skin in the continuous shedding of cells from the skin surface. Specific for amino acid residues with aromatic side chains in the PI position. SCCE cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-phe-|-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the activation of precursors to inflammatory cytokines.
[2]
NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skytt A., Stroemgvist M., Egelrud T.;
"Primary substrate specificity of recombinant human stratum corneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [GENOMIC DNA].
PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
MOSS P., Peeper B., Wang K.;
"Sequencing and expression analysis of the serine protease gene
cluster located in chromosome 19q13 region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Hansson L., Baeckman A., Ny A., Edlund M., Edholm E., Tornell J., Wallbrandt P., Egelrud T.;
"Epidermal overexpression of stratum corneum chymotryptic enzyme mice; a model for chronic ithchy dermatitis.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22623266; PubMed=12738725; Dong Y., Kaushal A., Brattsand M., Nicklin J., Clements J.A.; "Differential splicing of KLK5 and KLK7 in epithelial ovarian produces novel variants with potential as cancer blomarkers.";
                                                                                      TISSUE=Keratinocyte;
PubMed=10974542; DOI=10.1016/S0378-1119(00)00280-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clin. Cancer Res. 9:1710-1720 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95314630; PubMed=7794273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Ovarian carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cluster located in chrom
Gene 257:119-130(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                3ene 254:119-128(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                           regulation."
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-!- SUBCELLULAR LOCATION: Secreted. In ovarian carcinoma, secreted and
                                                                                                           Name=1; Synonyms=Long;
IsoId=P49862-1; Sequence=Displayed;
Name=2; Synonyms=Long;
IsoId=P49862-2; Sequence=VSP_013581;
IsoId=P49862-1; IsoId=P49862-1;
IsoId=P49862-1; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (By similarity).
(By similarity).
(By similarity).
(By similarity).
                        also observed at the apical membrane and in cytoplasm at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR00124; Peptidase_S1_A.
InterPro; IPR001214; Peptidase_S1_A.
Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00702; TRYPSIN.
PROSITE; PS00240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN BIS; 1.
Alternative splicing; Direct protein sequencing; Glycoprotein;
Hydrolase; Protease; Serine protease; Signal; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTId=VSP 013581.
-> W (in Ref. 6; AAH32005).
2D68B6B15A76A668 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0008236; F:serine-type peptidase activity; TAS. GO; GO:0008544; P:epidermis development; TAS. InterPro; IPR001254; Peptidase S1 S6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Charge relay system (Recharge relay system (Recharge relay system (Recharge relay system (N-linked (GlcNAc...) By similarity.                                                                                           Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Activation peptide.
Kallikrein 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 1 peptidase S1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L33404; AAC37551.1; -; mRNA.
EMBL; AF166330; AAD49718.1; -; Genomic_DNA.
EMBL; AF243527; AAG33360.1; -; Genomic_DNA.
EMBL; AF241214; AAN03662.1; -; Genomic_DNA.
EMBL; AF411214; AAN03662.1; -; mRNA.
EMBL; BAF411215; AAN03663.1; -; mRNA.
EMBL; BC032005; AAH32005.1; -; mRNA.
FIR; AS3968; AS3968.
HSSP; P00760; 1EZX.
MEROPS; SO1.300; --
ENSG00000169035; Homo sapiens.
HGNC; HGNC; 6368; KLK7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptidase S1.
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                                                 invasive front.
ALTERNATIVE PRODUCTS:
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253
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1112
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137
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221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    subfamily
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CARBOHYD
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CHAIN
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TISSUBE-Placenta;

TISSUB-Placenta;

TISSUB-Plac
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                                                                                                                                                                                                                                                                                                  QSKHEZ; QBNBY4;
10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Polyserase-2 precursor (EC 3.4.21.-) (Polyserine protease-2) (Protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genet. 36:40-45(2004).

Genet. 36:40-45(2004).

FUNCTION: Serine protease. Hydrolyzes the peptides N-t-Boc-Gln-Ala-Arg-AMC and N-t-Boc-Gln-Gly-Arg-AMC and, to a lesser extent, N-t-Boc-Ala-Phe-Lys-AMC, and N-t-Boc-Val-Leu-Lys-AMC. Has a preference for substrates with an Arg instead of a Lys residue in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Human polyserase-2, a novel enzyme with three tandem serine protease domains in a single polypeptide chain."; J. Biol. Chem. 280:1953-1961(2005).
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=15536082; DOI=10.1074/jbc.M409139200;
Cal S., Quesada V., Llamazares M., Diaz-Perales A., Garabaya C.,
Lopez-Otin C.;
                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [MRNA], ENZYME ACTIVITY, ENZYME REGULATION.
SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND N-GLYCOSYLATION.
                      DB 1; Length 253;
                                                                   0; Indels
                   100.0%; Score 41; DB 1 100.0%; Pred. No. 3.7;
                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                0;
Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                              MARSLLLPL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                  MARSLLLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rissum=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                 serine 36).
Name=PRSS36;
                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                                          HUMAN
POLS2_F
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         ENZYME REGULATION: Inhibited by serine proteinase inhibitor 4-(2-aminoethyl)-benzenesulfonyl fluoride, but not with EDTA or E-64. SUBCELLULAR LOCATION: Secreted. Extracellular matrix. Not attached
                                   (Potential). (Potential). (Potential).
                                                                                                                                                                                                                                                                                                                                    Pfam; PF00089; Trypsin; 3.

PRINTS; PR00722; CHYMOTRYPSIN.

SMARINS; PR00020; Tryp_SPc; 3.

PROSITE; PS50240; TRYPSIN DOM; 3.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

Extracellular matrix; Glycoprotein; Hydrolase; Protease; Repeat; Serine protease; Signal; Zymogen.
                                                                                                                                     -i- PTM: The 3 procease domains are not proteolytically cleaved.
-i- PTM: N-glycosylated.
-i- SIMILARITY: Belongs to the peptidase S1 family.
-i- SIMILARITY: Contains 3 peptidase S1 domains.
-i- CAUTION: Ref. 2 sequence differs from that shown due to a frameshift in position 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity)
similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIAF788019BD3A71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                 EMBL; AJ627034; CAF25303.1; -; mRNA.
EMBL; AK075142; BAC11431.1; ALT_FRAME; mRNA.
HSSP; P00750; 1RTF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-linked (GlCN)
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                    Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36;
                                                                                                                                                                                                                                                                                               MEROPS; S01.414; -.
HGNC; HGNC:26906; PRSS36.
InterPro; IPR001254; Peptidase_S1_£
InterPro; IPR001314; Peptidase_S1_K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91921 MW;
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                                                                                                                              (By similarity).
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855 AA;
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RESULT 7
BACE2 HUMAN
ID BACE2 HUMAN
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WEDLINE=20422477; PubMed=10965118;

WEDLINE=20422477; PubMed=10965118;

WEDLINE=20422477; PubMed=10965118;

Solans A., Estivill X., de La Luna S.;

Alzheimer's amyloid precursor protein beta-secretase.";

Lytogenet. Cell Genet. 89:177-184(2000).

EMBL; AP189277; AAF35836.1; -; mRNA.

RSP; P56817; 1FKN.

RSP; P56817; 1FKN.

RSP; P56817; 1FKN.

RO; GO:0016021; C:integral to membrane; ISS.

GO; GO:0016021; C:integral to membrane; ISS.

RO; GO:0016486; P:membrane protein ectodomain proteolysis; ISS.

RO; GO:0016486; P:peptide hormone processing; ISS.

RO; GO:0016486; P:peptide hormone processing; ISS.

RILEFPC; IPR009119; Pept_Al_BACE.

RILEFPC; IPR009121; Pept_Al_BACE.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Sun X., Wang Y., Qing H., Christensen M.A., Liu Y., Zhou W., Tong Y.,
Xiao C., Huang Y., Zhang S., Liu X., Song W.;
"Distinct transcriptional regulation and function of the human BACE2
and BACE1 genes.";
FASEB J. 19:739-749(2005).
BENBL; AY769996; AAX14808.1; -; Genomic_DNA.
                               Gaps
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Pred. No. 13;
2; Mismatches 0; Indels
                               Indels
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Last annotation update)
Pred. No. 1.4e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                            QSDIH8 HUMAN PRELIMINARY;
QSDIH8;
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Q9NZL1;
Similarity 88.5
8; Conservative
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Matches 7; Conservative
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4 LARALLLPL 12
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Best Local
Matches
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GO; GO:0005509; P:membrane protein ectodomain proteolysis; ISS.
GO; GO:0042985; P:negative regulation of amyloid precursor pr. . .; ISS.
GO; GO:0016486; P:peptide hormone processing; ISS.
InterPro; IPR009119; Pept Al BACE.
InterPro; IPR009121; Pept Al BACE.
InterPro; IPR00907; Pept App AS.
InterPro; IPR009007; Pept Aspartc_cat.
InterPro; IPR001641; Peptidase_A1.
Pfam; PF00026; Asp; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominldae;
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WEDLINE=20422477; PubMed=10965118;
Solans A., Betivil X., de La Luna S.;
Solans A., Estivil X., de La Luna S.;
A new aspartyl protease on 21422.3, BACE2, is highly similar to Alzheimer's amyloid precursor protein beta-secretase.";
Alzheimer's amyloid precursor protein beta-secretase.";
Sytogener. Cell Genet. 89:177-184(2000).
EMBL; AF188276; AAF35835.1; -; MRNA.
HSSP; P56817; 1FKN.
Ensembl; ENSCHOOO0182240; Homo sapiens.
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                                                                                                                                                                                                                                                                            396 AA; 43013 MW; 5023A7AF391CEAC9 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                        cat.
InterPro; IPR001969; Pept_Asp_AS.
InterPro; IPR003007; Pept_Aspartc_ca
InterPro; IPR0030461; PeptTdase_A1.
Pfam; PF00026; Asp; 1.
PRINTS; PR01817; BACE2.
PRINTS; PR01815; BACEPAMILY.
PRINTS; PR01815; PEPSIN.
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PRINTS; PR00792; PEPSIN.
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QƏNZL2 HUMAN PRELIMINARY;
QƏNZL2;
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4 LARALLLPL 12
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4 LARALLLPL 12
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MEDIINE=20144066; PubMed=10677483; DOI=10.1073/pnas.97.4.1456;
Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;
"Human appartic protease memapsin 2 cleaves the beta-secretase site of
beta-amyloid precursor protein.";
Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
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                                                                                                                                                                                                                    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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MEDLINE=2287265; PubMed=12973309; DOI=10.1101/gr.1293003;

Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,

Clark H.F., Gurney A.L., Crowley C., Currell B., Deuel B., Dowd P.,

Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

Lewis L., Liao D., Mark M.R., Robbie B., Sanchez C., Schoenfeld J.,

Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

Vandlen R.L., Watenanbe C., Wieand D., Woods K., Xie M.-H.,

Wood W.I., Godowski P.J., Gray A.M.;
                                                                                                                                                                                                                                                                                                                            MEDILINE-20057170; PubMed=10591213; DOI=10.1038/990107;
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"Membrane-anchored aspartyl protease with Alzheimer's disease beta-
                30-MAY-2000 (Rel. 39, Created)
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Beta secretase 2 precursor (EC 3.4.23.45) (Beta-site APP-cleaving enzyme 2) (Aspartyl protease 1) (Asp 1) (ASP1) (Membrane-associated aspartic protease 1) (Memapsin-1) (Down region aspartic protease).
Name-BACE2; Synonyms-ASP21; ORFNames=UNQ418/PRO852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kin H., Stephans J.C., Duan X., Harrowe G., Kim B., Grieshammer U., Siese K.:
                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Giese K.; "Identification of a novel aspartic-like protease differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20120043; PubMed=10656250; DOI=10.1006/mcne.1999.0811; Hussain I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D., Chapman C., Gloger I.S., Murphy K.E., Southan C.D., Ryan D.M., Smith T.S., Simmons D.L., Walsh P.S., Dingwall C., Christie G.; "Identification of a novel aspartic proteinase (Asp 2) as beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accarino M.P., Fumagalli P., Ottolenghi S., Taramelli R.; "Cloning of a gene from chromosome 21 Down region encoding transmembrane aspartyl protease."; Submitteed (FBS-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressed in human breast cancer cell lines.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Becretase.";
Mol. Cell. Neurosci. 14:419-427(1999).
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Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 402:533-537(1999).
                                                                                                                                                                             Homo sapiens (Human).
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TISSUB-Skin;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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""" "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Turner R.T. III, Loy J.A., Nguyen C., Devasamudram T., Ghosh A.K.,
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[8]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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AF178532; AAF29494.1;
AF204944; AAF26368.1;
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EMBL; AL163284; CAB90458.1;
EMBL; AL163285; CAB90554.1;
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MEROPS; A01.041; -.
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R GO; GO:0016021; C:membrane fraction; TAS.
R GO; GO:0016021; C:membrane fraction; TAS.
R GO; GO:0016050; P:membrane protein ectodomain proteolysis; IDA.
GO; GO:0016050; P:membrane protein ectodomain proteolysis; IDA.
GO; GO:0016464; P:megative regulation of amyloid precursor pr. .; IMP.
GO; GO:0016464; P:protein modification; TAS.
R GO; GO:001816; P:protein modification; TAS.
R GO; GO:001816; P:protein modification; TAS.
R InterPro; IPR001916; Pept_Al_BACE.
R InterPro; IPR001969; Pept_Al_BACE.
R InterPro; IPR001969; Pept_Al_BACE.
R InterPro; IPR001969; Pept_Al_BACE.
R InterPro; IPR001969; Pept_Al_BACE.
R PANTHER; PTHR13683; Pept[dase_Al; 1.
PER; PR001817; PR01817; Pept_Al_BACE; 1.
R PRINTS; PR01817; BACE2.
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Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Arthrobacter sp. FB24.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
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By similarity.

By similarity.

N-linked (GlCNAc. .) (Potential).
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13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
ATP-binding region, ATPase-like:Histidine kinase A, N-terminal.
ORFNames=ArthDRAFT_2772;
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Bacteria; Actinopacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Micrococcaceae; Arthrobacter.
NCBI_TaxID=290399;
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77.8%; Pred. No. 1.4e+02;
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2E903150823760D3 CRC64;
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STRAIN=FB24;
SI DOE Joint Genome Institute (PGF-ORNL);
Larimer F., Land M.;
ENSG0000182240; Homo sapiens
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Q4NGK9;
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                                      HGNC; HGNC:934; BACE2
MIM; 605668; -.
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518 AA;
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US DOE Joint
Ensembl;
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    OOR BOOK WAX WAX WAS A CONTRIBUTION OF THE CON
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
F2807.11 protein (F4P13.33)
Name=F2807.11; Synonyms=F4P13.33;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicacee; Arabidopsis.
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"Annotation of the draft genome assembly of Arthrobacter sp. Submitted (JUN-2005) to the BMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB 2; Length 1135;
Pred. No. 3e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                              85.4%; Score 35; DB 2; Length 593; 77.8%; Pred. No. 1.6e+02; tive 2; Mismatches 0; Indels
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SEQUENCE 1135 AA; 126119 MW; C5FDDC178D1E2D96 CRC64;
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EMBL, BT004227; AA042421. i.; mRNA.
InterPro, IPR002048; EF-hand.
PROSITE; PS00018; EF-HAND; UNKNOWN_1.
                                                                                                                                                                                                                                                   593 AA; 64710 MW; 2D81CDAA7841E21C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QB4W49 ARATH PRELIMINARY; PRT; 1135 AA.
Q84W49;
Q1-UN-2003 (TrEMBLrel. 24, Created)
01-UN-2003 (TrEMBLrel. 24, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein At3g01780 (Fragment).
                                                                                                                                                preliminary data.
EMBL; AAHG01000005; BAL96513.1; -; Genomic_DNA.
ATP-binding; Kinase.
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Name=031656_E11.113; Synonyms=P0496D04.53;
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
Morimura K., Ikeda H., Hattori M., Beppu T.;
Genome sequence of Symbiobacterium thermophilum, an uncultivable
bacterium that depends on microbial commensalism.";
Nucleic Acids Res. 32:4937-4944(2004).
BMBL, Ap066840; BAD40586.1; -; Genomic_DNA.
GO, GO:0016020; C.membrane; IEA.
GO, GO:0005215; F:transporter activity; IEA.
GO, GO:0006810; P:transporter activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 2; Length 129;
Pred. No. 58;
1; Mismatches 0; Indels
                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
U-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-FRB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein OJ1656_E11.113 (Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone:P0496D04.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003843; BAC24850.1; -; Genomic_DNA.
EMBL; AP004670; BAD30793.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l protein.
129 AA; 13891 MW; 6334E639E1A6DEAE CRC64;
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Last annotation update)
                                                                                                                                                                  129 AA
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OrderedLocusNames=STH1601;
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Bacteria; Actinobacteria; Symbiobacterium.
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PubMed=15383646; DOI=10.1093/nar/gkh830;
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25-0CT-2004 (TrEMBLrel. 28, Last seq
25-0CT-2004 (TrEMBLrel. 28, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 82.9%;
Local Similarity 87.5%;
Les 7; Conservative
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Q67P07_SYMTH PRELIMINARY;
Q67P07;
                                                                                                                                                             QBH584 ORYSA PRELIMINARY;
Q8H584;
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23 ARSLLLPM 30
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2 ARSLLLPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone:031656 Ell
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                                                                                                              RESULT 12
Q8H584_ORYSA
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A Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
A BILIB T., Engels R., Wang S., Nieleen C.E., Butler J., Endrizzi M.,
Qui D., Ianakiev P., Pedersen D., Melson M., Washburne M.,
A Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
A Kothe G.O., JedG G., Mewes W., Staben C., Marcotte E., Greenberg D.,
A Roy A., Foley K., Naylor J. Thomann N., Barrett R., Gnerre S.,
A Ramal M., Kamwysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
A Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
A Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
A DeSouza C.C., Glass L., Orbesch M.J., Berglund J., Voelker R.,
A Narden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
A Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
A Paulsen I., Sachs M.S., Lander E.S., Nubbaum C., Birren B.,
A Paulsen I., Sachs M.S., Lander E.S., Nubbaum C., Birren B.,
A Willey D.O., Alex L.A., Lander E.S., Nubbaum C., Birren B.,
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Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
                 Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.B.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Submitted (JAN-2001) to the BMBL/GenBank/DDB databases.
EMBL, AC010797; AAF03433.1; -; Genomic_DNA.
EMBL, AC009325; AAF03433.1; -; Genomic_DNA.
Interpro; IPR02048; EF-hand
PROSITE; PS00018; EF-hand.
SEQUENCE 1192 AA; 132863 MW; 4F67B124CBAFF154 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 German Neurospora genome project;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurospora crassa.
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes;
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                      85.4%; Score 35; DB 2; Length 1192; 77.8%; Pred. No. 3.1e+02; ive 2; Mismatches 0; Indels
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EMBL; BX908808; CAF0025.1; -; Genomic_DNA.
Hypothetical protein:
SEQUENCE 118 AA; 12596 MW; D1F84E47108B2145 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-FBE-2005 (TrEMBLrel. 29, Last annotation update)
Predicted protein (Hypothetical protein G21B4.400).
Name=NCU04420.1; Synonyms=G21B4.400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 AA.
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Best Local Similarity 87.5°
Lea 7; Conservative
                                                                                                                                                                                                                                                                                 Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   237 MARSLVLPV 245
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NUCLEOTIDE SEQUENCE
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Search completed: March 11, 2006, 00:38:56 Job time : 99.3333 secs
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-1-SUBCELLULAR LOCATION: Tightly associated with stromal side of the thylakoid membrane (By similarity).
EMB1, BX569694; CAROBS60.1; -; Genomic_DNA.
GO, GO:0005489; F:electron transporter activity; IEA.
GO, GO:0006489; F:electron transporter activity; IEA.
GO, GO:00066189; F:electron transport; IEA.
GO, GO:00066118; P:electron transport; IEA.
                                                                                                                                                                       Gaps
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QGFTAS_CANGA PRELIMINARY; PRT; 439 AA.

ID QGFTAS_CANGA PRELIMINARY; PRT; 439 AA.

AC QGFTAS_CANGA PRELIMINARY; PRT; 439 AA.

DT OS-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT OS-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DT OS-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DT OS-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DT OS-JUL-2004 (TrEMBLrel. 27, Last sequence update)

OF Samilar to sp[Q04673 Saccharomyces cerevisiae YLR005w SSL1.

GG OrderedLocusNames-CAGLUG040599;

OS Candida glabrata (Yeast) (Torulopsis glabrata).

OC Bukaryota; Fungi; Ascomycota; Saccharomycetes;

OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-222255697; PubMed=12917641; DOI=10.1038/nature01943; Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L., Chain P., Lamerdin J.E., Regala W., Allen B.E., McCarren J., Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.; "The genome of a motile marine Synechococcus."; An utere 424:1037-1042(2003).
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PROSITE; PS00198; 4FE4S FERREDOXIN; 1.
PROSITE; PS00198; 4FE4S FERREDOXIN; 1.
Metal-binding; Thylakoid; Transport.
SEQUENCE 348 AA; 37531 MW; 1E1903E684081A95 CRC64;
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                                                                                                            82.9%; Score 34; DB 2; Length 322; 77.8%; Pred. No. 1.4e+02; tive 1; Mismatches 1; Indels
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                                                    322 AA; 34949 MW; 80157DE1532812D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative ldpA protein.
OrderedLocusNames=SYNN2065;
Synechococcus ap. (Strain WH8102).
Bacteria, Cyanobacteria, Chroococcales, Synechococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                              348 AA
                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Q7U4K2;
                                                                                  Ouery Match
Best Local Similarity 77.00
Ti Conservative
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Matches 7; Conservative
Pfam; PF01032; FecCD; 1.
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298 MARRLLMPL 306
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1 MKRSLLIPL 9
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                          Complete proteome.
SEQUENCE 322 AA;
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O70482 SYN
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AC 07048
AC 07048
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DD 01-00

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                                                         CRAIN-ATCC 2001 / CBS 138;

PubMed=1522959; DOI=10.1038/nature02579;

PubMed=1522959; DOI=10.1038/nature02579;

Dujon B., Sherman D., Fischer G., Durtens P., Casaregola S.,

Lafontaine I., Angle M., Anthouard V., Babour A., Barbe V.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Barnay S., Blanchin S., Pairhead C., Ferry-Dumazet H., Groppi A.,

Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri H.,

Kerrest A., Koszul R., Lemaire M., Lesur I., Muller H.,

Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,

Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,

Bouchler C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,

Mincker P., Souciet J.-L.,

"Mincker P., Souciet J.-L.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; CR380953; CAG59466.1; -; Genomic_DNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006281; P:DNA repair; IEA.
GO; GO:0045449; P:regulation of transcription; IEA.
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PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004595; S811.
InterPro; IPR007198; S811 like.
InterPro; IPR002109; YFIIH_SSL1.
InterPro; IPR002035; VWF A.
InterPro; IPR007087; Znf_C2H2.
Pfan; PP04056; S811; 1.
PIRSF; PRISF015919; TFIIH_SSL1; 1.
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Best Local Similarity 77.8
Matches 7; Conservative
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us-09-905-083a-86.rai

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Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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US-09-918-243-86
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LENGTH: 9
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Sequence 2, Appli
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Sequence 2, Appli
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Sequence 3, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
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Sequence 67, Appl
Sequence 2, Appli
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                                                                                                       March 11, 2006, 00:41:16; Search time 21.222 Seconds (without alignments) 35.061 Million cell updates/sec
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Sequence 2,
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Sequence 2
Sequence 2
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Sequence 2
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             GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Second Patents AA:* | Cgn2_6/ptodata/1/iaa/5_COMB.pep:* | Cgn2_6/ptodata/1/iaa/6_COMB.pep:* | Cgn2_6/ptodata/1/iaa/H_COMB.pep:* | Cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* | Cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep:* | Cgn2_6/ptodata/1/iaa/RE_COMB.pep:* | Cgn2_6/ptodata/1/iaa/RE_COMB.pep:* | Cgn2_6/ptodata/1/iaa/ABC_COMB.pep:* | Cgn2_6/ptodata/1/iaa/ABC_COMB.pep:* | Cgn2_6/ptodata/1/iaa/backfiles1.pep:* | CGn2
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US-08-243-86
US-08-257-146-2
US-08-257-146-2
US-08-30-154-34-2
US-09-154-34-2
US-09-764-762-3
US-09-764-762-3
US-09-764-762-3
US-09-502-600-116
US-09-502-600-116
US-09-503-116
US-09-503-116
US-09-548-37-2
                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-548-366F-2
                                                                                                                                                                                                                                                                                            572060 segs, 82675679 residues
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                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                              protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
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Perfect score:
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                                  Sequence 2, Appli
Sequence 2, Appli
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Sequence 2, Appli
Sequence 196, App
Sequence 11075, A
Sequence 31977, A
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TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Ovarian Cancer
FILE REPERENCE: D6223(1P-C
CURRENT FILING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: US/09/502,600A
PRIOR PILING DATE: 09/039,211
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 86, Application US/09918243

Sequence 86, Application US/09918243

Sequence 86, Application US/09918243

SEMENAL INFORMATION:

APPLICANT: Cannon, Martin J.

APPLICANT: Cannon, Martin J.

APPLICANT: Cannon, Methods for the early diagnosis of ovarian cancer;

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

CURRENT APPLICATION NUMBER: US/09/918,243

CURRENT PILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 86

LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 41; DB 2; L
100.0%; Pred. No. 4.6e+05;
tive 0; Mismatches 0;
                                                  US-09-668-314C-6
US-09-668-314C-6
US-09-548-315-2
US-09-794-743-2
US-09-999-833A-196
US-09-945A-196
US-09-949-016-11075
US-09-149-476-355
US-09-149-476-355
                                                                                                                                                                                                                                                                    -09-134-000C-3659
-09-869-388-10
                                                                                                                                                                                                                              US-09-270-767-49194
US-09-869-388-8
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                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-502-600-86; Sequence 86, Application US/09502600A; Sequence 86, Application US/09502600A; Patent No. 6294344; GENERAL INFORMATION:
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HENDUL:

JUS-19-154-344-2

JUS-09-154-344-2

JUS-09-154-344-2

JUS-09-154-344-2

JUS-09-154-344-2

JUS-09-154-344-2

JUS-09-154-344-2

JUS-09-154-344-2

JUS-09-154-344-2

JUS-09-154-34-2

JUS-09-155-6

JUS-09-155
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                                                                                                                                                                                           COUNTER READABLE FORM:

MEDIUM TYPE: Diskette COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette COMPUTER: DISKETE COMPUTER: DISKETE COMPUTER: DOS

SOFTWANTING SYSTEM: DOS

SOFTWANT APPLICATION DATA:

APPLICATION NUMBER: US/08/824,874

FILING DATE: Filed Herewith

CLASSIFICATION DATA:

APPLICATION NUMBER: 14

FILING APPLICATION DATA:

APPLICATION NUMBER: FILE FILE STATE

FILING DATE: FILE STATE

TELECOMMUNICATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: 36,749

TELEPHONE: 415-85-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
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                                                                     STREET: 3174 Port
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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Matches 9; Conserv
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Patent No. 5834290
GENERAL INFORMATION:
APPLICANT: Bealtud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Excombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: 17
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New YOLK
STATE: New YOLK
COUNTRY: U.S.A.
ZIP: 10036-2787
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: DC-DOS/MS-DOS
OPERATING SYSTEM: DC-DOS/MS-DOS
OPERATING SYSTEM: DLC-1995
ILING DATE: 14-44
ATTORNEY/AGENT INFORMATION:
NAME: SETENCE, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELEPHONE: (212) 354-8113
TELEPHONE: (212) 354-8113
INFORMATION POR ENO ID NO: 2:
SEQUENCE CHARACTERISTICS:
T-RNCTH: 253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 41; DB 1; Length 253; Best Local Similarity 100.0%; Pred. No. 0.49; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                         Query Match 100.0%; Score 41; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 9; Conservative 0; Mismatches 0; Indels
                             NAME/KEY: CHAIN; OTHER INFORMATION: Residues 1-9 of the SCCE protein US-09-918-243-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08824874
PAFEDR NO. 5962300
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-557-146-2
                                                                                                                                                                                                                                                                                                                         1 MARSLLLPL 9
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1 MARSLLLPL 9
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US-08-824-874-3
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US-08-557-146-2
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                               100.0%; Score 41; DB 2; Length 253; 100.0%; Pred. No. 0.49; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                     US-09-210-084-3

Sequence 3, Application US/09210084

Sequence 3, Application US/09210084

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Lal, Preeti

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS OPERATING SYSTEM: DOS OFFWARE: PSEASED for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8

US-09-764-762-3

Sequence 3, Application US/09764762

PREENT NO. 6472195

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/624,874
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 9F-0252 US
REFERENCE/DOCKET NUMBER: 9F-0252 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
Query Match
Best Local Similarity 100....
See 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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STRANDEDNESS: single
                                                                                                                                                                         ||||||||||
1 MARSLLLPL 9
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LIBRARY: GenBank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94304
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APPLICANT: Dixon, Eric P.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: AMYLOID PRECURSOR ALDRESSE: ADDRESSE: Elilly and Company STREET: Lilly Corporate Center CITY: Indianapolis STARE: Indiana
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COUNTRY: United States of America
ZIP: 46285
COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OOFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMNUMICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEPHONE: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
FILING DATE: 04-APR-1995
ATTORNEY AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTATION NUMBER: 38,082
REFERENCE, DOCKET NUMBER: x9239
TELECOMMUNICATION INFORMATION:
TELEFHONE: 317-27-1090
TELEFAX: 317-27-1090
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acids
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US-08-930-188-2
; Sequence 2, Application US/08930188
; Patent No. 6093397
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amino acid
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Best Local Similarity 100.
Matches 9; Conservative
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MOLECULE TYPE: protein
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1 MARSLLLPL 9
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,
FILING DATE: 04-APR-1995
ATTORNEY, AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFRERENCE/DOCKET NUMBER: X9239
TELEPHONE: 317-27-1090
TELEPHONE: 317-27-1090
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 9; Conservative
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US-09-949-016-7716
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GENERAL INFORMATION:

APPLICANT: Dixon, Eric P.

APPLICANT: Little, Sheila P.

TILLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TILLE OF INVENTION: RELATED NUCLEIC ACIDS

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bil Lilly and Company
STREET: Lilly Corporate Center

CITY: Indiana

COUNTRY: Undiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Score 41; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0. Trann
                                                                                                                                                                                                                                     MEDIUM TYPE: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: FastESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 16-Jan-2001
CLASSIFICATION NAMER: 09/210,084
FILING DATE: 16-Jan-2001
CLASSIFICATION NAMER: 09/210,084
FILING DATE: APPLICATION DATA:
APPLICATION NAMER: 09/210,084
FILING DATE: AUNKNOWN:
APPLICATION NAMER: 96/210,084
FILING DATE: AUNKNOWN:
TELEFRANTON TOROMATION:
TELEFRANCE/DOCKET NUMBER: PF-0252 US
TELEFRANCE/DOCKET NUMBER: PF-0255
TELEFRANCE/DOCKET NUMBER: PF-0354
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04294
                  CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 253 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: GenBank
                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MARSLLLPL 9
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
PCT-US96-04294-2
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FARCHAL NO. GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 06/241,755
PRIOR APPLICATION NUMBER: 66/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PLILNG DATE: 2000-10-03
PRIOR PLILNG DATE: 2000-10-03
PRIOR PLILNG DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRACESEQ for Windows Version 4.0
SEQ ID NO 7716
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US-09-502-600-116
Sequence 116, Application US/09502600A
Patent No. 6294344
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer
TITLE OF INVENTION: Ovarian Cancer
FILLE REPRENCE: D6223CIP-C
FILLE REPRENCE: D6223CIP-C
CURRENT FILING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: US/09/502,600A
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US 08/416,257
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Patent No. 6812339
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                                                                                                                                                                                                                                             Score 35; DB 2; Length 475;
Pred. No. 20;
                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQUENCE 2. Application US/08999723A
Patent No. 6025180
GENERAL INFORMATION:
APPLICANT: Powell, David J.
APPLICANT: Chapman, Christopher
APPLICANT: Chapman, Conrad G.
TITLE OF INVENTION: ASPL
FILE REFERENCE: GH70262
CURRENT APPLICATION NUMBER: US/08/999,723A
CURRENT APPLICATION NUMBER: US/08/999,723A
CURRENT FILING DATE: 1997-10-06
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SSOFTWARE: Patentin Ver. 2.0
SSOFTWARE: 218
                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09443427

Sequence 2, Application US/09434427

Patent No. 6162630

GENERAL INFORMATION:

APPLICANT: POWELL, DAVID J.

APPLICANT: SOUTHAN, CHRISTOPHER

APPLICANT: EVANS, JOANNE R.

ITTLE OF INVENTION: ASPI

FILE REFERENCE: GH-70262-D1

CURRENT APPLICATION NUMBER: US/09/434,427

CURRENT PILING DATE: 1999-11-04

EARLIER PILING DATE: 1999-11-04

EARLIER PILING DATE: 1996-12-14

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FRASESEQ FOR WINDOWS VERSION 3.0

SEQ ID NO 2

LENGTH: 518
                             60/101,594
    PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/.
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin version 3.1
SEQ ID NO 67
LENGTH: 475
TYPE: PRT
CORGANISM: Homo sapiens
                                                                                                                                                                                                                                                 85.4%;
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT; ORGANISM: Homo sapiens
US-08-999-723-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :||:|||||
4 LARALLLPL 12
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ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                      1 MARSLLLPL 9
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US-08-999-723-2
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APPLICANT: Gurney, et al
APPLICANT: Gurney, et al
APPLICANT: Gurney, et al
APPLICANT: Gurney, et al
TITLE OF INVENTION: ALEXHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 28341/6280NCP
CURRENT APPLICATION NUMBER: US/09/668,314C
CURRENT APPLICATION NUMBER: US 60/169,232
PRIOR APPLICATION NUMBER: US 09/416,901
PRIOR PILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR APPLICATION NUMBER: PS 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
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US-09-918-243-116
| Sequence 116, Application US/09918243
| Patent No. 6677403
| GENERAL INFORMATION:
| APPLICANT: O'Brien, Timothy J. APPLICANT: Cannon, Martin J. APPLICANT: Gantin, Alessandro;
| TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer; FILE REFERENCE: D6223.CIP/C/D/CIP
| CURRENT APPLICATION UNMBER: US/09/918,243
| CURRENT FILING DATE: 2001-07-30
| PRIOR FILING DATE: 2001-07-13
| NUMBER OF SEQ ID NOS: 136
| SEQ ID NO 116
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                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                             87.8%; Score 36; DB 2; Length 9; 100.0%; Pred. No. 4.6e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                               ; OTHER INFORMATION: Residues 2-10 of the SCCE protein US-09-502-600-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Residues 2-10 of the SCCE protein US-09-918-243-116
PRIOR APPLICATION NUMBER: 09/039,211
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 116
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 67, Application US/09668314C Patent No. 6844148
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Best Local Similarity 100...
Thes 8; Conservative
                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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1 ARSLLLPL 8
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US-09-668-314C-67
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US-09-434-427-2
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Length 518;	), Indels
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Score 35; DB 2; Pred. No. 22;	2; Mismatches
85.4%;	ative
nilarity	Conserva
h Sir	7
Query Match Best Local Similarity 77.8%;	Matches

<sup>1</sup> MARSLLLPL 9 :||:||||| 4 LARALLPL 12 g ò

Search completed: March 11, 2006, 01:24:28 Job time : 22.222 secs

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Mon Mar 13 12:28:01 2006
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RESULT 2
US-09-905-083-86
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Sequence 96, Appl
Sequence 3, Appli
Sequence 2, Appli
Sequence 96, Appl
Sequence 97, Appl
Sequence 97, Appl
Sequence 95, Appl
Sequence 95, Appl
Sequence 116, Appli
Sequence 279409,
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Sequence 86, Appl
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Sequence 86, Appl
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Sequence 50699, A
Sequence 318442,
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                                                                                     March 11, 2006, 01:24:47; Search time 69.4444 Seconds (without alignments) 54.151 Million cell updates/sec
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US11_FUBCOMB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-918-21-86
US-10-831-075-86
US-10-62-511-96
US-10-62-511-96
US-09-764-762-3
US-10-071-214-2
US-10-071-214-2
US-10-071-214-8
US-10-071-214-8
US-10-071-214-8
US-10-10-264-283-90
US-10-10-264-283-95
US-10-10-264-283-95
US-10-948-518-95
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US-10-918-243-116
US-09-918-243-116
US-09-918-243-116
US-09-918-221-116
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-10-831-075-116
-10-424-599-279409
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Maximum Match 100%
Listing first 45 summaries
                                                         - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence 86, Application US/09905083

Patent No. US20020146708A1

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: O'Varian Cancer;

TITLE OF INVENTION: O'Brien Cancer;

TITLE OF INVENTION O'VAIRED CANCER: US/09/905,083

CURRENT APPLICATION NUMBER: US 09/502,600

PRIOR APPLICATION UNMERR: US 09/502,600

PRIOR APPLICATION UNMERR: US 09/502,600

PRIOR APPLIANG DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 86

TYPE: PRI
                                                                                                                                                                                                                                                                                US-09-918-243-86

i Sequence 86, Application US/09918243

j Patent No. US202020142317A1

j GENERAL INFORMATION:
   APPLICANT: O'Brien, Timothy J.
   APPLICANT: Cannon, Martin J.
   APPLICANT: Santin, Alessand for the early diagnosis of ovarian cance;
   TILE OF INVENTION: Methods for the early diagnosis of ovarian cance;
   FILE REFERENCE: D6223CIP/C/D/CIP
   CURRENT APPLICATION NUMBER: US/09/918,243
   CURRENT FILING DATE: 2001-07-30
   PRIOR APPLICATION NUMBER: US
   NUMBER OF SEQ ID NOS: 136
   SEQ ID NO 86
   LENGTH: 9
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NAME/KEY: CHAIN

OTHER INFORMATION: Residues 1-9 of the SCCE protein
US-09-918-243-86
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                       -10-433-757-13
-10-424-599-262566
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100.0%; Pred. No. 1.7e+06;
cive 0; Mismatches 0;
                                              US-10-791-488A-4
US-10-791-488A-4
US-10-817-979-67
US-10-749-14-2
US-09-794-927-2
US-09-794-743-2
US-09-794-743-2
US-09-794-743-2
US-09-794-925-2
US-09-174-25-196
US-09-978-196
US-09-978-196
US-09-978-196
US-09-978-196
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
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1 MARSLLLPL 9
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; Publication No. US20030223973A1
; Fublication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Santin, Alessandro
; TILE REFERENCE: D6223CIP/C/D/CIP/CIP
; CURRENT APPLICATION UMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR PILING DATE: 2003-02-21
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
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Sequence 86, Application US/10831075

Publication No. US20040224891A1

GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
FILE REFERENCE: D6223CIP/C/D/CIP3
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 10/372,521
PRIOR PILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 140

LENGTH: 9
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                                                                                                                          Length 9;
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CHAIN
OTHER INFORMATION: Residues 1-9 of the SCCE protein
                                     NAME/KEY: CHAIN
OTHER INFORMATION: Residues 1-9 of the SCCE protein US-09-905-083-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 1-9 of the SCCE protein US-10-372-521-86
                                                                                                                        Query Match
100.0%; Score 41; DB 3; I
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
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100.0%; Score 41; DB 5; Length 9;

Query Match

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FEATURE:
NAME/KEY: DOWAIN
LOCATION: (61). (78)
OTHER INFORMATION: Serine proteases trypsin family, histidine proteins. domain
OTHER INFORMATION: Journal of the serine proteases of 11.96
OTHER INFORMATION: 20, raw score of 11.96
FEATURE:
NAME/KEY: DOMAIN
COCHRIGH: (133)
OTHER INFORMATION: (134). (133)
OTHER INFORMATION: (146). (133)
OTHER INFORMATION: value=3.2e-31, PPam score of 101.0
US-10-450-763-53737
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                                                                                                                                                                                             Sequence 53737, Application US/10450763
; Bublication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyesq. Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES;
FILE REFERENCE: 790CIP3/US;
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR PILING DATE: 2000-03-31
; SOFTHARE: CUBCOM
; SSQ ID NOS: 60736
; SGO ID NOS 53737
                   IndelB
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 9; Conservative 0; Mismatches 0;
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Publication No. US20040038223A1
GENERAL INFORMATION:
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Patturajan, Meera
Spyrek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
Malyankar, Uziel M.
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Anderson, David W.
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
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Best Local Similarity 100.
Matches 9; Conservative
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Li, Li
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ORGANISM: Homo Bapiens
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US-10-262-511-96
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APPLICANT:
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APPLICANT:
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; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 98
; ENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-98
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1 MARSLLLPL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-764-762-3
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                                                                                                                                                                                                                                                                                                                APPLICANT: Bergh, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERBNCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
FILOR BEDLICATION NUMBER: US/10/262,511
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR APPLICATION NUMBER: 60/377,917
PRIOR PILING DATE: 2001-10-02
PRIOR PILING DATE: 2001-10-03
PRIOR PILING DATE: 2002-05-17
PRIOR PILING DATE: 2002-05-16
PRIOR PILING DATE: 2002-05-17
PRIOR PILING DATE: 2002-05-17
PRIOR PILING DATE: 2002-05-17
PRIOR PILING DATE: 2002-05-17
PRIOR PILING DATE: 2002-04-17
PRIOR PILING DATE: 2002-04-19
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SOFTWARE: CuraSeqList version 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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GENERAL INCOMPATION:
GENERAL INCOMPATION:
APPLICANT: PLOWMAN, GRECORY
APPLICANT: CARENEELS, SEAN
APPLICANT: CARENEELS, SEAN
APPLICANT: CHARVOCZAK, GLEN
APPLICANT: CHARVOCZAK, GLEN
APPLICANT: CHARVOCZAK, GLEN
APPLICANT: CHARVOCZAK, GLEN
APPLICANT: WIDARSANAM, SUCHA
ITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: 60/214,047
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR PILING DATE: 2001-06-26
PRIOR PILING DATE: 2000-06-26
                                                                                                                                                                                                                Shimkets, Richard A.
Rothenberg, Mark E.
Leach, Martin D.
Agee, Michele L.
                                                                      Miller, Charles E.
Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
                            Catterton, Elina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 9; Conservative
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CORGANISM: Homo sapiens
US-10-262-511-96
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LENGTH: 198
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APPLICANT:
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APPLICANT:
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APPLICANT:
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Query Match 100.0%; Score 41; DB 3; Length 253; Best Local Similarity 100.0%; Pred. No. 6.3; Matches 9; Conservative 0; Mismatches 0; Indele
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                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Jennifer L.
Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STRET: 3174 Porter Drive
CITY: Palo Alto
COUNTY: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Comparible
OPERATING SYSTEM: DOS
SOFTWARE: FRSESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/210,084

FILING DATE: «Unknown»

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REPERENCE/DOCKET NUMBER: PF-0252 US

TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                 US-09-764-762-3; Sequence 3, Application US/09764762; Patent No. US20020068341A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 415-855-0555
TELERAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 253 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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STRANDEDNESS: single
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APPLICANT: Marray, Richard H.
APPLICANT: Matray, Richard H.
APPLICANT: Matray, Richard H.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Edge Blotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer.
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer.
CURRENT FILING DATE: 2012-01250005
CURRENT PELLICA DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 60/35,027
PRIOR FILING DATE: 2001-11-15
PRIOR PILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-29
PRIOR PILING DATE: 2001-11-29
PRIOR PELLING DATE: 2001-11-29
PRIOR PELLING DATE: 2001-12-14
PRIOR PELLING DATE: 2001-12-14
PRIOR PELLING DATE: 2001-12-14
PRIOR PELLING DATE: 2001-11-29
PRIOR PELLING DATE: 2002-01-10
PRIOR PELLING DATE: 2002-02-13
PRIOR PELLING DATE: 2002-01-10
PRIOR PELLING DATE: 2002-02-13
PRIOR PELLING DATE: 2003-02-13
PROPERMER PELLING DATE: 2003-02-13
PROPERMER PELLING DATE: 2003-02-13
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210.21.590
CURRENT APPLICATION NUMBER: US/10/264,283
CURRENT PILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 111
SEQ ID NO 90
LENGTH: 253
TYPE: PRT
ORGANISM: HOMO SADIENS
US-10-264-283-90
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6.3;
                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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100.0%; Pred. No. 6.3
tive 0; Mismatches
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Publication No. US20030232350A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aziz, Natasha
Ginsberg, Wendy M.
Gish, Kurt C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glynne, Richard
Hevezi, Peter A.
                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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CORGANISM: Homo sapiens
US-10-295-027-498
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Best Local Similarity
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Sequence 2, Application US/10071214

Sequence 2, Application US/10071214

Sequence 2, Application O. US20030066099A1

GENERAL INFORMATION:
APPLICANT: HANSON, Lennart
APPLICANT: HANSON, Lennart
TILLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
FILE REPRENCE: HANSON-3A
CURRENT APPLICATION NUMBER: US/10/071,214
CURRENT PILING DATE: 2001-02-11
FRIOR FILING DATE: 2001-02-09
FRIOR APPLICATION NUMBER: US 60/267,422
FRIOR SEQ ID NOS: 50

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Deduced amino acid sequence from the C-terminal part of SCCE from OTHER INFORMATION: homo sapiens.
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US-10-264-283-90
US-10-264-283-90
Sequence 90, Application US/10264283
Publication No US20030144494A1
GENERAL INFORMATION:
APPLICANT: Algate, Pand A.
APPLICANT: Mannion, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
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US-10-071-214-48
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LENGTH: 253
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1 MARSLLLPL 9
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1 MARSLLLPL
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                                                                                                                                                        Sequence 48, Application US/10173999
Publication No. US20040005563A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Gos Biotechnology, Inc.
APPLICANT: Eos Biotechnology, Inc.
APPLICANT: Bos Biotechnology, Inc.
APPLICANT: Gos Biotechnology, Inc.
APPLICANT: Gos Biotechnology, Inc.
APPLICANT: Gos Biotechnology, Inc.
APPLICANT: Bos Biotechnology, Inc.
APPLICANT: Bos Biotechnology, Inc.
APPLICANT: Bos Biotechnology inc.
APPLICANT: Concer
FILIE OF INVENTION: Cancer
FILE REFERENCE: 018501-00242008
CURRENT APPLICATION NUMBER: US/10/173,999
CURRENT FILING DATE: 2002-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Publication No. US20040101874A1

General Information:
General Information:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Tang, Bing
APPLICANT: Glan, Bradford W.
APPLICANT: Glan, Gary M.
APPLICANT: Glan, Gary M.
APPLICANT: Taylor, Steven W.
APPLICANT: Glan, Gary M.
APPLICANT: Glan, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: INGERSE FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC
FILE REFERENCE: 660088 465
CURRENT APPLICANTON NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE FASELSEQ FOR Windows Version 4.0
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Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 41; DB 4; Length 253; 100.0%; Pred. No. 6.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2002-00-13
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/315,287
PRIOR APPLICATION NUMBER: US 60/315,287
PRIOR FILING DATE: 2001-08-27
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PALENTIN VET: 2.1
SEQ ID NO 48
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Homo sapiens US-10-173-999-48
  1 MARSLLLPL 9
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1 MARSLLLPL 9
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Best Local Similarity
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US-10-408-765A-639
                                                                                                                                           US-10-173-999-48
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APPLICANT: VICTORIA SWITH
APPLICANT: VICTORIA SWITH
APPLICANT: THOMAS D. WU
TITLE OF INVENTION: TREATMENT OF TUMOR
TITLE OF INVENTION NUMBER: US 60/404,809
PRIOR PELING DATE: 2002-08-19
PRIOR PELING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: US 60/413,192
PRIOR PLING DATE: 2002-09-23
PRIOR FILING DATE: 2002-09-10-15
PRIOR PLING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 60/426,847
PRIOR PLING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US 60/484,959
PRIOR FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 158
SEQ ID NO 95
LENGTH: 253
TWORP: DETAILS
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  0; Mismatches
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                                                                                                                                                                                   US-10-643-795A-95
Sequence 95, Application US/10643795A
Publication No. US20040241703A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              APPLICANT: FREDERIC J. DESAUVAGE
                                                                                                                                                                                                                                                                                                    GRETCHEN FRANTZ
KENNETH J. HILLAN
PAUL POLAKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
  9; Conservative
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Matches
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RESULT 2
US-10-412-748-14

Sequence 14, Application US/10412748

Publication No. US20060035219A1

GENERAL INFORMATION:
APPLICANT: Queensland University of Technology
APPLICANT: Clements, Judith A

TITLE OF INVENTION: Aberrant Kallikrein Expression
FILE REFERENCE: DAVI172.0034US

CURRENT FILING DATE: 2003-04-09

PRIOR PILING DATE: 2002-04-09

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PATENTING DATE: 2002-04-09

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PATENTING DATE: 2002-04-09

TYPE: PRIOR PILING DATE: 2002-04-09

TYPE: PRIOR PILING DATE: 2002-04-09

TYPE: PRIOR PILING DATE: 2002-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Human
US-10-412-748-11
                                                                                                                                                                                                                                                                                                                                        RESULT 1
US-10-412-748-11
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TYPE: PRT
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Sequence 14, Appl
Sequence 17, Appl
Sequence 111, Appl
Sequence 111, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 95, Appl
Sequence 96, Appl
Sequence 96, Appl
Sequence 12, Appl
Sequence 20677, A
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Sequence 1618, Ap
Sequence 10415, A
Sequence 184, App
Sequence 2477, App
Sequence 81, App
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Sequence 7434, Ap
Sequence 10450, A
Sequence 5367, Ap
                                                                             March 11, 2006, 01:27:17 ; Search time 8 Seconds (without alignments) 31.314 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/NS07_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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6 US-10-412-748-14
6 US-10-412-748-14
7 US-11-037-243-111
7 US-11-036-568A-1854
7 US-11-096-568A-1854
7 US-11-195-690-33
7 US-11-175-690-33
5 US-10-798-579A-2
5 US-10-798-579A-2
5 US-10-798-579A-2
6 US-10-798-579A-2
7 US-10-798-579A-2
8 US-10-798-579A-2
8 US-10-883-616-59
8 US-10-883-616-59
9 US-11-14-672-12
US-11-087-699-10415
US-11-096-568A-20677
US-11-087-099-10415
US-11-087-099-10415
US-11-087-099-2477
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US-11-096-568A-10450
US-11-096-568A-5367
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                                                                                                                                                                                                                                        161667 seqs, 27834885 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       OM protein - protein search, using sw model
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seq length: 200000000
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Match Length
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Perfect score:
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Maximum DB
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Sequence 16302, A Sequence 16301, A Sequence 16300, A Sequence 2645, Ap Sequence 5658, Ap Sequence 5656, Ap Sequence 2668, A Sequence 26809, A Sequence 278, Ap                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                             29391,
28435,
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Sequence 2
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Sequence
Sequence
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; Pred. No. 0.25;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                      Sequence 11, Application US/10412748

Publication No. US20060035219A1

GENERAL INFORMATION:
APPLICANT: Queensland University of Technology
APPLICANT: Clements, Judith A
TITLE OF INVENTION: Aberrant Kallikrein Expression
FILE REFERENCE: DAVI172.003AUS
CURRENT FILICATION NUMBER: US/10/412,748
CURRENT FILICATION NUMBER: AU PS1616/02
PRIOR PILING DATE: 2003-04-09
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
SEQ ID NO 11
                   US-11-096-568A-16300
US-11-096-568A-16300
US-11-096-568A-16300
US-11-096-568A-5658
US-11-096-568A-5658
US-11-096-568A-5650
US-11-096-568A-26809
US-11-096-568A-26809
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US-11-096-568A-26809
US-11-096-568A-278
US-11-096-568A-278
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US-11-096-568A-278
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US-11-096-568A-278
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US-11-096-568A-28435
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Best Local Similarity 100.0%;
Matches 9; Conservative 0;
   1 MARSLLLPL 9
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Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MARSLLLPL 9
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                             1 MARSLLLPL
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                                                         100.0%; Score 41; DB 6; Length 253; 100.0%; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 41; DB 7; Length 253; Best Local Similarity 100.0%; Pred. No. 0.25; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                               0; Indels
                                                                                                                                                                                                                                                              Sequence 17, Application US/10412748

Publication No. US20060035219A1

GENERAL INFORMATION:
APPLICANT: Queensland University of Technology
APPLICANT: Clements, Judith A

TITLE OF INVENTION: Abstrant Kallikrein Expression
FILE REFERENCE: DAVI172.003AUS
CURRENT FILING DATE: 2003-04-09

PRIOR APPLICATION NUMBER: US/10/412,748

CURRENT FILING DATE: 2003-04-09

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn version 3.2

LENGTH: 253
                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WHYTE, DAVID
APPLICANT: WHYTE, DAVID
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CHARYDCAK, GLEN
APPLICANT: WANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
TITLE PEFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/11/037,243
CURRENT FILING DATE: 2005-05-26
PRIOR APPLICATION NUMBER: US/09/888,615
PRIOR PILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-26
SOFTWARE: PARCHIN VOR: 2.1
SEQ ID NO 98
LENGTH: 253
TYPE: PRT
ORGANISM: HOMO SADIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-11-037-243-98
US-11-037-243-98
Sequence 99, Application US/11037243;
Publication No. US20050287546A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
                                                     Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                     1 MARSLLLPL 9
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US-10-412-748-14
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                                                                                                                                                                                                                              RESULT 3
US-10-412-748-17
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US-11-096-568A-1854
US-11-096-568A-1854
Sequence 1854, Application US/11096568A
Sequence 1864, Application US/11096568A
Sequence 1864, Application No. US20060048240A1
GENERAL INFORMATION:
THE SET INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F.
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
SEQ ID NOS: 34471
SEQ ID NO 1854
LENGTH: 138
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Pred. No. 9.8;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Zea mays subsp. mays
FATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(138)
LOCATION: (1)...(138)
JUCHER INDERMATION: Ceres Seq. ID no. 15179472
US-11-096-568A-1854
JOS-11-03/243-11, Application US/11037243
Fublication No. US20050287546A1
GENERAL INFORMATION
JAPPLICANT: BLOWMAN, GREGORY
APPLICANT: CARENEEEL, SEAN
APPLICANT: CARENEEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: GUNERLON: US/11/037,243
CURRENT APPLICATION NOWEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/10/988,615
PRIOR APPLICATION NUMBER: US/10/988,615
PRIOR FILING DATE: 2001-06-26
PRIOR PRIOR DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE PARENTIN VET. 2.1
SED ID NO 111
LENGTH: 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.8%;
88.9%;
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88.9%;
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Sequence 2, Application US/10798579A
Sequence 2, Application US/10798579A
Publication No. US20060005281A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kirin Beer Kabushiki Kaisha; Japan International Research Center for APPLICANT: Kirin Beer Kabushiki Kaisha; Japan International Research Center for APPLICANT: Maricultural Sciences
TITLE OF INVENTION: using environmental stress-resistant gene
FILE REPERENCE: PH-2034
CURRENT APPLICATION NUMBER: US/10/798,579A
CURRENT FILING DATE: 2004-03-12
PRIOR FILING DATE: 2003-03-14
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 2
LENGTH: 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Publication No. US20060005265A1
Fublication No. US20060005265A1
Fublication No. US20060005265A1
FUBBREAL INFORMATION:
APPLICANT: Han, Zhoa
APPLICANT: Wang, Yuexia
APPLICANT: Wang, Yuexia
TITLE OF INVENTION: Ryegrass CBF3 Gene: Identification and Isolation
FILE REFERENCE: MSO-08807
CURRENT APPLICATION NUMBER: US/10/883,512
CURRENT FILING DATE: 2004-07-01
NUMBER OF SEQ ID NOS: 199
SOFTWARE: Patentin Version 3.3
SEQ ID NO 95
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Pred. No. 2.2;
1; Mismatches
                                                           PRIOR FILING DATE: 2003-02-02
PRIOR APPLICATION NUMBER: US 60/472,816
PRIOR FILING DATE: 2003-05-23
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-09-24
PRIOR FILING DATE: 2003-09-30
FILING DATE: 2003-03-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.6%;
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Best Local Similarity 77.8
Matches 7; Conservative
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185 MAEGMLLPL 193
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Matches 6; Conserv
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US-10-883-512-95
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                              Sequence 2, Application US/11198819
Publication No. US20050287582A1
GENERAL INFORMATION:
APPLICANT: Adea, Gosse Jan
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes,
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAK Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.0%; Score 32; DB 7; Length 303; 77.8%; Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                       CUCMIANI: C.C..
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
COMPUTER: IEM PC COMPATIBLE
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/11/198,819
FILING DATE: 04-AUG-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-11-175-690-33
i Sequence 33, Application US/11175690
i Publication No. US20060014254A1
GENERAL INFORMATION:
APPLICANT: Haselline et al.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF605
CURRENT FILING DATE: 2005-07-07
PRIOR APPLICATION NUMBER: US/11/175,690
CURRENT FILING DATE: 2005-07-07
PRIOR FILING DATE: 2004-01-20
PRIOR FILING DATE: 2004-01-22
PRIOR FILING DATE: 2003-01-22
PRIOR FILING DATE: 2003-01-22
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APPLICATION NUMBER: US/08/985,950
FILING DATE: 05-DEC-1997
PRIOR APPLICATION NUMBER: US 60/041,279
FILING DATE: 21-WARCH-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,252
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAMME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 100670K
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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amino acid
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Matches 7; Conservative
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CITY: Palo Alto
STATE: California
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TYPE: PRT ORGANISM: Arabidopsis thaliana
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Best Local Similarity 66.7
Matches 6; Conservative
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185 MAEGMLLPL 193
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Bublication No. US20060008874A1

GENERAL INCORMATION:
APPLICANT: CREELMAN, Robert A
APPLICANT: GUTTERSON, Meal I
APPLICANT: GUTTERSON, Meal I
APPLICANT: GUTTERSON, Neal I
APPLICANT: GUTTERSON, NUMBER: US/10/838,616
CURRENT PRILING DATE: 2004-05-04
PRIOR APPLICATION NUMBER: S104-065-04
PRIOR FILING DATE: 2003-10-14
PRIOR FILING DATE: 2003-10-14
PRIOR FILING DATE: 2003-10-14
PRIOR FILING DATE: 2003-04-10
PRIOR FILING DATE: 2003-04-10
PRIOR FILING DATE: 2003-06-14
PRIOR FILING DATE: 2003-06-14
PRIOR FILING DATE: 2003-06-14
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-03-22
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Sequence 96, Application US/10883512

Sequence 96, Application US/10883512

Publication No. US20060005265A1

GENERAL INFORMATION:

APPLICANT: Bughrara, Suleiman

APPLICANT: Han, Zhoa

APPLICANT: Wang, Yuexia

TITLE OF INVENTION: Ryegrass CBF3 Gene: Identification and Isolation

FILE REFERENCE: MSU-08807

CURRENT APPLICATION NUMBER: US/10/883,512

CURRENT PILING DATE: 2004-07-01

NUMBER OF SEQ ID NOS: 199

SOFTWARE: Patentin version 3.3

SEQ ID NO 96

LENGTH: 216
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Pred. No. 40;
1; Mismatches 2; Indels
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; LENGTH: 216
; TYPE: PRT
; OYGANISM: Arabidopsis thaliana
US-10-883-512-95
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                                                                                                                  Query Match 73.2%;
Best Local Similarity 66.7%;
Matches 6; Conservative
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185 MAEGMLLPL 193
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185 MAEGMLLPL 193
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APPLICANT: BUBER, Omaira
APPLICANT: BINEDA, Omaira
TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF DROUGHT STRESS
FILE REFERENCE: MBIO058-CIP
CURRENT FILING DATE: 2003-10-13
PRIOR PAPLICATION NUMBER: 10/412,699
PRIOR PAPLICATION NUMBER: 09/506,720
PRIOR APPLICATION NUMBER: 09/506,720
PRIOR PILING DATE: 2000-02-17
PRIOR PILING DATE: 1999-05-20
PRIOR PILING DATE: 1999-05-20
PRIOR PILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,392
PRIOR PILING DATE: 2000-03-22
PRIOR PILING DATE: 2000-03-22
PRIOR PILING DATE: 2000-03-22
PRIOR PELING DATE: 2000-03-22
PRIOR PILING DATE: 2000-03-23

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PRIOR APPLICATION NUMBER: 09/533,392
PRIOR FILING DATE: 2000-033.22
PRIOR FILING DATE: 1999-03-22
PRIOR PILING DATE: 1999-03-23
PRIOR PILING DATE: 1999-03-23
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 2000-11-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 68
SOFTWARE: Patentin version 3.2
SEQ ID NO 59
LENGTH: 216
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Pred. No. 40;
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APPLICANT: HEARD, Jacqueline
APPLICANT: RIECHMANN, Jose Luis
APPLICANT: CREELMAN, Robert
APPLICANT: CREELMAN, ROBERT
APPLICANT: CANALES, ROGER
APPLICANT: REPETTI, Peter
APPLICANT: KUMIMOTO, ROGERICK W
APPLICANT: RUMIMOTO, ROGERICK W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 426, Application US/10714887 Publication No. US20060015972A1 GENERAL INFORMATION:
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US-211-114-672-12

US-211-114-672-12

US-211-114-672-12

US-211-114-672-12

US-211-114-672-12

US-211-114-672-13

US-211-114-672

US-21-114-672

US-21-114-672

US-21-114-672

US-214-672

US-214-672

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; Bublication No. US20060015973A1
; GENERAL INFORMATION:
    APPLICANT: SHINOZAKI, Kazuko;
    APPLICANT: SHINOZAKI, Kazuko;
    APPLICANT: SAKUMA, Yoh
; TITLE OF INVENTION: Environmental stress-tolerant plants;
    FILE REFERENCE: 382.1029CIP
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: US/10/664,771
; PRIOR PILING DATE: 2003-09-19
; PRIOR PILING DATE: 1999-04-28
; PRIOR FILING DATE: 1999-04-28
; PRIOR FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 75
; SEQ ID NO S: 75
                                                                                                                                                                                 Query Match 73.2%; Score 30; DB 6; Length 216; Best Local Similarity 66.7%; Pred. No. 40; Matches 6; Conservative 1; Mismatches 2; Indels
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Pred. No. 40;
1; Mismatches 2; Indels
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                                      ; FEATURE:
; OTHER INFORMATION: CBF3 polypeptide
US-10-714-887-426
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; ORGANISM: Arabidopsis thaliana
US-11-114-672-12
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Arabidopsis thaliana
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Best Local Similarity 66.7
Matches 6; Conservative
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185 MAEGMLLPL 193
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Best Local Similarity
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US-10-887-475B-2
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Search completed: March 11, 2006, 01:38:43 Job time : 8 secs



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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model Run on:

March 11, 2006, 00:10:50; Search time 86.6667 Seconds (without alignments) 45.628 Million cell updates/sec

US-09-905-083A-99 42

1 QRIKASKSF 9 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2443163 seqs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

geneseq11980s:\* geneseq12000s:\* geneseq2001s:\* geneseq2001s:\* geneseq12002s:\* geneseq12003s:\* geneseq12003s:\* geneseq12005s:\* A Geneseq 21: 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Aae08334 Human str	Aae08304 Human str	Adr68891 Human str	Adr68860 Human str	Ada05740 Human NOV	4	Adi39727 Stratum c	Adi37151 Stratum c	Ada05738 Human NOV	Adn62902 Human NOV	Ada05736 Human NOV	Adn62900 Human NOV	Ada05744 Human NOV	Adn62908 Human NOV	Adv21100 Human str	Aab98502 Human Str	Ada05742 Human NOV	Adn62906 Human NOV	Ada05732 Human NOV	Adn62896 Human NOV	Ada05734 Human NOV	Adn62898 Human NOV	Aar67888 Human str	Aaw05383 Human amy
SUMMARIES	ΙΙ		AAE08334	AAE08304	ADR68891	ADR68860	ADA05740	ADN62904	ADI39727	ADI37151	ADA05738	ADN62902	ADA05736	ADN62900	ADA05744	ADN62908	ADV21100	AAB98502	ADA05742	ADN62906	ADA05732	ADN62896	ADA05734	ADN62898	AAR67888	AAW05383
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	Length DB	1	6	σ	σ	σ	97	97	144	144	181	181	198	198	224	224	224	225	247	247	250	250	252	252	253	253
•	* Query Match		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score		42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42
	Result No.		г	8	m	4	S	9	7	œ	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

## ALIGNMENTS

Human stratum corneum chymotrypsin enzyme peptide #99 (residues 91-99). Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia. AAE08334 standard; peptide; 9 AA. 01-NOV-2001 (first entry) AAE08334; RESULT 1 AAE08334 

Homo sapiens.

WO200159158-A1.

16-AUG-2001.

07-FEB-2001; 2001WO-US003977.

11-FEB-2000; 2000US-00502600

(UYAR-) UNIV ARKANSAS.

O'brien TJ;

WPI; 2001-514676/56.

Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.

Disclosure; Page 124; 127pp; English.

The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metaetsais, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide

Sequence 9 AA;

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Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:130.
                                                                                                                                                               (UYAR-) UNIV ARKANSAS
                                                                                                                                                                                                                                                                                                                                                                                                            chymotrytic enzyme).
                                                                                                                                                                                                    WPI; 2004-653294/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
hes 9; Conserv
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                                                                                  WO2004075723-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9 AA;
                                                                  Homo sapiens.
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                                                                                                                                                                                   O'brien TJ,
                                                                                                      10-SEP-2004
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                                                                                                                                                                         Human stratum corneum chymotrypsin enzyme peptide #69 (residues 91-99).
                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                          Diagnosing cancer comprises detecting stratum corneum chymotrypsin
                                                                                                                                                                                           Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; trancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia.
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       100.0%; Score 42; DB 4; Length 9; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 2e+06;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; Page 117; 127pp; English.
                                                                                                                AAE08304 standard; peptide; 9 AA.
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                                                                                                                                                      (first entry)
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Query Match
Best Local Similarity 100.
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                                                                 ORIKASKSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human SCCE peptide
                                                                                                                                                                                                                                                      WO200159158-A1
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                                                                                                                                                      01-NOV-2001
                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                         16-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                    O'brien TJ;
                                                                                                                                    AAE08304;
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ADR68891
ID ADR6
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The invention relates to a novel method for vaccinating an individual against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating an individual with a SCCE peptide, which elicits an immune response in the individual. A peptide of the invention acts as a stratum corneum chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or at risk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligonuclectide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or pancreatic cancer, and other cancers in which SCCE is overexpressed. The peptides are also useful in the monitoring and development of immunotherapies for ovarian and other malignancies. The present sequence represents a peptide fragment of serine protease SCCE (stratum corneum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
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serine protease; stratum corneum chymotrytic enzyme; SCCE; immune response; ovarian cancer; lung cancer; prostate cancer; pancreatic cancer; colon cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Santin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADR68860 standard; peptide; 9 AA.
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The invention relates to a novel method for vaccinating an individual against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating an individual with a SCCE peptide, which elicits an immune response in the individual. A peptide of the invention acts as a stratum corneum chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or a trisk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligonucleotide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or pencreatic cancer, and other cancers in which SCCE is overexpressed. The peptides are also useful in the monitoring and development of immunotherapies for ovarian and other malignancies. The present sequence represents a peptide fragment of serine protease SCCE (stratum corneum corneum
                                                                                                                                                                                                                                           Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
                                                                                                                                                                                                                                                                                                                                     Claim 5; SEQ ID NO 99; 117pp; English
                                                                                                                                                          Santin A;
                       20-FEB-2004; 2004WO-US005134
                                                                21-FEB-2003; 2003US-00372521
                                                                                                                                                          Cannon MJ,
                                                                                                          (UYAR-) UNIV ARKANSAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chymotrytic enzyme)
                                                                                                                                                        O'brien TJ,
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Sequence 9 AA;

100.0%; Score 42; DB 8; Length 9; 100.0%; Pred. No. 2e+06; 0; Indels 0; Mismatches Query Match Best Local Similarity 100.00 9; Conservative 1 QRIKASKSF 9 ઠે

ORIKASKSF 9

ADA05740 standard; protein; 97 AA 06-NOV-2003 (first entry) ADA05740; 

human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obseity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia. Human NOV18e protein SEQ ID NO:100.

Homo sapiens

WO2003029424-A2

10-APR-2003.

02-OCT-2002; 2002WO-US031373

2001US-0326483P. 2001US-0327435P. 2001US-0327449P. 2001US-0327917P. 02-OCT-2001; 2 05-OCT-2001; 2 05-OCT-2001; 2 09-OCT-2001; 2 2001US-0328056P. 2001US-0328849P. 2001US-0330141P. 2001US-0330140P. 2001US-0341058P. 2001US-0349575P. 2001US-0349575P. 2001US-034957P. 2001US-034637P. 2002US-0373815P. 2002US-0373817P. 2002US-0373817P. 2002US-0374977P. 2002US-0381037P. 2002US-0381038P. 16-MAY-2002; 2002US-0381042P. 17-MAY-2002; 2002US-0381642P. 28-MAY-2002; 2002US-0383656P. 29-MAY-2002; 2002US-0383831P. 2002US-0391335P 09-0CT-2001; 2 09-0CT-2001; 2 12-0CT-2001; 2 17-0CT-2001; 2 18-0CT-2001; 2 24-0CT-2001; 2 24-0CT-2001; 2 24-0CT-2001; 2 29-0CT-2001; 2 22-APR-2002; 16-MAY-2002; 17-APR-2002; 19-APR-2002; 19-APR-2002; 19-APR-2002; 19-APR-2002; 16-MAY-2002; 

(CURA-) CURAGEN CORP.

Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterron E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK; Smithson G, Millet I, Pe Patturajan M, Spytek KA, Ort T, Gorman L, Zerhuse

WPI; 2003-381626/36. N-PSDB; ADA05739.

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Gaps ö New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics

Claim 1; Page 171; 586pp; English.

The present invention describes Novy procesurs, where X can be 1 co 35 described above and a carrier; (2) a kit comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NoVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an anthbody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a disease associated with altered levels of expression of the above comprising the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a disease associated with altered levels of expression of the above comprising an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of contrivity of the polypeptide; (12) a method for modulating contrivity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide; NovX contrivity of the polypeptide described above; (13) methods of treating contrivity or of latency or predisposition to a pathology associated with the above polypeptide; norectic, and antilipaemic activities, and can be used in gene therapy. The conditions and mutilipaemic activities, and can be used in gene therapy. The conditions associated with a human disease. The polypeptide or the nucleic acid molecule may be used to disagnose, treat or prevent metabolic conditions, caphology, acid molecule may be used to disagnose. The present invention describes NOVX proteins, where X can be 1 to 55

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neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the present invention.
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05-OCT-2001; 2001US-0327435P.
09-OCT-2001; 2001US-0327443P.
09-OCT-2001; 2001US-0327917P.
09-OCT-2001; 2001US-0328029P.
09-OCT-2001; 2001US-0328044P.
12-OCT-2001; 2001US-0328044P.
15-OCT-2001; 2001US-0328049P.
15-OCT-2001; 2001US-033914P.
17-OCT-2001; 2001US-033916P.
24-OCT-2001; 2001US-034956P.
24-OCT-2001; 2001US-034957P.
17-APR-2002; 2001US-034957P.
19-APR-2002; 2002US-037381P.
19-APR-2002; 2002US-037381P.
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22-APR-2002, 2002US-037497PP.
16-MAY-2002, 2002US-0381037P.
16-MAY-2002, 2002US-0381038P.
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                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                          Sequence 97 AA;
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Dipippo VA;
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                                                                                                                 MILLER C B.
RASTELLI L.
STONE D J.
PENA C C B A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E.
                                                                                                                                                                                          EISEN A.
GANGOLLI B A.
RIEGER D K.
SPADERNA S K.
                                                                MALYANKAR U M.
                                                                                                                                                                      AGEE M L.
BERGHS C.
DIPIPPO V A.
                                     PATTURAJAN M.
                                                                                   ZERHUSEN B D.
ANDERSON D W.
                                             SPYTEK K A.
EDINGER S R.
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                                                                                                      CATTERTON E.
                                                          ELLERMAN K.
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                                                                                                                                                               LEACH M D.
MILLET I.
PEYMAN J A
KEKUDA R.
                                                                            GORMAN L.
                                                                                                ZHONG M.
                                GUO X
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(GANG/)
(RIEG/)
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Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease N-PSDB; ADN62903.

Claim 1; SEQ ID NO 100; 395pp; English.

The invention relates to isolated NOVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent, diagnose or NOVX polypeptides. For example, NOVX polypeptides and activity of NOVX polypeptides. For example, NOVX polypeptides and activity of NOVX by supplementing the patient our control or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by indiagnostic assays to detect and quantitate the presence of binding with the cells own genes and preventing their expression. NOVX polymucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators the production of antibodies and in assays to identify modulators anti-NOVX polypeptide expression and activity of NOVX. The anti-NOVX polypeptide expression and activity of NOVX cused to modulate NOVX polymucleotide expression and activity of NOVX polypeptides and purpose and presence of NOVX in samples. The anti-NOVX polypeptide antibodies may be used as diagnose and treat: metabolic disorders, diaberes, obesity, infectious diseases, anorexia, cancer, cancer, saberes; anobesity, immune disorders, haematopoietic disorders, and the various dyslipidaemias, metabolic

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ADI37151 standard; protein; 144 AA
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Matches
                                                   RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel activated immune T cells or dendritic cells directed toward extracellular serine protease termed tumour antigen derived gene-14 (TADG-14). The method of the invention involves exposing the immune cells to a TADG-14 protein fragment, where exposure to the TADG-14 protein fragment activates the immune cells. The invention of activated immune T cells or dendritic cells. The invention allows screening to identify proteases overexpressed in carcinoma. The present sequence is stratum corneum
disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Production of activated immune cells or dendritic cells by exposing immune cells to tumor antigen derived gene protein fragment consisting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immune T cell; dendritic cell; extracellular serine protease; tumour antigen derived gene-14; TADG-14; carcinoma; stratum corneum chymotryptic enzyme; scce.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stratum corneum chymotryptic enzyme (scce) catalytic domain.
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                                                                                                                                                             100.0%; Score 42; DB 8; Length 97; 100.0%; Pred. No. 0.28; ive 0; Mismatches 0; Indels
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98US-00137944.
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Best Local Similarity 100.
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Best Local Similarity
9; Conserve
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                                                                                                                    Sequence 97 AA;
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The invention relates to extracellular serine protease termed tumour antigen derived gene-14 (TADG-14) and its nucleic acid. Composition comprising TADG-14 peptide is useful for treating a neoplastic state in individual. The neoplastic state is chosen from ovarian cancer, cancer, lung cancer, colon cancer, prostate cancer in which TADG-14 is overexpressed. The present sequence is Stratum corneum chymotryptic enzyme (scce) catalytic domain. This sequence is used in the envention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated DNA encoding tumor antigen derived gene-14 protein, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for treating neoplastic state (such as ovarian cancer, breast cancer, lung cancer, colon cancer, prostate cancer) in an individual.
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                                                                                                                                                   Serine protease; tumour antigen derived gene-14; TADG-14; neoplastic state; cancer; ovary; breast; lung; colon; prostate; chymotryptic enzyme; scce; enzyme.
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                                                                                                    Stratum corneum chymotryptic enzyme (scce) catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 42; DB 8; Length 144; 100.0%; Pred. No. 0.42; cive 0; Mismatches 0; Indels
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21-AUG-1998; 98US-00137944.
18-JUL-2000; 2000US-00618259.
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Conservative 0
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Best Local Similarity
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                                                                                                                                                                                                                                                                Homo sapiens.
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ADI37151;
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QRIKASKSF 9

polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential threapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the above polypeptide. Now mammal; and [14) a method for producing the above polypeptide. Now sequences have antidiabetic, nortodici, antibacterial, virucide, immunomodulator, cytostatic, noctropic, neuroprotective, antiparkinsonian and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic alsorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders such as Alzheimer's disease or Parkinson's cyclobes, in chromosome mapping, tissue typing, preventive medicine and present invention.

Expresent invention.

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The present invention describes NOVX proteins, where X can be 1 to 55 described above and a carrier; (2) a kit comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a call comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of an order of acid molecule in a disease associated with altered levels of expression of the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerbusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
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                                                                                                                                                                                                                                                       05-0CT-2001; 20010S-0327449P.
09-0CT-2001; 2001US-0327917P.
09-0CT-2001; 2001US-0328029P.
09-0CT-2001; 2001US-0328049P.
12-0CT-2001; 2001US-0328049P.
15-0CT-2001; 2001US-033914P.
17-0CT-2001; 2001US-033914P.
18-0CT-2001; 2001US-033926P.
24-0CT-2001; 2001US-0341059P.
24-0CT-2001; 2001US-0341059P.
24-0CT-2001; 2001US-0341059P.
24-0CT-2001; 2001US-034162P.
17-APR-2001; 2001US-034162P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373816P.
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2001US-0327449P.
2001US-0327917P.
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22-APR-2002; 2002US-0374977P.
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16-MAY-2002; 2002US-0381038P.
16-MAY-2002; 2002US-0381042P.
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01-OCT-2002; 2002US-00262511,
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                                                                                                             WO2003029424-A2.
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                                                                            Homo sapiens
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human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X; Gaps ö 100.0%; Score 42; DB 6; Length 181; 100.0%; Pred. No. 0.54; ive 0; Mismatches 0; Indels ADN62902 standard; protein; 181 AA. 2001US-0326483P.
2001US-0327449P.
2001US-0327449P.
2001US-0328029P.
2001US-0328044P.
2001US-0328444P.
2001US-0328444P.
2001US-0328444P.
2001US-033849P.
2001US-033942P.
2001US-0330309P.
2001US-0330309P.
2001US-0341058P. 01-OCT-2002; 2002US-00262511 01-JUL-2004 (first entry) 9; Conservative 80 1 QRIKASKSF 9 Best Local Similarity 72 QRIKASKSF wasting disorder. Sequence 181 AA; US2004038223-A1. 02-0CT-2001; 2 05-0CT-2001; 2 05-0CT-2001; 2 09-0CT-2001; 2 09-0CT-2001; 2 12-0CT-2001; 2 11-0CT-2001; 2 11-0CT-2001; 2 18-0CT-2001; 2 22-OCT-2001; 24-OCT-2001; 24-OC Human NOV18d. Homo sapiens. 26-FEB-2004 ADN62902; Query Match Matches RESULT 10 ADN62902 ઠ 셤

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Peyman JA, Kekuda R, Ju J, Li L, Guo X;
A, Edinger SR, Ellerman K, Malyankar UM;
seen BD, Anderson DW, Zhong M, Catterton E;
111 L, Stone DJ, Pena CEA, Shenoy SG;
ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
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Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA,
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Be
Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
29-OCT-2001; 2001US-0349575P.
01-NOV-2001; 2001US-0346357P.
17-APR-2002; 2002US-0373260P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373817P.
19-APR-2002; 2002US-037384P.
22-APR-2002; 2002US-0374977P.
16-MAY-2002; 2002US-0381037P.
16-MAY-2002; 2002US-0381038P.
17-MAY-2002; 2002US-0381038P.
                                                                                                                                                                                28-MAY-2002; 2002US-0383656P.
29-MAY-2002; 2002US-0383831P.
25-JUN-2002; 2002US-0391335P.
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EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
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GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
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SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
LEACH M D.
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BERGHS C.
DIPIPPO V A.
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PATTURAJAN M.
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ANDERSON D W.
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PEYMAN J A.
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MILLER C E.
RASTELLI L.
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CATTERTON E.
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The invention relates to isolated NOVX polypeptides and polynucleotides. NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and polynucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules
Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                         Claim 1; SEQ ID NO 98; 395pp; English.
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may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX purelectides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polypucleotide expression and activity of NOVX polypeptides. The anti-NOVX polypeptide antibodies may also be used as diagnose and treat: metabolic disorders, diabetes, obseity, infectious disorders, and the various dislipidaemias, metabolic disorders, and the various dislipidaemias, metabolic disorders associated with obseity, the metabolic syndrome X and chisturbances associated with obseity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence of a human NOVX protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 42; DB 8; Length 181; 100.0%; Pred. No. 0.54; tive 0; Mismatches 0; Indels
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2001US-0327449P.
2001US-0328029P.
2001US-0328064P.
2001US-0328064P.
2001US-032849P.
2001US-0329414P.
2001US-0330309P.
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2001US-0343629P.
2001US-0349575P.
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 181 AA;
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05-0CT-2001;
09-0CT-2001;
09-0CT-2001;
09-0CT-2001;
12-0CT-2001;
15-0CT-2001;
18-0CT-2001;
22-0CT-2001;
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24-OCT-2001;
29-OCT-2001;
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ADN62900 standard; protein; 198 AA.

RESULT 12

ADN62900

01-JUL-2004 (first entry)

ADN62900;

Human NOV18c

human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;

wasting disorder

Homo sapiens

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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                            New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
01-NOV-2001; 2001US-0346357P.

17-APR-2002; 2002US-0373810P.

19-APR-2002; 2002US-0373817P.

19-APR-2002; 2002US-0373817P.

19-APR-2002; 2002US-0373826P.

19-APR-2002; 2002US-037384P.

22-APR-2002; 2002US-0374877P.

16-MAY-2002; 2002US-0381033P.
                                                                                            2002US-0381042P.
2002US-0381642P.
2002US-0383656P.
2002US-0383831P.
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                                                                                                                                                                    (CURA-) CURAGEN CORP.
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N-PSDB; ADA05735.
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                                                                                                     17-MAY-2002; 2
28-MAY-2002; 2
29-MAY-2002; 2
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The present invention describes NOVX proteins, where X can be 1 to 55 C (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more described above and a carrier; (3) an isolated nucleic acid molecule above; (3) an isolated nucleic acid molecule described above; (5) a cell or comprising the nucleic acid molecule described above; (5) a cell or comprising the nucleic acid molecule described above; (5) a cell or comprising the nucleic acid molecule described above; (5) a cell or presence or amount of the above polypeptide cor nucleic acid molecule in a fasease associated with altered levels of expression of the above or adease associated with altered levels of expression of the above and polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therspeutic agent for above polypeptide cor nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (11) a method of a pathology that the polypeptide; (12) a method for modulating cor a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating to requences have antidabated; anorderic, antibacterial, vincled, and antilipaemic activities, and can be used in gene therapy. The corpusement above polypeptide is useful in manufacturing a medicament for treating a pathology associated with the above polypeptide or the nucleic syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to disquence. The polypeptide corpused manufacturing a medicament for treating activities, and can be used and vibracian and polypeptide or or prevent metabolic acid molecule may be used to disquence the polypeptide corpused with a human disease. The polypeptide or probes, in mune disord
Claim 1; Page 170; 586pp; English.
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2001US - 0327435P
2001US - 0327449P
2001US - 0328029P
2001US - 0328054P
2001US - 0328056P
2001US - 0328449P
2001US - 0328449P
2001US - 0328449P
2001US - 0329414P
2001US - 0330142P
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2001US-0349575P.
2001US-0346357P.
2002US-037386PP.
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2002US-0383656P.
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PATTURAJAN M.
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EDINGER S R.
ELLERMAN K.
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PEYMAN J A.
KEKUDA R.
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다.
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12-0CT-2001;
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18-0CT-2001;
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24-OCT-2001;
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09-OCT-2001;
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19-APR-2002;
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The invention relates to isolated NoVX polypeptides and polymucleotides.

NoVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the abstrant expression and activity of NoVX polypeptides. For example, NoVX polypeptides and control of NoVX by supplementing the patient our production or to rectify mutations. Conversely, antiense NA molecules may be administered to down regulate expression of NoVX polypeptides by binding with the cells own genes and preventing their expression. NoVX polymucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NoVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators cantinovx polypeptides and antagonists and clivity of NoVX. polypeptides. The anti-NoVX polypeptide antibodies and antagonists may also be used as diagnose and treat: metabolic disorders, diabetes, obesity, infectious diagnose and treat: metabolic disorders, diabetes, obesity, infectious diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, Alabeimer's bisease, Parkinson's Disporder, immune disorders, haematopoietic disorders, and the various dyslipidaemias, metabolic disorders, habreimer's bisease, parkinson's and prevent disorders, and the various dyslipidaemias, metabolic wasting disorders associated with obesity, the metabolic syndrome X and charting disorders associated with charcing diseases and various cancer. They may also be used as antibacterial agents. The present sequence of a human NoVX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ortr T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
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Best Local Similarity 100...
--- 9; Conservative
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GANGOLLI E A.
RIEGER D K.
                                                                                                                                                                                                             PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
LEACH M D.
  MALYANKAR U M.
                                                       ZERHUSEN B D. ANDERSON D W.
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BERGHS C.
DIPIPPO V A.
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RASTELLI L.
STONE D J.
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N-PSDB; ADN62899.
                                                                                                                   CATTERTON E.
                                  GORMAN L.
                                                                                                  ZHONG M.
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(ROTH/)
(LEAC/)
(AGEE/)
(BERG/)
                                                                                              (ZHON/)
(CATT/)
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(RAST/)
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immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obseity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Bisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                    human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                                                                                                             Human NOV18g protein SEQ ID NO:104.
                                                                  ADA05744 standard; protein; 224 AA.
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2001US-0327435P.
2001US-0328029P.
2001US-0328044P.
2001US-0328044P.
2001US-0328044P.
2001US-0328044P.
2001US-0328044P.
2001US-0339042P.
2001US-0341058P.
2001US-0343626P.
2001US-0343629P.
2001US-034362P.
2001US-034362P.
2001US-034362P.
2001US-034362P.
2001US-034837P.
2002US-0373817P.
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2002US-0391335P.
2002US-00262511.
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                                                                                                                   06-NOV-2003 (first entry)
      91 ORIKASKSP 99
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17-OCT-2001;
18-OCT-2001;
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29-OCT-2001;
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Dipippo VA;

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26-FEB-2004

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The present invention describes NOVX proteins, where X can be 1 to 55 cengr NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) at the composition described above; (3) an isolated nucleic acid containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell like to be peoply peptide described above; (5) a cell like to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a disease associated with altered levels of expression of the above adisease associated with altered levels of expression of polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for aberrant physiological interactions of the polypeptide or nucleic acid molecule in a first mammalian subject; (9) a construct the polypeptide described above; (11) a method of a pathology that is related to an aberrant expression or a pathology associated with the polypeptide; (12) a method for modulation of a pathology associated with the above polypeptide; (11) a method of producing the above polypeptide is useful in manufacturing a method for producing the above polypeptide is useful in manufacturing a method for producing the above polypeptide or the nucleic and antilipaemic activities, and can be used in gene therapy. The pulpaemic activities, and can be used in gene therapy. The pulpaemic and molecule may be used to diagnose, treat or prevent metabolic acid molecule may be used to diagnose, treat or prevent metabolic dylational and plantacogenerative disorders such as Alzheimer's achexia, cancer, also a diabetes or obseity, inferience and antilibaemic and inference and antilibaemic and inference and an ab
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             New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
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100.0%; Pred. No. 0.67;
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                                                                                                                              Claim 1; Page 172; 586pp; English.
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort I, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
                                                                              2001US - 0326483P . 2001US - 0327435P . 2001US - 03274435P . 2001US - 0328029P . 2001US - 0328044P . 2001US - 0328044P . 2001US - 0328044P . 2001US - 0328444P . 2001US - 0338044P . 2001US - 0346557P . 2001US - 0346557P . 2002US - 0373815P . 2002US - 0373817P . 2002US - 0373817P . 2002US - 0373814P . 2002U
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2002US-0381042P.
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2002US-0383656P.
2002US-0383831P.
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EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
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GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
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RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
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ZERHUSEN B D.
ANDERSON D W.
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PATTURAJAN M.
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BERGHS C.
DIPIPPO V A.
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MILLET I.
PEYMAN J A.
KEKUDA R.
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09-0CT-2001; 2
12-0CT-2001; 2
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18-0CT-2001; 2
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24-OCT-2001;
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01-NOV-2001;
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Shenoy SG;
                                                                                                                                                                                                                   The invention relates to isolated NOVX polypeptides and polynucleotides.
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                                                                                                                             Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
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     Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy
ts RA, Rothenberg ME, Leach MD, Agee ML, Berghs C,
A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 42; DB 8; Length 224; 100.0%; Pred. No. 0.67;
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                                                                                                                                                                                Claim 1; SEQ ID NO 104; 395pp; English.
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77 QRIKASKSF 85
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Best Local Similarity
9; Conserve
                                                                           2004-213931/20.
                                                                                              N-PSDB; ADN62907
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                                            Eisen A,
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New isolated polypeptides, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining predisposition to diseases or conditions of the prostate such as prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to PS133 protein, a member of the human serine protease family and its corresponding nucleic acid sequence. PS133 polypeptide is useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to diseases or conditions of the prostate such as prostatic cancer. The present sequence is the human stratum corneum chymotrypsin protein. This sequence is used to align with PS133 consensus protein.
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                     /note = Catalytically functional motif
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Stroupe SD;
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Job time : 87.6667 secs
                                                                                                                                                     20-FEB-2001; 2001US-00789210.
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174. .179
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COLPITTS T L.
FRIEDMAN P N.
GRANADOS E.
KLASS M R.
RUSSELL J C.
STEWART K D.
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                                                                 US2004241646-A1.
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                                                                                                                                                                                                 06-OCT-1997;
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Russell JC,
                                                                                                           02-DEC-2004
                                                                                                                                                                                                                                                                                                             (GRAN/)
(KLAS/)
(RUSS/)
(STEW/)
(STRO/)
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Domain
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March 11, 2006, 00:24:40; Search time 14.1111 Seconds (without alignments) 61.367 Million cell updates/sec Run on:

US-09-905-083A-99 Perfect score:

1 QRIKASKSF 9 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:\*
1: pir1:\*
2: pir2:\*
1: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		protein T24A6.11 [	kallistatin precur	probable DNA-direc	tetrachloro-p-hydr	beta-SNAP protein	mak16-like protein	probable phosphate	BET1 protein - yea		probable dehydroge	hypothetical prote		neutral endopeptid	lactococcal endope	endopeptidase PepO		pyruvate dehydroge		dystrophin, muscle	ᇋ	16K protein - toba	NADH2 dehydrogenas	hypothetical prote	thiogalactoside ac	thiogalactoside ac	quinolinate phosph	WD repeat protein	hypothetical prote
SUMMARIES	ΩΙ	A53968	D89004	A49518	D72571	A40625	S32368	T50147	F81409	C39610	C71463	H97051	T48159	T40129	C86850	A47098	F53290	T19678	D82776	H84545	S02041	AF2269	B46322	H81251	C64176	C90678	G85528	E84339	AE2568	T22587
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d	Query Match	100.0	81.0	78.6	76.2	73.8	73.8	73.8	73.8	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	ď.	69.0	69.0	e,	69.0	69.0	•	69.0	69.0
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G97300 JC5282	G71081 B82883	T48273 I37216	AB2028	T46476	AC1419	E86294	C86168	S67164	A40985	T15297	824600	T13931
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69.0	69.0 69.0	69.0	0.69	0.69	69.0	0.69	0.69	0.69	69.0	0.69	0.69	0.69
7 7 7 7	5 7 8 8	8 8 8 8	5	53	29	29	53	29	53	53	53	53
30	33	3.4	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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C;Accession: A53968
R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T. D. Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzym: A;Reference number: A53968; MUID:94308225; PMID:8034709
                                                                                                                                                                                                                                    A;Accession: A53966
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <HAN>
A;Cross-references: UNIPROT: P49862; UNIPARC: UPI000001BC4; GB:L33404; NID:g521214; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                     N;Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-Jul_1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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serine proteinase SCCE precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Cross-references: GDB:377730
A, Map position: 7q35-7q35
C, Superfamily: trypsin; trypsin homology
P,30-245/Domain: trypsin homology <PRY>
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: GDB: PRSS6; SCCE
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91 QRIKASKSF 99

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RESULT 2

protein T24A6.11 [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004

C; Accession: D89004

Riancommous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see webbaites genome.wustl.edu/gsc/C\_elegans/ and www\_sanger.ac.uk/Projects/C\_elegans/ A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A; Accession: D89004 A; Status: preliminary

A; Molecule type: DNA

A,Residues: 1-373 <STO>
A,Residues: 1-373 <STO>
A,Cross-references: UNIPROT:061942; UNIPARC:UPI000017A667; GB:chr\_V; PIDN:AAC17798.1; PII
A,Note: contains similarity to C4-type zinc fingers
C;Genetics:
A,Gene: T24A6.11

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awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ku
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyru
A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                         A;Accession: D72571
A;Status: preliminary
A;Molecus: treiminary
A;Residues: 1-895 <KAW>
A;Residues: 1-895 <KAW>
A;Residues: 1-895 <KAW>
A;Cross-references: UNIPROT:Q9YAU1; UNIPARC:UPI000005E0F5; DDBJ:AP000062; NID:g5105244; I
A;Experimental source: strain K1
A;Genetics:
A;Genetics:
A;Genetics:
C;Genetics:
C;Superfamily: Halobacterium DNA-directed RNA polymerase chain A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tetrachloro-p-hydroquinone reductive dehalogenase (BC 1.-...) - Flavobacterium sp.
N.Alternate names: glutathione S-transferase homolog; TeCH reductive dehalogenase
C;Species: Flavobacterium sp.
C;Date: 21. Sep-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Accession: A40625
R;Orser, C.S.; Dutton, J.; Lange, C.; Jablonski, P.; Xun, L.; Hargis, M.
J. Bacteriol: 175, 2640-2644, 1993
A;Title: Characterization of a Flavobacterium glutathione S-transferase gene involved rec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: A40625
A;Status: preliminary
A;Nolecule types: nucleic acid
A;Nolecule types: nucleic acid
A;Residues: 1-248 <ORS>
A;Residues: 1-248 <ORS>
A;Cross-references: UNIPARC:UPI000017A939; GB:M98559; NID:g148689; PIDN:AAA24921.1; PID:ç
A;Experimental source: ATCC 39723
A;Note: sequence extracted from NCBI backbone (NCBIN:130432, NCBIP:130433)
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species Boo primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S32368 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S32368 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S32368 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
R;Whitcheart, S.W.; Griff, I.C.; Brunner, M.; Clary, D.O.; Mayer, T.; Buhrow, S.A.; Rothmadrus 362, 353-355, 1993
A;Title: SNAP family of NSF attachment proteins includes a brain-specific isoform.
A;Reference number: S32367; MUID:93205122; PMID:8455721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 2; Length 298;
Pred. No. 35;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 2; Length 895;
Pred. No. 63;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.8%; Score 31; DB 2; Length 248;
66.7%; Pred. No. 29;
tive 2; Mismatches 1; Indels
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C;Superfamily: alpha-soluble NSF attachment protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 73.8%;
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 75.0%;
Matches 6; Conservative
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885 QRVKASKA 892
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Matches 6; Conserv
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-298 < WHI>
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A;Cross-references: GDB:266537; OMIM:147935
A;Cross-references: GDB:266537; OMIM:147935
A;Cross-references: GDB:266537; OMIM:147935
C;Superfamily: Gerpin
C;Superfamily: serpin
C;Superfamily: serpin
C;Keywords: blocked amino end; glycoprotein; pyroglutamic acid; serine proteinase inhibi
F;11-20/Domain: signal sequence #status predicted AMIP
F;21-47/Product: kallistatin #status predicted AMIP
F;21-47/Product: kallistatin #status predicted AMIP
F;21-47/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;33,108,157,238/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;388/Inhibitory site: Phe (tissue kallikrein) #status experimental
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A49518; A55560; A545093
R;Chai, K.X.; Chen, L.M.; Chao, J.; Chao, L.
J. Biol. Chem. 268, 24498-24505, 1993
A;Title: Kallistatin: a novel human serine proteinase inhibitor. Molecular cloning, tiss A;Accession: A49518; MUD:94043294; PMID:8227002
A;Accession: A49518
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: UNIPARC:UPI000012DC02, GB:L28101, NID:g609489; PIDN:AAC41706.1, PID: R;Zhou, G.X.; Chao, L.; Chao, J. Biol. Chem. 267, 258973-25896, 192
A,Title: Kallistatin: a novel human tissue kallikrein inhibitor. Purification, character A,Reference number: A45093; MUID:93100304; PMID:1334488
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A;Residudes: 389-403 - 2810>
A;Cross-references: UNIPARC:UP100000353AC; PIDN:AAB24557.1; PID:g261993
A;Note: sequence extracted from NCBI backbone (NCBIP:120847)
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A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA
A;Residues: 1-427 <CH2>
                                                                             81.0%; Score 34; DB 2; Length 373; 77.8%; Pred. No. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.6%; Score 33; DB 2; Length 427;
66.7%; Pred. No. 18;
cive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-427 < CCHA>
A; Cross-references: UNIPROT: P29622; UNIPARC: UPI000012DC02;
R; Chai, K.X.; Ward, D.C.; Chao, J.; Chao, L.
Benonics 23, 370-378, 1994
A; Title: Molecular cloning, sequence analysis, and chromoso
A; Reference number: A55560; MUID: 95137583; PMID: 7835886
                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
A49518
kallistatin precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 78.6
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                   Conservative
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QEIKSSKSF 17
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                                                                                                             Local Similarity
les 7; Conserv
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                 A; Map position:
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Matches
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A;Title: Identification and structure of four yeast genes (SLY) that are able to suppress A;Reference number: A39610; MUID:91117254; PMID:1990290
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                                                                                                                                                                             Rikowley, N.
submitted to the EMBL Data Library, August 1994
A;Reference number: $48442
A;Recession: $48453
A;Rocession: $48453
A;Molecule type: DNA
A;Residues: 1.142 - ROWA
A;Cross-references: UNIPARC:UPI000012689C; GB:Z47047; EMBL:Z38113; NID:g603997; PID:g763C
R;Voss, H.; Tamames, J.; Teodoru, C.; Valencia, A.; Sensen, C.; Wiemann, S.; Schwager, C
Yeast 11, 61-78, 1995
A;Title: Nucleotide sequence and analysis of the centromeric region of yeast chromosome 1
A;Reference number: S50795; MUID:95282515; PMID:7762303
A;Accession: S58677
A;Estus: nucleic acid sequence not shown; translation not shown
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A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia track A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: C71463
A;Status: preliminary
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*Residues: 1-31. ARN>
A;Cross-references: UNIRROT:084847; UNIPARC:UPI00000D33B9; GB:AE001357; GB:AE001273; NID
A;Experimental source: serotype D, strain UW-3/Cx
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probable dehydrogenase, YULF B. subtilis ortholog [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-142 <VOS>
A;Crose-references: UNIPARC:UPI000012689C; EMBL:X79743
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
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Pred. No. 64;
2; Mismatches 1; Indels
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C,Superfamily: cell cycle control PP-loop ATPase MesJ/YaeO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: SGD:BET1; SLY12
A;Cross-references: SGD:S0001266; MIPS:YIL004c
A;Map position: 9L
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Best Local Similarity 66.7%;
Matches 6; Conservative
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                                                            A;Accession: C39610
A;Molecule type: DNA
A;Residues: 1-142 <DAS>
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C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Species: Ja.Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: F81409
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 655-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A;Reference number: A81250; MUD:20150912; PMID:10688204
A;Accession: F81409
A;Accession: F81409
A;Accession: F81409
A;Molecule type: DNA
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A;Cross-references: UNIPROT:Q9PHQ2; UNIPARC:UPI00000C21AA; GB:AL139075; GB:AL11168; NID
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q9UTE6; UNIPARC:UP1000069FE1; EMBL:AL132798; PIDN:CAB60698
A;Experimental source: strain 972h(-); cosmid c222
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                                                                                                                                                                                                      maki6-like protein [imported] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 12-Jul-2004
C;Accession: T50147
R;Hamlin, N; Churcher, C.M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, November 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
C39610
BET1 protein - yeast (Saccharomyces cerevisiae)
NALternate names: protein YIA4c; protein YIL004c; SLY12 protein
NyAlternate names: protein YIA4c; protein YIL004c; SLY12 protein
C;Species: Saccharomyces cerevisiae
C;Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 09-Jul-2004
C;Accession: C39610; S48453; S58677
R;Dascher, C.; Ossig, R.; Gallwitz, D.; Schmitt, H.D.
Mol. Cell. Biol. 11, 872-885, 1991
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                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: 225043
A;Accession: T50147
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-302 <HAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: ribosomal biogenesis protein MAK16
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Matches 7; Conservative
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KRVKASHSF 27
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ORIKLSKNY 86
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QRIKASKSF
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Matches 6; Conserv
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A,Gene: SPDB:SPAC222.06
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Search completed: March 11, 2006, 00:40:54 Job time : 15.1111 secs
           A; Introns: 42/3; 126/3; 157/3; 308/3
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T40129
hypothetical protein SPBC2F12.12c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: 30-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40129
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
Submitted to the EMBL Data Library, June 1997
A;Reference number: Z21907
A;Reference number: Z21907
A;Recession: T40129
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-517
A;Molecule type: DNA
A;Residues: 1-517
A;Cross-references: UNIPROT:014342; UNIPARC:UP1000013A210; EMBL:Z97211; PIDN:CAB10159.1;
A;Experimental source: strain 972h-; cosmid c2F12
C;Genetics:
A;Gene: SPDB:SPBC2F12.12c
A;Map position: 2
C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C; Accession: H97051
R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
F; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Accession: H97051
A; Accession: H97051
A; Accession: H97051
A; Accession: H97051
A; CKUR>
A; Cross-references: UNIPROT: Q97JP2; UNIPARC: UPI00000CA131; GB:AE001437; PIDN:AAK79203.1;
A; Experimental source: Clostridium acetobutylicum ATCC824
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48159
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, Iseference number: Z24486
A;Reference number: Z24486
A;Reference number: Z24486
A;Ression: T48159
A;Residues: L-427
A;Molecule type: DNA
A;Residues: 1-427
A;Residues: 1-427
A;Residues: UNIPROT: O9M035; UNIPARC: UPI00000A2376; EMBL: AL161746
A;Genetics:
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Match 71.4%; Score 30; DB 2; Length 331; Local Similarity 75.0%; Pred. No. 66; 1; Indels es 6; Conservative 1; Mismatches 1; Indels
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A;Gene: CAC1231
C;Superfamily: Escherichia coli ygjR protein
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Best Local Similarity 66...
6; Conservative
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140 RRVKASVSF 148
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A; Introns: 317/1
A; Note: T1008.80
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Matches
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Jactococcal endopeptidase (EC 3.4...) - Lactococcus lactis subsp. cremoris (strain P8-2. C.Species: Lactococcus lactis subsp. cremoris C.Species: Lactococcus lactis subsp. cremoris C.Species: D3-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004 C.Accession: A47098
C.Accession: A47098
A.Fitle: Cloning and sequencing of the gene for a lactococcal endopeptidase, an enzyme with A.Reserior number: A47098; MUID:93209954; PMID:8458851
A.Accession: A47098
A.Status: preliminary
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A;Residues: 1-627 <MIE>
A;Cross-references: UNIPROT:Q09145; UNIPARC:UPI000016F8B8; GB:L04938; NID:g293013; PIDN:f
C;Genetics:
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Query Match 71.4%; Score 30; DB 2; Length 517; Best Local Similarity 77.8%; Pred. No. 1e+02; Matches 7; Conservative 0; Mismatches 2; Indels
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75.0%; Pred. No. 1.2e+02;
tive 1; Mismatches 1;
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C,Keywords: hydrolase; oligopeptide transport
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Best Local Similarity 75.0
Matches 6; Conservative
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March 11, 2006, 00:11:15 ; Search time 95.2222 Seconds (without alignments) 66.684 Million cell updates/sec Run on:

US-09-905-083A-99 42 1 QRIKASKSF 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

يد	P49862 homo sapien	Q91ve3 mus musculu	Q9cju4 pasteurella			Q82xb0 nitrosomona	Q678h2 lymphocysti	-			_	Q54h89 dictyosteli	Q8eup9 mycoplasma		_							-		O8i6k2 holotrichia	-	Q62hp6 burkholderi		Q7qxy1 giardia lam		00	Q5cw22 cryptospori
SUMMAKIES	KLK7 HUMAN	KLK7 MOUSE	Y1897 PASMU	Q88Q37 PSEPK	Q4KA21_PSEF5	Q82XB0_NITEU	Q678H2_9VIRU	RLAO THEAC	KAIN HUMAN	KAIN_PONPY	Q54TF9 DICDI	QS4H89_DICDI	Q8EUP9 MYCPE	Q4S703_TETNG	RL10_MYCPE	Q6FDRS ACIAD	040B71 LEIMA	Q4HKD5_CAMLA	Q7RKQ8_PLAYO	Q8IBN4_PLAF7	Q7VRX5_CANBF	Q8SAQ6_CHLRE	Q5X079_LEGPL	Q816K2 HOLDI	Q6D7X6_ERWCT	Q62HP6_BURMA	Q63W23_BURPS	Q7QXY1_GIALA	Q9YAU1_AERPE	Q4PEQ8_USTMA	Q5CW22_CRYPV
ength DB	253 1	249 1		294 2	•	•	310 2	314 1	427 1	427 1	•	٠. س	671 2	•													772 2		895 2		3395 2
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Q4rul0 tetraodon n Q6dgm1 brachydanio			Q519u9 entamoeba h				Q937x0 sphingomona	Q975x7 sulfolobus	Q8n8n1 homo sapien	P81126 bos taurus
Q4RUL0_TETNG Q6DGM1_BRARE	Q6AXNO_RAT Q6P3B2_MOUSE	Q8TB05 HUMAN Q4S4E7 TETNG	Q519U9_ENTHI	Q71MF6_HUMAN	Q6FBIO ACIAD	PCPC_SPHCR	Q937X0 9SPHN	Q975X7 SULTO	Q8N8N1 HUMAN	SNAB_BOVIN
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143 155	176 176	177	201	212	235	247	248	254	276	298
73.8	73.8	73.8	73.8	73.8	73.8	73.8	73.8	73.8	73.8	73.8
31	31	31	31	31	31	31	31	31	31	31
33	34 35	36 37	38	39	40	41	42	43	44	45

# ALIGNMENTS

NOTECTION STANDARD; PRT; 253 AA.  KIKT HUMAN  KIKT HUMAN  P49862; QBNSN9; QBNRY1; 01-OCT-1996 (Rel. 34, Lest sequence update) 02-OCT-1996 (Rel. 34, Lest sequence update) 03-SEVENT (RESO SEQUENCE (MRNA) (ISOFORM 1), AND PROTISSUE-SKIN; 04-OCT-1996 (RENNA) (ISOFORM 1), AND PROTISSUE-SKIN; 05-OCT-1996 (RENNA) (ISOFORM 1), AND PROTISSUE-SKIN; 05-OCT-1996 (GENOMIC DNA), TISSUE SPECITISSUE-Keratinocyte; 05-OCT-199420-19426 (1994). 07-OCT-1001-1001-1001-1001-1001-1001-1001-10
NOTECOTION STANDARD; PRT; 253 AA.  KIZY HUMAN  KIZY HUMAN  KIZY HUMAN  P49862; QBNSN9; QBNEV7; 01-OCT-1996 (Rel. 34, Last sequence update) 02-OCT-1996 (Rel. 34, Last sequence update) 03-OCT-1996 (Rel. 34, Last sequence update) 04-OCT-1996 (Rel. 34, Last sequence in the serior of set characterization of set characterization of set characterization, mapping, tissue expression and characterization. 05-OCT-109-10-1056/S0378-1119(00)00382 (Ban L., Lee I., Smith R., Argonza-Barrett R., Lee Sequencing and expression analysis of the serior cluster located in chromosome 19q13 region."; 05-OCT-109-108-109-109-109-109-109-109-109-109-109-109
NOTENTIAL STANDARD; PRT; 253 AA.  KIZT HUMAN  KIZT HUMAN  KIZT HUMAN  P49862; QBNSN9; QBNEV7; 01-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-1996 (Rel. 48, Last annotation update) 01-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-1996 (Rel. 48, Last annotation update) 01-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-1996 (Rel. 34, Last sequence update) 02-OCT-1996 (Rel. 34, Last sequence update) 03-OCT-1996 (Rel. 34, Last sequence in the second of store in the second of sequence in the second of second of sequence in the second of second of second of sequence in the second of sequence in the second of
NOTICEDTIDE SEQUENCE [GENOMIC DAY], PRT; 253 AA.  KLK7 HUMAN  YAHANA  KLK7 HUMAN  P49862; QBNSN9; QBNEV9; 01-OCT-1996 [Rel. 34, Last sequence update) 01-OCT-1996 [Rel. 48, Last sequence update) 13-SEP-2005 [Rel. 48, Last annotation update) KAIlikrein 7 precursor [EC 3.4.21) (hK7) (Street of the companies of the companies (Human)  Bundersyptic enzyme) (hSCE).  NCBL TaxID=9606; [1]  NUCLEOTIDE SEQUENCE [WENA] (ISOFORM 1), AND PROTINGE SEQUENCE [GENOMIC DNA], TISSUE SPECIF (1)  NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIF (2)  NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIF (2)  NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIF (2)  NUCLEOTIDE SEQUENCE [GENOMIC DNA].  PUDMed=10054574; DOI=10.1016/S0378-1119(00)00382 (2018 EV.) Pasper B., Wang K.; Argonza-Barrett R., Legal L., Smith R., Argonza-Barrett R., Legal L., Shith R., Shith R., Argonza-Barrett R., Legal L., Shith R., Shith
NCLEOTIDE SEQUENCE (MRNA) (STANDARD), PRT; 253 AA.  KLK7 HUMAN  Y49862; QBNSN9; QBNEV9; 01-OCT-1996 (Rel: 34, Created) 01-OCT-1996 (Rel: 34, Last sequence update) 13-SEP-2006 (Rel: 34, Last sequence update) 13-SEP-2006 (Rel: 34, Last sequence update) 13-SEP-2006 (Rel: 48, Last annotation update) Name=KLK7; Synonyma=PRSS6, SCCE; Homo sapiens (Human): Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Burerchontoglires; Primates; Homo sapiens (Human): Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Burerchontoglires; Primates; Homo sapiens (Human): NCBI TaxID=9606; [1] NUCLEOTIDE SEQUENCE (MRNA) (ISOFORM 1), AND PROT TISSUE-SKIN; MEDLINE=94308225; PubMed=8034709; HABSSON L., Stroemqvist M., Baeckman A., Wallbra Bgelrud T.; "Cloning, expression, and characterization of stroymetryptic enzyme. A skin-specific human serin." J. Biol. Chem. 269:19420-19426(1994). [2] NUCLEOTIDE SEQUENCE (GENOMIC DNA), TISSUE SPECIF PubMed=10974542; DOI=10.1016/S0378-1119(00)00382 (Yousef G.M., Scorilas A., Magklara A., Soosaipill Diamandis E. P.; Sequencing and expression analysis of the serin requlation."; Gene 254:119-128(2000). [3] NUCLEOTIDE SEQUENCE (GENOMIC DNA). HAMSSON L., Baeckman A., NA A., Edlund M., Edhol Wallbrandt P., Eaglrud T.; "Sequencing and expression analysis of the serin cluster located in chromosome 19913 region."; Gene 257:119-130(200). [4] NUCLEOTIDE SEQUENCE (GENOMIC DNA). HANDSON L., Baeckman A., NA A., Edlund M., Edhol Wallbrandt P., Eaglrud T.; "Spidermal overexpression of stratum corneum chymics; a model for chronic ithchy dermatitis."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ ds (Submitted (DEC-2000) to the EMBL/GenBank/DDBJ (Submitted (DEC-2000) to the EMBL/GENBANDANDANDANDANDANDANDANDANDANDANDANDANDA
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NCILT 1  NUMAN  NEWAN  NEWAN  NEWAN  NEWAN  NEWAN  NEWAN  NEWAN  NOTED-1996 (Rel. 34, Created)  O1-OCT-1996 (Rel. 34, Last sequence update)  13-SEP-2005 (Rel. 34, Last sequence update)  13-SEP-2005 (Rel. 48, Last annotation update)  Name-KLK7, Synowne=PRSS6, SCCE;  Name-KLK7, Synowne=PRSS6, SCCE;  Homo sapiens (Human)  Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Euarchontoglires; Primates; Homo sapiens (Human)  NCIL TaxID=9606;  [1]  NUCLEOTIDE SEQUENCE (MRNA) (ISOFORM 1), AND PROT TISSUE-Skin;  MEDLINE-94308225; PubMed=8034709;  Hansson L., Stroemqvist M., Baeckman A., Wallbra Bggllrud T.;  "Cloning, expression, and characterization of st chymotryptic enzyme. A skin-specific human serin."  J. Biol. Chem. 269:19420-19426(1994).  [2]  NUCLEOTIDE SEQUENCE (GENOMIC DNA), TISSUE SPECIF TISSUE-Skaratinocyte;  PubMed=10974542; DOI=10.1016/S0378-1119(00)00382 (Yousef G.M., Scorilas A., Magklara A., Soosaipil Diamandis E.P.;  ROJAMAND SECALID-1016/S0378-1119(00)00382 (August E.)  NUCLEOTIDE SEQUENCE (GENOMIC DNA).  Hansson L., Baeckman A., Ny A., Edlund M., Edhol Wallbrand P., Rageland, T.;  "Sequencing and expression and expression and cluster located in chromosome 19413 region.";  Gene 25:119-130(200).  [4]  NUCLEOTIDE SEQUENCE (GENOMIC DNA).  Hansson L., Baeckman A., Ny A., Edlund M., Edlund M., Edlund M., Mallbrand P., Ragelard P., Segland T.;  "Sequencing and expression of stratum corneum chy wallbrand P., Regelard (Dr., Regelard T.;  "Submitted (DEC-2000) to the EMBL/GenBank/DDBJ de (S)  NUCLEOTIDE SEQUENCE (MENNA) (ISOFORMS I AND 2), Submitted (DEC-2000) to the EMBL/GenBank/DDBJ (S)  NUCLEOTIDE SEQUENCE (MENNA) (ISOFORMS I AND 2), SUBMICEDPARAIN CALCIDORS.
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NCLEATION STANDARD; PRT; 253 AA.  KLK7 HUMAN  KLK7 HUMAN  FAHENA  KLK7 HUMAN  P49862; QBNSNB: 34, Created)  01-OCT-1996 (Rel: 34, Last sequence update)  13-SEP-2005 (Rel: 34, Last sequence update)  13-SEP-2005 (Rel: 34, Last sequence update)  13-SEP-2005 (Rel: 34, Last sequence update)  KAILIkrein 7 precursor (EC 3.4.21) (hK7) (Streated)  Name=KLK7; Synowns=PRSS6, SCCE;  Homo sapiens (Human):  Bukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Eurrchontoglires; Primates; Homo sapiens (Human):  NCIL TAXID=9606;  [1]  NUCLEOTIDE SEQUENCE (MRNA] (ISOFORM 1), AND PROT TISSUE=Skin;  MEDLINE=941308225; PubMed=8034709;  Hansson L., Stroemqvist M., Baeckman A., Wallbra Bggllvdf T.;  "Cloning, expression, and characterization of st chymotryptic enzyme. A skin-specific human sering."  "Cloning, expression, and characterization of st chymotryptic enzyme. A skin-specific human sering."  "Cloning, expression, and characterization of st chymotryptic enzyme. A skin-specific human sering."  "Cloning, expression, and characterization of st chymotryptic enzyme. A skin-specific human kallikrein grandation."  [2]  NUCLEOTIDE SEQUENCE [GENOMIC DNA].  Hansson L., Baeckman A., Ny A., Edlund M., Edhol Wallbrand P., Regeliand T.;  "Sequencing and expression of stratum corneum chymics: a model for chronic ithchy dermatitis.";  Submitted (DEC-2000) to the EMBL/GenBank/DDBJ de [5]  NUCLEOTIDE SEQUENCE [FRNOMIC DNA].  "Biddermal overexpression of stratum corneum chymics: a model for chronic ithchy dermatitis.";  "Submitted (DEC-2000) to the EMBL/GenBank/DDBJ (15)  NUCLEOTIDE SEQUENCE [CENOMIC ithchy dermatitis.";  Submitted (DEC-2000) to the EMBL/GenBank/DDBJ (15)
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YTHUMAN  YTHUMAN  YTHUMAN  YELY HUMAN  O1-OCT-1996 (Rel. 34, Last sequence update)  I3-SEP-2005 (Rel. 48, Last annotation update)  Xallikrein 7 precursor (EC 3.4.21) (kY) (Strachyretypein censyme) (hSCCE)  Name=KLK7; Synonyms=PRSS6, SCCE;  NAME ARAZO2 (HUMAN)  NUCLECTIDE SEQUENCE [WENA] (ISOFORM 1), AND PROTINGENTIES SEQUENCE [WENA] (ISOFORM 1), AND PROTINGENTES SEQUENCE [WENA] (ISOFORM 1), AND PROTINGENTIES SEQUENCE [GENOMIC DNA], TISSUE SPECIF (Chymotryptic enzyme. A skin-specific human sering a chymotryptic enzyme. A skin-specific human sering a sequence (GENOWIC DNA), TISSUE SPECIF (1994).  [2]  NUCLECTIDE SEQUENCE (GENOMIC DNA), TISSUE SPECIF (1994).  [3]  NUCLECTIDE SEQUENCE (GENOMIC DNA), ANGREE SPECIF (1994).  "The KLK7 (PRSS6) gene, encoding for the stratum enzyme is a new member of the human kallikreing characterization, mapping, tissue expression and regulation.";  Gene 254:119-128 (2000).  Gene 254:119-128 (2000).  [4]  NUCLECTIDE SEQUENCE (GENOMIC DNA).  PubMed=11054574; DOI=10.1016/S0378-1119(00)00382  Gan L., Lee I., Smith R., Argonza-Barrett R., Lee I., Septer B., Wang K., Redlund R., Redlund R
NUT 1  NUT 1  NUT 1  NUT 1  NUT 1  P49662; QONNEYD;  O1-OCT-1996 (Rel. 34, Last sequence update)  Name-KLK7; Synonyms=PRSS6, SCCE;  Homo sapiens (Human).  Bukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Euarchontoglires; Primates; Homo.  NCETT TaxID=9606;  [1]  NUCLEUTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT TISSUE-Skin;  MEDIINE=94308225; PubWed=8034709;  Hansson L., Stroemqvist M., Baeckman A., Wallbra Egglind T.;  "Cloning, expression, and characterization of st chymotryptic enzyme. A skin specific human serin.  J. Biol. Chem. 269:19420-19426 (1994).  [2]  NUCLEOTIDE SEQUENCE [GENOMIC DNA]; TISSUE SPECIF TISSUE-Keratinocyte;  PubMed=10974542; DOI=10.1016/S0378-1119(00)00382 (1994).  NUCLECTIDE SEQUENCE [GENOMIC DNA].  PubMed=1054542; DOI=10.1016/S0378-1119(00)00382 (1994).  NUCLEOTIDE SEQUENCE [GENOMIC DNA].  NUCLEOTIDE SEQUENCE [GENOMIC DNA].  NUCLEOTIDE SEQUENCE [GENOMIC DNA].  Sequencing and expression analysis of the serin cluster located in chromosome 19q13 region."; Gene 257:119-130(2000).  (4)  NUCLEOTIDE SEQUENCE [GENOMIC DNA].  Hansson L., Lee I., Smith R., Argonza-Barrett R., Lee Nose Section and Expression analysis of the serin cluster located in chromosome 19q13 region."; Gene 257:119-130(200).  Hansson L., Baeckman A., Ny A., Edlund M., Edhol Hansson L., Baeckman A., Ny A., Edlund M., Portarnal P.,
YTHUMAN  KTAT HUMAN  KLAT HUMAN  KLAT HUMAN  KLAT HUMAN  KLAT HUMAN  KLAT HUMAN  KASSA; GONEND; GNEVT;  01-OCT-1996 (Rel. 34, Last sequence update)  01-OCT-1996 (Rel. 34, Last sequence update)  13-SEP-2005 (Rel. 34, Last sequence update)  13-SEP-2005 (Rel. 34, Last sequence update)  13-SEP-2005 (Rel. 34, Last sequence update)  Kallikrein 7 precursor (EC 3.4.21) (hK7) (Strecknotryptic enzyme) (hSCCE).  Name=KLK7; Synonyms=PRSS6, SCCE;  Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Euarchontoglires; Frimates; Moust. LaxID=9606;  [1]  NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT TISSUE-Skin;  MEDLINE=94108225; PubMed=8034709;  MHADISON L., Stroemqvist M., Baeckman A., Wallbra Beglaind; expression, and characterization of strohymotryptic enzyme. A skin-specific human serin.  J. Biol. Chem. 269:19420-19426(1994).  [2]  NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIF TISSUE-Keratinocyte; DoI=10.1016/S0378-1119(00)00382 (Gene 254:119-128(2000).  [3]  NUCLEOTIDE SEQUENCE [GENOMIC DNA], PubMed=11054574; DOI=10.1016/S0378-1119(00)00382 (Gene 254:119-128(2000).  [4]  NUCLEOTIDE SEQUENCE [GENOMIC DNA], Radoon."; Gene 257:119-130(2000).  [5]  NUCLEOTIDE SEQUENCE [GENOMIC DNA], Hansson L., Baeckman A., Ny A., Edlund M., Edhol Wallbrandt P., Begelrand T., Ny A., Kallond M., Edhol Wallbrandt P., Begelrand T., Ny A., Kallond M., Edhol Wallbrandt P., Begelrand T., Ny A., Kallond M., Edhol Wallbrandt P., Regelrand T., Rell Maleson L., Rell Male
YOUT 1  YOUT 1  YOUNG NEW STANDARD; PRT; 253 AA.  FURN_HUMAN  STANDARD; SURNYT; O1-0CT-1996 (Rel. 34, Last sequence update) Name-KLK7; Synonyms=PRSS6, SCCE; Homo sapiens (Human). BURATYOTA; Metazoza (Hordata; Craniata; Vertebra Mammalia; Butheria; Evarchontoglires; Primates; Homo NCESUTIDE SEQUENCE (MENA] (ISOFORM 1), AND PROT TISSUE-Skin; MEDLINE-94308225; PubMed=8034709; Hansson L.; Stroemqvist M., Baeckman A., Wallbra Bgellud T.; Egellud T.; Cloning, expression, and characterization of st chymotryptic enzyme. A skin-specific human serin. J. Biol. Chem. 269:19420-19426(1994). USUESEREATINGOYE; PubMed=10074542; DOI=10.1016/S0378-1119(00)00280 YOUSE G.M.; Scorilas A., Magklara A., Soosaipil Diamandis B.P.; "The KLK7 (PRSS6) gene, encoding for the stratum enzyme is a new member of the human kallikrein gcharacterization, mapping, tissue expression and characterization, mapping, tissue expression and characterization, mapping, tissue expression and characterization, mapping, K.; Gene 254:119-128(2000).  O13 PubMed=11054574; DOI=10.1016/S0378-1119(00)00382 Gan L., Lee I., Smith R., Argonza-Barrett R., Bequencing and expression analysis of the serin cluster located in chromosome 19q13 region."; Gene 257:119-130(2000). WINCLEOTIDE SEQUENCE (GENOMIC DNA). NUCLEOTIDE SEQ
YOUNT 1  KLYT HUMAN  P49862; QBNSN9; QBNFV7;  01-OCT-1996 (Rel. 34, Last sequence update)  01-OCT-1996 (Rel. 34, Last sequence update)  13-SEP-2005 (Rel. 34, Last sequence update)  13-SEP-2005 (Rel. 34, Last sequence update)  Kallikrein 7 precursor (EC 3.4.21) (hK7) (Strachynome-PKLK7; Synonyms=PRSS6, SCCE;  Homo sapiens (Human).  Bukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Euarchontoglires; Primates; Homo.  NCBL TaxID=9606;  [1]  NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT TISSUE-Skin;  MEDLINE=94308225; PubMed=8034709;  Hansson L., Stroemqvist M., Baeckman A., Wallbra Egglind T., Stroemqvist M., Baeckman A., Wallbra Egglind T., Stroemqvist Chordata; Cloning, expression, and characterization of strohymotryptic enzyme. A skin-specific human serin.  [2] ROLLEOTIDE SEQUENCE (GENOMIC DNA), TISSUE SPECIF TISSUE-Keratinocyte;  PubMed=10974542; DOI=10.1016/S0378-1119(00)00280  Yousef G.M., Scorilas A., Magklara A., Soosaipil Diamandis E.P.  "The KLK7 (PRSS6) gene, encoding for the stratum enzyme is a new member of the human kallikrein genzyme is a new member of the human kallikrein generacterization, mapping, tissue expression and regulation.";  "The I., Lee I., Smith R., Argonza-Barrett R., Lee I., Smith R., Argonza-Barrett R., Lee I., Smith R., Argonza-Barrett R., Lee I., Sequencing and expression analysis of the serin cluster located in chromosome 19q13 region.";  Gene 254:119-130(2000).  [4]  NUCLEOTIDE SEQUENCE (GENOMIC DNA).  Hansson L., Baeckman A., NY A., Edlund M., Edhol Hansson L., Baeckman A., NY A., Edlund M., Edbol
YTHUMAN  KTAT HUMAN  KLYAT HUMAN  KLYAT HUMAN  KLYAT HUMAN  KLYAT HUMAN  KABORSN9; QBNFN9;  01-0CT-1996 (Rel. 34, Last sequence update)  01-0CT-1996 (Rel. 34, Last sequence update)  13-8EP-2005 (Rel. 34, Last sequence update)  Kallikrein 7 precursor (EC 3.4.21) (hK7) (Strachyrota; Metazoa; (hSCCE;  Name=KLK7; Synonyms=PRSS6, SCCE;  Name=KLK7; Synonyms=PRSS6, SCCE;  NOBL TaxID=9606;  [1]  NUCLECTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT TISSUE-Skin;  MEDLINE=94108225; PubMed=80134709;  Hansson L., Stroemqvist M., Backman A., Wallbra Bgelrud T., Stroemqvist M., Backman A., Wallbra Bgelrud T., Stroemqvist M., Backman A., Wallbra Bgelrud T., Stroemqvist M., Backman A., Wallbra Bgelrud T. Stroemqvist M., Backman A., Wallbra Bgelrud T. Stroemqvist M., Magklara A., Soosaipil Jumed=10974542; DoI=10.1016/S0378-1119(00)00286  Yousef G.M., Scorilas A., Magklara A., Soosaipil Diamandis B.P.;  "The KLK7 (PRSS6) gene, encoding for the straum enzyme is a new member of the human kallikrein gcharacterization, mapping, tissue expression and regulation.";  Gene 254:119-128(2000).  RUGEOTIDE SEQUENCE [GENOMIC DNA].  NUCLEOTIDE SEQUENCE [GENOMIC DNA].  Requering and expression analysis of the serin cluster located in chromosome 19413 region.";  Gene 257:119-130(2000).  [4]
YTHUMAN  KLYT HUMAN  KLYT HUMAN  KLYT HUMAN  KLYT HUMAN  KLYT HUMAN  KLYT HUMAN  STANDARD;  PA GRE1, 24, Last sequence update)  11-68F2-2005 (Rel. 34, Last acquence update)  11-68F2-2005 (Rel. 34, Last acquence update)  11-68F2-2005 (Rel. 34, Last annotation update)  11-68F2-2005 (Rel. 34, Last annotation update)  Kallikrein 7 precursor (ECS. 3.4.21) (kK7) (Streckland Edgate)  Name-KLK7; Synonyms=PRSS6, SCCE;  Homo sapiens (Human).  Bukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Buarchontoglires; Primates; Homo.  NUCLECTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT TISSUE-Skin;  MEDIINE-94308225; PubMed=8034709;  Hansson L., Stroemqvist M., Baeckman A., Wallbra Egglund T.;  Cloning, expression, and characterization of st chymotryptic enzyme. A skin-specific human serin.  J. Biol. Chem. 269:19420-19426(1994).  Listud T.;  BubMed=1007452; DOI=10.1016/S0379-1119(00)00382  Yousef G.M., Scorilas A., Magklara A., Soosaipil Diamandis E.P.;  "The KLK7 (PRSS6) gene, encoding for the stratum enzyme is a new member of the human kallikrein gcharacterization, mapping, tissue expression and regulation.";  Gene 254:119-128(2000).  Sequencing and expression analysis of the serin cluster located in chromosome 19q13 region.";  Gene 257:119-130(2000).  MUCLECTIDE SEQUENCE (GENOMIC DNA).  NUCLECTIDE SEQUENCE (GENOMIC DNA).
YTHUMAN  KLYT HUMAN  STANDARD;  01-OCT-1996 (Rel. 34, Last sequence update)  01-OCT-1996 (Rel. 34, Last sequence update)  13-SEP-2005 (Rel. 34, Last sequence update)  13-SEP-2005 (Rel. 34, Last sequence update)  13-SEP-2005 (Rel. 34, Last sequence update)  Kallikrein 7 precursor (EC 3.4.21) (kK7) (Streckynerypetic enzyme) (hSCCE);  Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Euarchontoglires; Primates; Homo.  NCBI_TAXID-9606;  [1]  NUCLECTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT TISSUE-Skin;  MEDLINE=94308225; PubMed=8034709;  MHADISON L., Stroemqvist M., Baeckman A., Wallbra Egglind T.;  Cloning, expression, and characterization of strocymetryptic enzyme. A skin-specific human serin.  J. Biol. Chem. 269:19420-19426(1994).  [2]  NUCLECTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIF TISSUE-Keratinocyte;  NUCLECTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIF TISSUE-Keratinocyte;  NUCLECTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIF TISSUE-Keratinocyte;  NUCLECTIDE SEQUENCE [GENOMIC DNA].  PubMed=105442; DOI=10.1016/S0378-1119(00)00382 (Gene 254:119-128 (GENOMIC DNA).  PubMed=11054574; DOI=10.1016/S0378-1119(00)00382 (Gene 254:119-130(2000).  [3]  NUCLECTIDE SEQUENCE [GENOMIC DNA].  PubMed=11054574; DOI=10.1016/S0378-1119(00)00382 (Gene 257:119-130(2000).
YTHUMAN  YTHUMAN  YTHUMAN  YELY HUMAN  O1-OCT-1996 (Rel. 34, Last sequence update)  O1-OCT-1996 (Rel. 34, Last sequence update)  O1-OCT-1996 (Rel. 34, Last sequence update)  I3-SEP-2005 (Rel. 48, Last annotation update)  Xallikrein 7 precursor (EC 3.4.21) (kK7) (Strachymorryptic enzyme) (HSCES;  Name=KLK7; Synonyms=PRSS6, SCCE;  Name=KLK7; Synonyms=PRSS6, SCCE;  NAME ALAZOA (HONDA)  NUCLECTIDE SEQUENCE (MENA) (ISOFORM 1), AND PROT  TISSUB=Skin;  MUCLECTIDE SEQUENCE (MENA) (ISOFORM 1), AND PROT  TISSUB=Skin;  MUCLECTIDE SEQUENCE (GENOMIC DNA), TISSUB SPECIF  Cloning, expression, and characterization of st  Chymotryptic enzyme. A skin-specific human serin  J. Biol. Chem. 269:19420-19426(1994).  [2]  NUCLECTIDE SEQUENCE (GENOMIC DNA), TISSUB SPECIF  PUBMED=1007452; DOI=10.1016/S0378-1119(00)00280  YOUSEG G.M., Scorilas A., Magklara A., Soosaipil  Diamandis B.P.;  "The KLK7 (PRSS6) gene, encoding for the stratum enzyme is a new member of the human kallikrein generacterization, mapping, tissue expression and regulation.";  Gene 254:119-128(2000).  [3]  NUCLEOTIDE SEQUENCE (GENOMIC DNA).  PUBMED=11054574; DOI=10.1016/S0378-1119(00)00382  Gan L., Lee I., Smith R., Argonza-Barrett R., Le Moss P., Paeper B., Wangy K.;  "Sequencing and expression analysis of the serin cluster located in chromosome 19q13 region.";  Gene 257:119-130(2000).
YOUNT 1  YOUNG 198509; OBNEVD;  YOUNG 198509; OBNEVD;  YOUNG 198621, OBNEVD;  YOUNG 198621, OBNEVD;  YOUNG 198621, OBNEVD;  O1-OCT-1996 (Rel. 34, Last sequence update)  O1-OCT-1996 (Rel. 34, Last sequence update)  O1-OCT-1996 (Rel. 34, Last sequence update)  Yallikrein 7 precursor (EC 3.4.21) (hK7) (Strachynortyptic enzyme) (hSCCE);  Name-KLK7; Synonyms=PRSS6, SCCE;  HOMO Sapiens (Human).  BUKARYOTA; MEAZOA; Chordata; Craniata; Vertebra Mammalia; Butheria; Buarchontoglires; Primates; HOMO.  NCBL TaxID=9606;  [1]  NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT TISCUE-Skin;  MEDLINE=94308225; PubMed=8034709;  Hansson L., Stroemqvist M., Baeckman A., Wallbra Egglind T.;  "Cloning, expression, and characterization of strohymotryptic enzyme. A skin-sepecific human serin. J. Biol. Chem. 269:19420-19426(1994).  [2]  NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIF TISSUE-Keratinocyte;  PubMed=10974542; DOI=10.1016/S0378-1119(00)00382 (Abracterization, mapping, tissue expression and regulation.";  "The KLK7 (PRSS6) gene, encoding for the stratum enzyme is a new member of the human kallikrein genezaterization, mapping, tissue expression and regulation.";  NUCLEOTIDE SEQUENCE [GENOMIC DNA].  Sequencing and expression analysis of the serin cluster located in chromosome 19q13 region.";  Gene 257:119-130(2000).
YTHUMAN  KTAT HUMAN  KTAT HUMAN  KLANA  KLAT HUMAN  KLAT HUMAN  KLAT HUMAN  KLAT HUMAN  STANDARD;  P49662;  O1-OCT-1996 (Rel. 34, Last sequence update)  I3-SEP-2005 (Rel. 34, Last sequence update)  NADELTYPEIC enzyme) (RCS 3.4.21) (hK7) (Stractoryota) Metazon (ROS 3.4.21) (hK7) (Stractoryota) Metazon (ROS 3.4.21) (hK7) (Stractoryota) Metazon L. (Stroemqvist M., Backman A., Wallbra Bgelrud T., Stroemqvist M., Magklara A., Soosaipil U., Biol. Chem. 269:19420-19426(1994).  [2]  NUCLEOTIDE SEQUENCE (GENOMIC DNA), TISSUE SPECIF PubMed=10974542; DOI=10.1016/S0378-1119(00)00382 (Sene 254:119-128(2000).  [3]  NUCLEOTIDE SEQUENCE (GENOMIC DNA), Metarett R., Lee I., Smith R., Argonza-Barrett R., Lee I., Smith R., Argonza-Barrett R., Lee I., Smith R., Argonza-Barrett R., Lee I., Seeper B., Wang K.; Seperior Indianal and expression analysis of the serin Schuster located in Chromosome 19913 region."; Cluster located in Chromosome 19913 region.";
NTT 1  YOUNDAN  KLYT HUMAN  STANDARD; PRT; 253 AA.  F49862; QBNEN9; QBNEV7; 01-0CT-1996 (Rel. 34, Last sequence update) 01-0CT-1996 (Rel. 34, Last sequence update) 01-0CT-1996 (Rel. 34, Last sequence update) 13-SEP-2005 (Rel. 34, Last annotation update) 13-SEP-2005 (Rel. 34, Last annotation update) 13-SEP-2005 (Rel. 34, Last annotation update) Kallikrein 7 precursor (ECS.  Name-KLK7; Synonyms=PRSS6, SCCE; HOMO Sapiens (Human).  BUKARYOTA; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Buarchontoglires; Primates; HOMO.  NUCLECTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT TISSUE-SKin;  MEDLINE-94308225; PubMed=8034709; HANSSON L.; Stroemqvist M., Baeckman A., Wallbra Egglund T.;  BGLIND T.; Stroemqvist M., Baeckman A., Wallbra Egglund T.;  Lalol. Chem. 269:19420-19426(1994).  J. Biol. Chem. 269:19420-19426(1994).  J. MUCLECTIDE SEQUENCE (GENOMIC DNA).  PubMed=1004574; DOI=10.1016/S0378-1119(00)00382 (Annotation and expression and pubmed=11054574; DOI=10.1016/S0378-1119(100)00382 (Annotated in Chromosome 19913 region.";  Cluding and expression analysis of the serincluscing and expression and expression and expre
NUT 1  KLYAT HUMAN  KABISN9; QBNFN9; QBNFV7;  01-OCT-1996 (Rel. 34, Last sequence update)  01-OCT-1996 (Rel. 34, Last sequence update)  13-SEP-2005 (Rel. 34, Last annotation update)  Kallikrein 7 precursor (EC 3.4.21) (hK7) (Strachynortyptic enzyme) (hSCCB).  Name-KLK7; Synonyms-PRSS6, SCCE;  Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Euarchontoglires; Primates; Homo.  NCBL TaxID=9606;  [1]  NUCLECTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT TISSUE-Skin;  MEDLINE=94308225; PubMed=8034709;  Hansson L., Stroemqvist M., Baeckman A., Wallbra Egglind T., Stroemqvist M., Baeckman A., Wallbra Egglind T., Stroemqvist Coloning, expression, and characterization of strokymotryptic enzyme. A skin-specific human serin.  J. Biol. Chem. 269:19420-19426(1994).  [2] Biol. Chem. 269:19420-19426(1994).  NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIF TISSUE Fectatinocyte;  PubMed=10974542; DOI=10.1016/S0378-1119(00)00280  Yousef G.M., Scorilas A., Magklara A., Soosaipill Diamandis E.P., Rose member of the human kallikrein gcharacterization, mapping, tissue expression and regulation.";  Gene 254:119-128(2000).  [3] NUCLEOTIDE SEQUENCE [GENOMIC DNA].  Sequencing and expression analysis of the serin
YTHUMAN  YTHUMAN  YTHUMAN  YELY HUMAN  YELSEP-1996 (Rel. 34, Last sequence update)  01-0CT-1996 (Rel. 34, Last sequence update)  13-SEP-2005 (Rel. 48, Last annotation update)  13-SEP-2005 (Rel. 48, Last annotation update)  YELSEP-2005 (Rel. 48, Last annotation update)  Name=KLK7; Synonyms=PRSS6, SCCE;  Name=KLK7; Synonyms=PRSS6, SCCE;  NAME ARAZOO: Chordata; Craniata; Vertebra Mammalia; Butheria; Euarchontoglires; Primates;  NCBI_TAXID=9606;  [1]  NUCLECTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT TISSUE=Skin;  MEDLINE=94108225; PubMed=8034709;  Hansson L., Stroemqvist M., Bacckman A., Wallbra Egelrud T.;  "Cloning, expression, and characterization of st chymotryptic enzyme. A skin-specific human serin J. Biol. Chem. 269:19420-19426(1994).  [2]  NUCLECTIDE SEQUENCE (GENOMIC DNA], TISSUE SPECIF TISSUE-Keratinovyte;  PubMed=1007442; DOI=10.1016/S0378-1119(00)00280 Yousef G.M., Scorilas A., Magklara A., Soosaipil Diamandis E.P.;  "The KLK7 (PRSS6) gene, encoding for the stratum enzyme is a new member of the human kallikrein granterion.";  Gene 254:119-128(2000).  Gene 254:119-128(2000).  NUCLEOTIDE SEQUENCE [GENOMIC DNA].  PubMed=11054574; DOI=10.1016/S0378-1119(00)00382 Gan L., Lee I., Smith R., Argonza-Barrett R., Le Mose P., Neapers En. Manay K.;  "Secuencing and expression analysis of the serin
NUT. 1  KLYT HUMAN  KLYT HUMAN  KLYT HUMAN  KLYT HUMAN  KLYT HUMAN  KLYT HUMAN  P49862; QBNENJ;  01-0CT-1996 (Rel. 34, Last sequence update)  13-5EP-2005 (Rel. 34, Last amnotation update)  13-5EP-2005 (Rel. 34, Last amnotation update)  Kallikrein 7 precursor (ECS 3.4.21) (hK7) (Strachynorymae-FRSS6, SCCE;  Homo sapiens (Human).  Bukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Evarchontoglires; Primates; Homo.  NUCLECTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT TISSUE-SKin;  MEDLINE=94308225; PubWed=8034709;  Hansson L., Stroemqvist M., Baeckman A., Wallbra Egglund T.;  "Cloning, expression, and characterization of st chymotryptic enzyme. A skin specific human serin. J. Biol. Chem. 269:19420-19426(1994).  [2]  NUCLECTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIF TISSUE-Keratinocyte;  PubMed=10074542; DOI=10.1016/S0378-1119(00)00382 (Paracterization, mapping, tissue expression and regulation.";  enzyme is a new member of the human kallikrein grantation.";  Gene 254:119-128(2000).  [3]  NUCLECTIDE SEQUENCE [GENOMIC DNA].  NUCLECTIDE SEQUENCE [GENOMIC DNA].  NUCLECTIDE SEQUENCE [GENOMIC DNA].  NUCLECTIDE SEQUENCE [GENOMIC DNA].  NUCLECTIOR SEQUENCE [GENOMIC DNA].
YTHUMAN  YTHUMAN  YTHUMAN  YTHUMAN  YELY HUMAN  YELY HOR HELL 34, Last sequence update)  13-68F-2005 (Rel. 34, Last sequence update)  13-68F-2005 (Rel. 34, Last sequence update)  13-68F-2005 (Rel. 34, Last sequence update)  Xallikrein 7 precursor (EC 3.4.21) (hK7) (Streckynerypetic enzyme) (hSCCE).  Name=KLK7; Synonyms=PRSS6, SCCE;  Homo sapiene (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Euarchontoglires; Frimates; MOBI_TAXID=9606;  [1]  NUCLECTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT TISSUE-Skin;  MEDLINE=94308225; PubMed=8034709;  MEDLINE=94308225; PubMed=8034709;  MEDLINE=94308225; PubMed=8034709;  MEDLINE=94308225; PubMed=8034709;  MUCLECTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIF TISSUE-Kezatinocyte; Orly 1016/S0378-1119(00)00280  YOURE G.M., Scorilas A., Magklara A., Soosaipill Diamandis E.P.; A. Magklara A., Soosaipill PubMed=11054574; DOI=10.1016/S0378-1119(00)00382  Gan L., Lee I., Smith R., Mano K., Magklar B., Wano K., Argonza-Barrett R., Lee I., Mosk R.
YTHUMAN  YTHUMAN  YTHUMAN  YLX7 HUMAN  YLX7 HUMAN  YLX7 HUMAN  YLX7 HUMAN  YLX7 HUMAN  YH CARL 134, Created)  O1-OCT-1996 (Rel. 34, Last sequence update)  I3-SEP-2005 (Rel. 34, Last sequence update)  Xallikrein 7 precursor (EC 3.4.21) (hK7) (Strachyner-ryptic enzyme) (hSCCE)  Name=KLK7; Synonyms=PRSS6, SCCE;  Name=KLK7; Synonyms=PRSS6, SCCE;  NAME Acazoos (Chordata; Craniata; Vertebramanalia; Butheria; Eurrchontoglires; Primates; Homo.  NCBI_TaxID=9606;  [1]  NUCLECTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTINGSUB=Skin;  MEDLINE=94308225; PubMed=8034709;  Hansson L., Stroemqvist M., Bacckman A., Wallbramanalia; expression, and characterization of strohymotryptic enzyme. A skin-specific human serind.  J. Biol. Chem. 269:19420-19426(1994).  [2]  NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUB SPECIF PubMed=10974542; DOI=10.1016/S0378-1119(00)00280 Yousef G.M., Scorilas A., Magklara A., Soosaipil Diamandis E.P.;  "The KLK7 (PRSS6) gene, encoding for the stratumenzyme is a new member of the human kallikrein generalation.";  Gene 254:119-128(2000).  [3]  NUCLEOTIDE SEQUENCE [GENOMIC DNA].  NUCLEOTIDE SEQUENCE [GENOMIC DNA].  NUCLEOTIDE SEQUENCE [GENOMIC DNA].  Hans and member of the human kallikrein generalation.";  Gene 254:119-128(2000).  [3]  NUCLEOTIDE SEQUENCE [GENOMIC DNA].  PubMed=11054574; DOI=10.1016/S0378-1119(00)00382  Gan L., Lee I., Smith R., Argonza-Barrett R., Le
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NUT. 1  KLY THUMAN  KLYT HUMAN  KLYT HUMAN  KLYT HUMAN  KLYT HUMAN  KLYT HUMAN  RAJ16.2 34. Created)  01-0CT-1996 (Rel. 34, Last sequence update)  13-6EP-2006 (Rel. 34, Last amnotation update)  13-6EP-2006 (Rel. 34, Last amnotation update)  Kallikrein 7 precursor (EC 3.4.21) (hK7) (Strachynctryptic enzyme) (hSCCE).  Name-KLK7; Synonyms-PRSS6, SCCE;  Homo sapiens (Human).  Eukaryota; Metazoa: Chordata; Craniata; Vertebra Mammalia; Butheria; Buarchontoglires; Primates; Homo.  NCBL TaxID=9606;  [1]  NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT TISSUB-Skin;  MEDLINE=94308225; PubMed=8034709;  Hansson L., Stroemqvist M., Baeckman A., Wallbra Egglind T.;  "Cloning, expression, and characterization of strohymotryptic enzyme. A skin-sepcific human serin. J. Biol. Chem. 269:19420-19426(1994).  [2]  RUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIF TISSUE-Keratinocyte;  PubMed=10974542; DOI=10.1016/S0378-1119(00)00280  Yousef G., Scorilas A., Magklara A., Soosaipil Diamandis E. P. Scorilas A., Magklara A., Soosaipil Characterization, mapping, tissue expression and regulation.";  [3]  NUCLEOTIDE SEQUENCE [GENOMIC DNA].
YTHUMAN  YTHUMAN  YTHUMAN  YELY HUMAN  OL-OCT-1996 (Rel. 34, Last sequence update)  OL-OCT-1996 (Rel. 34, Last sequence update)  OL-OCT-1996 (Rel. 34, Last sequence update)  I3-SEP-2005 (Rel. 48, Last annotation update)  Xallikrein 7 precursor (EC 3.4.21) (hK7) (Strachyner ENGARCH ENGA
NT. 1  Y. HUMAN  Y. GNBFVJ;  O1-OCT-1996 (Rel. 34, Last sequence update)  O1-OCT-1996 (Rel. 34, Last sequence update)  O1-OCT-1996 (Rel. 34, Last sequence update)  O1-OCT-1996 (Rel. 34, Last annotation update)  X. Allikrein 7 precursor (ECS)  Name-KLK7; Synonyms=PRSS6, SCCE;  HOMO Sapiens (Human).  RUKANYOTA; Metazoza; Chordata; Craniata; Vertebra Mammalia; Butheria; Evarchontoglires; Primates; HOMO  NCBL TaxID=9606;  NUCLECTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT TISSUE-Skin;  MEDLINE-94308225; PubMed=8034709;  Hansson L.; Stroemqvist M., Baeckman A., Wallbra Bgellud T.;  Egglund T.;  Egglund T.;  Edling, expression, and characterization of st chymotryptic enzyme. A skin-specific human serin.  J. Biol. Chem. 269:19420-19426(1994).  J. Biol. Chem. 269:19420-19426(1994).  NUCLECTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIF TISSUE-Keratinocyte;  PubMed=10974542; DOI=10.1016/S0378-1119(00)00280  Yousef G.M., Scorilas A., Magklara A., Soosaipil Diamandis B.P.;  TISSUE-KERATION, mapping, tissue expression and characterization, mapping, tissue expression and characterization.  Secondary of the human kallikrein gene 254:119-128(2000).
YTT 1  YTHUMAN  YTHUMAN  YTHUMAN  YEACT HUMAN  O1-OCT-1996 (Rel. 34, Last sequence update)  O1-OCT-1996 (Rel. 34, Last sequence update)  O1-OCT-1996 (Rel. 34, Last sequence update)  I3-SEP-2005 (Rel. 34, Last annotation update)  Xallikrein 7 precursor (EC 3.4.21) (kY) (Strachyneryptic enzyme) (HACCE).  Name=KLK7; Synonyms=PRSS6, SCCE;  Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Euarchontoglires; Primates; MonCL TaxID=9606;  [1]  NUCLECTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT TISSUE-Skin;  MEDLINE=94308225; PubMed=8034709;  MEDLINE=94308225; PubMed=8034709;  MEDLINE=94308225; PubMed=8034709;  MEDLINE=94308225; PubMed=8034709;  MEDLINE=SEQUENCE [GENOMIC DNA], TISSUE SPECIF Chymotryptic enzyme. A skin-specific human serin.  J. Biol. Chem. 269:19420-19426(1994).  [2]  NUCLECTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIF TISSUE=Keratinocyte;  YOURE G.M., Scorilas A., Magklara A., Soosaipil Diamandis E.P.;  When the text of the human kallikrein generyme is a new member of the human kallikrein generyme is a new member of the human kallikrein genergaterization, mapping, tissue expression and regulation.";  Second P. Second
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NTT 1  YOUNDAN  KLYT HUMAN  STANDARD;  PRT; 253 AA.  F49862;  OBNEVD;  O1-OCT-1996 (Rel. 34, Last sequence update)  I3-SEP-2005 (Rel. 34, Last annotation update)  Kallikrein 7 precursor (EC 3.4.21) (hK7) (Strachynortyptic enzyme) (hSCCE);  Name-KLK7; Synonyms=PRSS6, SCCE;  Homo sapiens (Human).  Bukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Buarchontoglires; Primates; Homo.  NCBL TaxID=9606;  [1]  NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT TISSUE-Skin;  MEDLINE=94308225; PubMed=8034709;  Hansson L., Stroemqvist M., Baeckman A., Wallbra Egglind T.;  "Cloning, expression, and characterization of strohydrive enzyme. A skin-sepecific human serin. J. Biol. Chem. 269:19420-19426(1994).  [2]  NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIF TISSUE-Keratinocyte;  PubMed=10974542; DOI=10.1016/S0378-1119(00)00286  Yousef G.M., Scorilas A., Magklara A., Soosaipil Diamandis E.P.;  "The KLK7 (PRSS6) gene, encoding for the stratum enzyme is a new member of the human karlikrein genzyme is a new member of the human karlikrein genzyme is a new member of the human karlikrein genzyme is a new member of the human karlikrein genzyme is a new member of the human karlikrein genzyme is a new member of the human karlikrein genzyme is a new member of the human karlikrein genzyme is a new member of the human karlikrein genzyme is a new member of the human karlikrein genzyme is a new member of the human karlikrein genzyme is a new member of the human karlikrein genzyme is a new member of the human karlikrein genzyme is a new member of the human karlikrein genzyme is a new member of the stratum
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NUT. 1  NUT. 1  NUT. 1  NUT. 1  NUT. 1  NUT. 1  NUCLEOTIDE (Rel. 34, Created)  O1-OCT-1996 (Rel. 34, Last sequence update)  O1-OCT-1996 (Rel. 34, Last annotation update)  Name-KLK7; Synonyms=PRSS6, SCCE;  Homo sapiens (Human).  Bukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Evarchontoglires; Primates; Homo.  NCBL TaxID=9606;  [1]  NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT TISSUB-Skin;  MEDLINE=94308225; PubMed=8034709;  Hansson L., Stroemqvist M., Baeckman A., Wallbra Egglind T., Stroemqvist M., Baeckman A., Wallbra Egglind T.;  "Cloning, expression, and characterization of stroymotryptic enzyme. A skin-specific human serin. J. Biol. Chem. 269:19420-19426(1994).  [2]  NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIF TISSUE-Keratinocyte;  PubMed=10974542; DOI=10.1016/S0378-1119(00)00286  Yousef G.M., Scorilas A., Magklara A., Soosaipil Diamandis B.P.  The KLK7 (PRSS6) gene, encoding for the stratum
NTT 1  YTHUMAN  YTHUMAN  YTHUMAN  YANDARD;  P49662;  OHNEVD;  OH-OCT-1996 (Rel. 34, Last sequence update)  OH-OCT-1996 (Rel. 34, Last sequence update)  OH-OCT-1996 (Rel. 34, Last sequence update)  OHOCT-1996 (Rel. 34, Last sequence update)  I3-SEP-2005 (Rel. 48, Last annotation update)  Xallikrain 7 precursor (EC 3.4.21) (kY) (Strachyner-typtic enzyme) (hSCCE;  Name=KLK7; Synonyms=PRSS6, SCCE;  Name=KLK7; Synonyms=PRSS6, SCCE;  NAME Acazoa (Chordata; Craniata; Vertebramammalia; Butheria; Euarchontoglires; Primates;  NCBI_TaxID=9606;  [1]  NUCLECTIDE SEQUENCE [WRNA] (ISOFORM 1), AND PROT  TISSUB=Skin;  MEDLINE=94308225; PubMed=8034709;  MEDLINE=94308225; PubMed=8034709;  MEDLINE=94308225; PubMed=8034709;  MEDLINE=94308225; PubMed=8034709;  MEDLING: Appression, and characterization of st chymotryptic enzyme. A skin-specific human serin J. Biol. Chem. 269:19420-19426(1994).  [2]  NUCLECTIDE SEQUENCE [GENOMIC DNA], TISSUB SPECIF PubMed=1097452; DOI=10.1016/S0378-1119(00)00286 Yousef G.M., Scorilas A., Magklara A., Scosaipill PubMed=1097452; DOI=0.1016/S0378-1119(00) Doiamandis B.P.;  "The Strandardis B.P.;  "The Strandard B.P.;  "The Strandard B.P.;  "The Strandard B.P.;  "The Break B.P.;  "The Break B.P.;  "The
NT. 1  Y. HUMAN  Y. GNBFUP;  O1-OCT-1996 (Rel. 34, Last sequence update)  O1-OCT-1996 (Rel. 34, Last sequence update)  O1-OCT-1996 (Rel. 34, Last sequence update)  O1-OCT-1996 (Rel. 34, Last annotation update)  X. Allikrein 7 precursor (ECS)  Y. Allikrein 7 precursor (ECS)  HOMO Sapiens (Human).  BUKARYOTA; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Evarchontoglires; Primates; HOMO  NCBL TaxID=9606;  NUCLECTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT TISSUE-Skin;  MEDLINE-94308225; PubMed=8034709;  Hansson L.; Stroemqvist M., Baeckman A., Wallbra Bgellud T.;  Equind T.;  Equind T.;  Stroemqvist M., Baeckman A., Wallbra Bgellud T.;  Elal. Chom. 269:19420-19426(1994).  J. Biol. Chem. 269:19420-19426(1994).  NUCLECTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIF TISSUE-Keratinocyte;  PubMed=10974542; DOI=10.1016/S0378-1119(00)00280  Yousef G.M., Scorilas A., Magklara A., Soosaipil)
NUT 1  Note 1996 (Rel. 34, Created)  10-0CT-1996 (Rel. 34, Last sequence update)  Name-ELEP-2005 (Rel. 48, Last annotation update)  Rallikrein 7 precursor (EC 3.4.21) (hK7) (Strectyne)  Name-KLK7; Synonyms-PRSS6, SCCE;  Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Euarchontoglires; Primates; NCBI_TaxID=9606;  [1]  NUCLEDTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT TISSUE-Skin;  MEDLINE=94308225; PubMed=8034709;  MEDLINE=94308225; PubMed=8034709;  MEDLINE=94308225; PubMed=8034709;  MEDLINE=94308225; PubMed=8034709;  MICLEOTIDE SEQUENCE (GENOMIC DNA], TISSUE SPECIF TISSUE-Keratinocyte; DOI=10.1016/S0378-1119(00)00280 Pubmed=10974542; DOI=10.1016/S0378-1119(00)00280 Pubmed=10974542; DOI=10.1016/S0378-1119(00)00280 Pubmed=10974542; DOI=10.1016/S0378-1119(00)00280
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NTT 1  Y THUMAN  Y THUMAN  X TANDARD;  P49662;  001-0CT-1996 (Rel. 34, Created)  01-0CT-1996 (Rel. 34, Last sequence update)  01-0CT-1996 (Rel. 34, Last sequence update)  13-SEP-2005 (Rel. 34, Last sequence update)  13-SEP-2005 (Rel. 48, Last annotation update)  Xallikrein 7 precursor (EC 3.4.21) (hK7) (Strachyner-ryptic enzyme) (hSCCE);  Name=KLK7; Synonyms=PRSS6, SCCE;  Name=KLK7; Synonyms=PRSS6, SCCE;  Name=KLK7; Synonyms=PRSS6, SCCE;  NAME ARAZOA: (Chordata; Craniata; Vertebramammalia; Butheria; Euarchontoglires; Primates;  NCBI_TaxID=9606;  [1]  NUCLECTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT  TISSUB=Skin;  MEDLINE=94308225; PubMed=8034709;  MEDLINE=94308225; PubMed=8034709;  MEDLINE=94308225; PubMed=8034709;  Hansson L., Stroemqvist M., Baeckman A., Wallbra  Eqelrud T.;  "Cloning, expression, and characterization of st  Chymotryptic enzyme. A skin-specific human serin  J. Biol. Chem. 269:19420-19426(1994).  [2]  NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIF  PubMed=10974542: DOI=10.1016/S0378-1119(00)00280
YTHUMAN STANDARD; PRT; 253 AA.  KLAT HUMAN STANDARD; PRT; 253 AA.  P49862; QBNSN9; QBNFV7; 01-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-1996 (Rel. 34, Last sequence update) 13-SEP-2005 (Rel. 34, Last annotation update) 13-SEP-2005 (Rel. 48, Last annotation update) 13-SEP-2005 (Rel. 48, Last annotation update) Kallikrein 7 precursor (EC 3.4.21) (hK7) (Strachyme-KLK7; Synonyme-PRSS6, SCCE; Name-KLK7; Synonyme-PRSS6, SCCE; NAME SULPARANAI (HAMA) (ISOFORM 1), AND PROT NCBI TaxID=9606; [1] NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROT SEGILUM T.; "Cloning, expression, and characterization of st chymotryptic enzyme. A skin-specific human serin J. Biol. Chem. 269:19420-19426(1994).  INCLEDTINE SEQUENCE [GENOMIC DNA], TISSUE SPECIF TISSUE-Keratinocyte;
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NT. 1  Y. HUMAN  Y. GNNFV7;  O1-OCT-1996 (Rel. 34, Last sequence update)  O1-OCT-1996 (Rel. 34, Last sequence update)  O1-OCT-1996 (Rel. 34, Last sequence update)  I. SEP-2005 (Rel. 34, Last annotation update)  X. Allikrein 7 precursor (EC 3.4.21) (hK7) (Stracymerryptic neryme) (hSCCE);  Name-KLK7; Synonyme-PRS6, SCCE;  Name-KLK7; Synonyme-PRS6, SCCE;  Name-KLK7; Synonyme-PRS6, SCCE;  Name-KLK7; Synonyme-PRS6, SCCE;  NAME SAPICAN (HUMAN).  Eukaryota; Metazoa; Chordata; Craniata; Vertebramania; Eutheria; Eurchontcoglires; Primates;  NCBI TaxID=9606;  [1]  NUCLEOTIDE SEQUENCE [MENA] (ISOFORM 1), AND PROT TSSUE-SKin;  MEDILINE=93108225; Pubbwed=8034709;  Hansson L., Stroemqvist M., Baeckman A., Wallbra Bgelrud T.;  "Cloning, expression, and characterization of st chymotryptic enzyme. A skin-specific human serin.  J. Biol. Chem. 269:19420-19426 (1994).  [2]  NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIF
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NUT. 1  Y. HUMAN  Y. HUMAN  Y. HUMAN  Y. HUMAN  Y. HUMAN  Y. HUMAN  Y. GNBYN9; QNBNFY; QNBNFY; QNBNFN9; QNBNPN9; QNBNFN9; QNBNPN9; QNBNPN9
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NUT 1  Y THUMAN
YUMAN   1
Y_HUMAN STAND P49862; QBNSN9; QBNF 01-OCT-1996 (Rel. 34 01-OCT-1996 (Rel. 34 13-SEP-2005 (Rel. 48 KAllikrein 7 precurs Chymotryptic enzyme) Name=KLK7; Synonyme Homo sapiens (Human)
YULT I  X7 HUMAN  XLK7 HUMAN  P49862; Q8N5N9; Q8NFV7;  01-OCT-1996 (Rel. 34, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation updat Kallikrein 7 precursor (EC 3.4.21) (hK7)  Chymotryptic enzyme) (hSCCB).  Home exLK7; Synonymap HSS6, SCCE; Home saniens (Human)
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SULT 1 K7_HUMAN KLK7 HUMAN STANDARD; PRT; 253
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SULT 1 K7_HUMAN
RESULT 1
RESULT 1
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Genomic\_DNA.

AAK69624.1;

mRNA.

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EMBL; EMBL;

PIR; A53968; A53968.

1EZX.

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HGNC; HGNC:6368; KLK7.

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MEDLINE=228825; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDLINE=228825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Bromstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Andrews S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villaton D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Malkealey R.W., Touchman J.W., Green E.D., Dickson M.C., A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Helton E., Jones S.J.M., Marra M.A., Schein J.E., Jones C. Han IS,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chymotryptic enzyme.";
Biochem Biophys, Res. Commun. 211:586-589(1955).

-! FUNCTION: May catalyze degradation of intercellular cohesive structures in the cornilited layer of the skin in the continuous shedding of cells from the skin surface. Specific for amino acid residues with aromatic side chains in the Pl position. SCCE cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-Phe-|-Tyr-26, and 26-Tyr-|-Thr-27, Could play a role in the activation of precursors to inflammatory cytokines.

-!- SUBCELLULAR LOCATION: Secreted. In ovarian carcinoma, secreted and also observed at the apical membrane and in cytoplasm at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=1; Synonyms=Long;
Isod=P49862-1; Sequence=Displayed;
Name=2; Synonyms=Short;
Isold=P49862-1; Sequence=USP 013581;
TISSUE SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermia. Also expressed in the brain, mammary gland, cerbellum, spinal cord and kidney. Lower levels in salivary gland, uterus, thymus, thyroid, placenta, trachea and testis. Up-regulated in ovarian carcinoma, especially late-stage serous carcinoma, compared with normal ovaries and benign adenomas (at the protein level).
INDUCTION: By estrogens and glucocorticoids in a breast carcinoma
                  Dong Y., Kaushal A., Brattsand M., Nicklin J., Clements J.A.; "Differential splicing of KLKS and KLK7 in epithelial ovarian cancer produces novel variants with potential as cancer biomarkers."; Clin. Cancer Res. 9:1710-1720(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDDINE=97314630; PubMed=7794273;
Skytt A., Stroemqvist M., Egelrud T.;
"Primary substrate specificity of recombinant human stratum corneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 1 peptidase S1 domain.
  MEDLINE=22623266; PubMed=12738725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nvasive front
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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Q91VE3; Q9R048;
10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kallikrein 7 precursor (EC 3.4.21.-) (Stratum corneum chymotryptic
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(By similarity).
(By similarity).
(By similarity).
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C -> W (in Ref. 6; AAH32005).
2D68B6B15A76A668 CRC64;
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Charge relay system
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Kallikrein 7.
Peptidase S1.
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InterPro; IPR001314; Peptidase_SIA
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Name=Klk7; Synonyms=Prss6, Scce;
Mus musculus (Mouse).
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Best Local Similarity 100.
Matches 9; Conservative
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253 AA;
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EMBL; L33404; AAC37551.1; -; mRNA. EMBL; AF166330; AAD49718.1; -; Genomic\_DNA.

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Dermatol. 113:152-155(1999)

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REPLINE-22154683; PubMed=12466851; DOI=10.1038/nature01266; RRAIN-C57BBL/63; TISSUB=Head; MEDLINE-22354683; PubMed=12466851; DOI=10.1038/nature01266; RAGAZAKI Y. Puruno M., Kasukawa T., Adachi J., Bono H.; Kondo S., Radazaki Y., Puruno M., Kasukawa T., Adachi H., Yamanaka I., Kiyosawa H., Nakaido I., Osatoo N., Saitoo R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Golobori T., Rabadracelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Badarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Rohrim I.M., Kanapin A., Matsuda H., Bataloo S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S., R. Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gasterland T., Gariboldi M., Jackson I.J., Jarvis B.D., R. Anai A., Kawaji H., Kawasawa Y., Kedaierski R., King B.L., Kanai A., Kawaji H., Kawasawa Y., Kedaierski R., King B.L., Kanai A., Kawaji H., Marchionni L., McKenzie L., Miki H., Rasasawa T., Nedierski R., Pontius J.U., Qi D., Ramachandran S., Andgohima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Rasashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Asharaka Y., Watanabe Y., Watanabe Y., Wallining L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I., Yang I., Yang I., Yang I., Walliming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I., And M., Malming L.G., Mynshaw-Boris A., Yanagisawa M., Yang I., Yang I., And M., Asharaka M., Sakai K., Sasaki D., Shibata K., Shinaqawa A., Shinaqawa A., Yanagisawa A., Yasusaki A., Sakai K., Sasaki D., Shibata K., Shinaqawa A., Yasusaki A., Sakai K., Sasaki D., Shibata K., Shinaqawa A., Yasusaki A., Sakai K., Sasaki D., Shibata K., Shinaqawa A., Yasusaki A., Sakai K., Sasaki D., Shibata K., Shinaqawa A., Yasusaki A., Sakai K., Sasaki D., Shibata K., Shinada A., Hara A., Har
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Baeckman A., Stranden P., Bratteand M., Hansson L., Egelrud T.;
"Molecular cloning and tissue expression of the murine analog to human
stratum corneum chymotryptic enzyme.";
                                                                                     Hansson L., Baeckman A., Ny A., Edlund M., Edholm E., Tornell J.,
Wallbrandt P., Egelrud T.;
"Epidermal overexpression of stratum corneum chymotryptic enzyme in
mice; a model for chronic ithchy dermatitis.";
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
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MEDLINE=99399282; PubMed=10469296;
[2]
NUCLEOTIDE SEQUENCE (GENOMIC DNA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 420:563-573(2002).
                                                         STRAIN=129/SvJ
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                          the Buropean Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
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        or infections and catalyze the degradation of intercellular cohesive structures in the cornified layer of the skin in the continuous shedding of cells from the skin surface. Specific for amino acid residues with aromatic side chains in the Pl position. SCCE cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-Phe-|-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the activation of precursors to inflammatory cytokines.

-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- TISSUE SPECIFICITY: Expressed in skin and, at lower levels, in lung, kidney, brain, heart and spleen. In skin, expressed in high suprabasal keratinocytes and in the luminal parts of hair follicles. Not detected in liver and skeletal muscle.
-!- SIMILARITY: Belongs to the peptidase SI family. Kallikrein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kallikrein 7 (By similarity).
Serine protease (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
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18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Activation peptide
Kallikrein 7 (By si
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InterPro; IPR001254; Peptidase_S1_S6.
InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                         mRNA.
Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ensembl; ENSMUSG00000030713; Mus musculus.
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-; mRNA.
-; mRNA.
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp, SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
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87 QKIKATKSF 95
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Y1897 PAS
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MEDLINE=22423060; PubMed=12534463;
DOI=10.1046/1462-2920.2002.0036.x;
Melbon K.E., Weinel C., Paulsen IT., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Fraser C.M.;
                                                                                                                                                                                               May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein PM1897.
N-palmitoyl oysteine (Potential).
S-diacylglycerol cysteine (Potential)
9200661E14A10P405 CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas putida (strain KT2440).
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
                         Bacteria; Protecobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE006227; AAK03981.1; -; Genomic DNA.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Complete proteome; Hypothetical protein; Lipoprotein; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                   STRAIN=Pm70;
MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
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Environ. Microbiol. 4:799-808(2002).
-!- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
EMBL; AE016776; AAN66286.1; -; Genomic_DNA.
TIGR; P90661; -.
GO; GO:0003700; F:transcription factor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 1; Length 107;
Pred. No. 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                             NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcriptional regulator AmpR, putative. OrderedLocusNames=PP0661;
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18 18 N-P
18 18 N-P
107 AA; 12214 MW; 9
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77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 PSEPK
QB8Q37 PSEPK PRELIMINARY;
Q88Q37;
OrderedLocusNames=PM1897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 77.8
es 7; Conservative
                      Pasteurella multocida.
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27 QRIEAGKSF 35
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                                                                                                                                                                                                                                                                                       (Potential).
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Best Local
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088037 PS
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Gaps
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PubMed=1590861; DOI=10.1038/nbtl110;
PubMed=1590861; DOI=10.1038/nbtl110;
Paulsen I.T. Press C., Ravel J., Kobayashi D., Myers G.S.,
Mavrodi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
Durkin S., Brinkec L.M., Daugherty S.C., Sullivan S.B., Resovitz M.,
Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,
Khouri H.M., Pierson E., Pierson L. III, Thomashow L., Loper J.;
"Complete genome sequence of the plant commensal Pseudomonas
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA. GO:0006350; P:transcription; IEA. InterPro: IPR000847; HTH_LY9R. InterPro: IPR000847; HTH_LY9R. InterPro: IPR011991; Wing_hlx_DNA_bd. InterPro: IPR011991; Wing_hlx_DNA_bd. Pfam; PF00126; HTH_1; 1. Pfam; PF0013465; Ly9R. Substrate; 1. PR081TE; PS50931; HTH_LYSR; 1.
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13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Transcriptional regulator, LysR family.
ORFNames=PFL 3812;
Pseudomonas fluorescens (strain Pf-5).
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales;
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Nitrosomonadaceae, Nitrosomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Activator; Complete proteome; DNA-binding; Transcription;
Transcription regulation.
SEQUENCE 294 AA; 32996 MW; 33695F24D26560EF CRC64;
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Nat. Biotechnol. 23:473-878 (2005).
EMBL: CP000076; AAV93076.1; -; Genomic DNA.
SEQUENCE 296 AA; 33530 MW; 3941F0FIEA3E92F0 CRC64;
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QBZXBO;
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Q4KA21;
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259 QRIEASESF 267
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUCLEOTIDE SEQUENCE [MRNA], AND FUNCTION.
MEDLINE=94043294; PubMed=8227002;
Chai K.X., Chen L.-M., Chao J., Chao L.;
Kallistatin: a novel human serine proteinase inhibitor. Molecular cloning, tissue distribution, and expression in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P29622; Q53XBS; Q86TR9; Q96B2S;
01-APR-1993 (Rel. 25, Created)
13-SEP-2005 (Rel. 48, Last smooterion update)
13-SEP-2005 (Rel. 48, Last annotation update)
Kallistatin precursor (Serpin A4) (Kallikrein inhibitor) (Protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: Ribosomal protein PO is the functional equivalent of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E.coli protein L10.
                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Buryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.6%; Score 33; DB 1; Length 314
87.5%; Pred. No. 1.18+02; Uinmarches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20479972; PubMed=11029001; DOI=10.1038/35035069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AL445064; CAC11503.1; -; Genomic_DNA.
HAMAP; MF_00280; -; 1.
InterPro; TPR001730; Ribosomal_L10.
Pfam; PF00466; Ribosomal_L10; 1.
Complete proteome; Ribonucleoprotein; Ribosomal protein.
SEQUENCE 314 AA; 34583 MW; F40D048660E0B6EB CRC64;
                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-Gid: ribosomal protein P0 homolog (L10E).
Name=rplP0; OrderedLocusNames=Ta0359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] STRAIN-DSM 1728;
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Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                      Thermoplasma acidophilum.
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                                                                                                                                                                   STANDARD;
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183 QKIKSSKNF 191
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KAIN HUMAN
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PubMed=15194775; DOI=10.1128/JVI.78.13.6982-6994.2004;
PubMed=15194775; DOI=10.1128/JVI.78.13.6982-6994.2004;
PubMed=15194775; DOI=10.1128/JVI.78.13.6982-6994.2004;
Complete Genome Sequence of Lymphocystis Disease Virus Isolated from China...;
J. virol. 78:6982-694(2004).

G. GO:0005576; C:extracellular region; IEA.

GO: GO:0005576; C:extracellular region; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
Lymphocystis disease virus - isolate China.
Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Lymphocystivirus.
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                                                                           DOI=10.1128/JB.18S.9.2759-2773.2003;
Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,
Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.,
"Complete genome sequence of the ammonia-oxidizing bacterium and
obligate chemolithoautotroph Nitrosomonas europaea.";
                                                                                                                                                                                                                                         EMBL; BX321857; CAD84288.1; -; Genomic_DNA.

RESP; GSS310; 1155.

RESP; GSS310; 1155.

RGO; GO:0016302; C:membrane; IEA.

RGO; GO:0016301; F:ATP binding; IEA.

RGO; GO:0016301; F:Kinase activity; IEA.

RGO; GO:000155; F:two-component sensor molecule activity; IEA.

RGO; GO:000155; F:two-component sensor molecule activity; IEA.

RGO; GO:000165; H:se.

RGO; GO:000165; F:two-component sensor molecule activity; IEA.

RINEEPPO; IRR00364; H:se.

RGO; GO:000165; H:se.

RGO; GO:000165
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PR051TE; P800261; GLYCO_HORMONE_BETA_1; 1.
Hypothetical protein.
SEQUENCE 310 AA; 34349 MW; 714DAC2A33E42C11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77013 MW; 6989E95EB6543ED4 CRC64;
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Last sequence update)
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                          STRAIN=ATCC 19718 / IFO 14298;
MEDLINE=22586410; PubMed=12700255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00344; BCTRLSENSOR.
SMART; SM00065; GAF; 1.
SMART; SM00387; HATPase c; 1.
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Q678H2_9VIRU PRELIMINARY;
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Best Local Similarity 66.7.
Page 6; Conservative
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Gaps

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Length 314;

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GO; GO:0005515; F:protein binding; TAS.
GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; TAS.
InterPro; IPR00215; Prot inh serpin.
PANTHER; PTHR1461; Prot Inh serpin; 1.
                                                                                        BX248009; CAD62337.1; -; mRNA.
BX248760; CAD66567.1; ALT INIT; mRNA.
BC014992; AAH14992.1; -; mRNA.
                              L19684; AAA59454.1; -; mRNA.
L28101; AAC41706.1; -; Genomic_DNA.
                                                                                                                                                                                                          HSSP; P01011; 3CAA.
Ensembl; ENSG0000100665; Homo sapiens.
HGNC; HGNC:8948; SERPINA4.
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66.7%;
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108
157
238
382
427 AA;
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CARBOHYD
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CONFLICT
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KITAUSDES-2010016

KITAUSDES K.D., Felingold E.A., Grouse L.H., Derge J.G.,

A Altechul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

KAN Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M., Jusdin T.B., Toshiyuki S., Carninci P., Frange C.,

Rapleton M., Foares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Roberts S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Roberts S., Worley K.C., Hale S., Garcian A.M., Gay L.J., Hulyk S.W.,

KICHARGS S., Worley K.C., Hale S., Garchen A.M., Gay L.J., Hulyk S.W.,

KICHARGS S., Worley K.C., Hale S., Garchenko Y., Bouffard G.G.,

Rablesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rochiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,

Robertstield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,

Robertstield M. Schein J.E., Jones S.J.M., Marra M.A.;

Robertstield M. Schein J.E., Jones S.J.M., Marra M.A.;
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                           [2]

WUCLEOTIDE SEQUENCE [GENOMIC DNA].

WUCLENTES 5137583; PubMed=7835886;

Chai K.X., Ward D.C., Chao J., Chao L.;

Chai K.X., Ward D.C., chao J., Chao L.;

"Molecular cloning, sequence analysis, and chromosomal localization of

"Molecular cloning, sequence analysis, and chromosomal localization of

the human protease inhibitor 4 (kallistatin) gene (PI4).";

Genomics 23:370-378 [1994].
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MEDLINE=22660472; PubMed=12754519; DOI=10.1038/mbt827;
Zhang H., Li X.-J., Martin D.B., Aebersold R.;
Zhang H., Li X.-J., Martin D.B., Aebersold R.;
Identification and quantification of N-linked glycoproteins using hydrazide chemistry, stable isotope labeling and mass spectrometry.";
Nat. Biotechnol. 21:660-666(2003).
Nat. Biotechnol. 21:660-666(2003).
Lissue kallikrein. Inhibition is achieved by formation of an equimolar, heat- and SDS-stable complex between the inhibitor and the enzyme, and generation of a small C-terminal fragment of the inhibitor due to cleavage at the reactive site by tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: Monomer and some homodimers.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
-!- PTM: The V-terminus is blocked.
-!- MISCELLANEOUS: Heparin blocks kallistatin's complex formation with tissue kallikrein and abolishes its inhibitory effect on tissue kallikrein's activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhou G.X., Chao L., Chao J.; "Kallikrein inhibitor. Purification, "Kallistatin: a novel human tissue kallikrein inhibitor. Purification, characterization, and reactive center sequence."; J. Biol. Chem. 267:25873-25880(1992).
                                                                                                                                                                                                                                                                                                   TISSUE=Fetal liver;
Li W.B. . Gruber C. Jessee J., Polayes D.;
Full-length cDNA libraries and normalization.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the serpin family.
                                                                                                                                                                                                                                               [3]NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                          [4]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
Biol. Chem. 268:24498-24505(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB=Plasma;
MEDLINE=93100304; PubMed=1334488;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kallikrein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Colon;
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and

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=SERPINA4;
Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                            Gaps
                                                                                                           Reactive bond.
N-linked (GlcNAc. ..) (Potential).
N-linked (GlcNAc. ..) (Potential).
                                                                                                                                                             N-linked (GlcNAc. . .).
N-linked (GlcNAc. . .) (Potential).
S -> T (in Ref. 1 and 2).
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Pfam; Pruduls, Corresponding SMRT; SMO0284; SERPIN; 1.

PROSITE; PS00284; SERPIN; 1.

Direct protein sequencing; Glycoprotein; Protease inhibitor; Serine protease inhibitor; Serpin; Signal.

20 Potential.
                                                                                                                                                                                                                                           Score 33; DB 1; Length 427;
Pred. No. 1.5e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                              68EBE7AF956BFB77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             FAIN PONPY STANDARD; PRT; 427 AA. OSRCR2;
13-SEP-2005 (Rel. 48, Created)
13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Kallistatin precursor (Serpin A4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
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InterPro; IPR000215; Prot_inh_serpin.
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removed

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1 QRIKASKSF 9
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                                                                                                                                                                                                   RESULT 12
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Sucgang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
A Bunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
Bankier A.T., Lebmann R., Hamin N., Davies R., Gaudet P., Fey P.,
Bankier A.T., Lebmann E., Hamin N., Davies R., Gaudet P., Fey P.,
Richornou A., Nie K., Hall N., Anjard C., Hemphill L., Bason N.,
Rarborcher P., Desany B., Just E., Morio T., Rost R., Churcher C.,
Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindaay R.,
Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
Nardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,
Loulseged H., Mungall K., Oliver K., Price C., Quail M.A.,
Unushihara H., Hernandaz J., Rabbinowitsch E., Seeffen D., Sanders M.,
M. J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
Shaulsky G., Schleicher M., Weinstcok G., Rosenthal A., Cox E.C.,
Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
M. Marker D., Moegel A.A., Barrell B., Kuspa A.;
M. Marker D., Moegel A.A., Barrell B., Kuspa A.;
M. Marker D., Moegel A.A., Barrell B., Kuspa A.;
M. Marker D., Moegel A.A., Barrell B., Kuspa A.;
M. Marker D., Moegel A.A., Barrell B., Kuspa A.;
M. Marker D., Moegel A.A., Barrell B., Kuspa A.;
M. Marker D., Moegel A.A., Barrell B., Kuspa A.;
M. Marker D., Moegel A.A., Barrell B., Kuspa A.;
M. Marker D., Moegel A.A., Barrell B., Kuspa A.;
M. Marker D., Moegel A.A., Barrell B., Kuspa A.;
M. Marker D., Moegel A.A., Barrell B., Kuspa A.;
M. Marker D., Moegel A.A., Barrell B., Kuspa A.;
M. Marker D., Moegel A.A., Barrell B., Kuspa A.;
M. Marker D., Moegel A.A., Barrell B., Kuspa A.;
M. Marker D., Moegel A.A., Barrell B., Kuspa A.;
M. Marker D., Moegel A.A., Barrell B., Kuspa A.;
M. Marker D., Moegel A.A., Barrell B., Kuspa A.;
M. Marker D., Moegel A.A., Barrell B., Marrell B., Marker D., Moegel A.A., Barrell B., Marrell B., Marrell B
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                                                                                                                      PROSITE; PS00284; SERPIN; 1.
Glycoprotein; Protease inhibitor; Serine protease inhibitor; Serpin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                         427 Kallistatin.
389 Reactive bond (By similarity).
33 N-linked (GlCNAc. .) (Potential).
108 N-linked (GlCNAc. .) (Potential).
157 N-linked (GlCNAc. .) (Potential).
338 N-linked (GlCNAc. .) (Potential).
48558 MW, 24E05E0197F927ED CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 1; Length 427;
Pred. No. 1.5e+02;
3; Mismatches 0; Indels
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EMBL, ARFIO1000075; BAL66649.1; -; Genomic_DNA.
GO; GO:0031072; F:heat shock protein binding; IEA.
GO; GO:0006457; F:unfolded protein binding; IEA.
GO; GO:0006457; P:protein folding; IEA.
Chaperone; Hypothetical protein.
SEQUENCE 45 AA; 50097 MW; BDIA93PAF109CA13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
ORFNames=DDB0204663;
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetcoza; Dictyosteliida; Dictyostelium.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
PANTHER; PTHR11461; Prot_inh_serpin; 1. PPART; SPR00079; SERPIN; 1. SMART; SW00093; SERPIN; 1. PROSITE; PS00284; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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Matches 7; Conservative
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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427
389
33
1108
1157
238
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              427 AA;
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                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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SIGNAL
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1054TFP DIC.

10654TFP DIC.

10754TFP DIC.

10754TFP DIC.

10754TFP DIC.

10754TFP DIC.

107554TFP                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Bichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A., Sucgang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q., Tunggal B., Xummerfeld S., Madera M., Konfortov B.A., Rivero F., Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P., Pilcher K., Chen G., Saunders D., Sodergren E., Davis P., Rerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N., Rarborner P., Desany B., Just E., Morio T., Rost R., Churcher C., Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I., Muzny D., Mourier T., Pain A., Iu M., Harper D., Lindsay R., Hauser H., Arnandez K., Quilles M., Mohan M.B., Saito T., Buchrieser C., Loulseged H., Mungall K., Oliver K., Price C., Quail M.A., Loulseged H., Mungall K., Oliver K., Price C., Quail M.A., Sanders M., Ma J., Kohara Y., Shapp S., Simmonds M., Spiegler S., Tivey A., Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y., Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C., A., Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.; The genome Of the social amoeba Dictyostelium discoideum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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MEDLINE=22354719; PubMed=12466555; DOI=10.1093/nar/gkf667;
Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 0:0-0(2005).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Bacteria, Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.6%; Score 33; DB 2; Length 513; 66.7%; Pred. No. 1.8e+02; ive 2; Mismatches 1; Indels
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Hypothetical protein.
SEQUENCE 513 AA; 58802 MW; 994053C8156F1DDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                          13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
ORFNames=DDB0219472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Heavy-metal transporting P-type ATPase.
OrderedLocusNames=MYPE8710;
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Best Local Similarity 66.77,
6; Conservative
                                                                                                                                                                                                                                                              Q54H89_DICDI PRELIMINARY;
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QBEUP9;
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489 KRVKVSKSF 497
103 KRIKACKSF 111
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1D 08ECP9 M
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1D 01-MAR-21
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EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
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                                                                                                                                                                                                                                                                                                                                                                                                                                               1618 1618 AA; 177245 MW; C89436939816A448 CRC64;
                                                                       EMBL; CAAE01014723; CAG03579.1; -; Genomic_DNA.
InterPro; IPR001660; SAM.
InterPro; IPR001452; SH3.
InterPro; IPR001151; SH3_2.
Pfam; PF07653; SAM_1; 2.
Pfam; PF07653; SH3_2; 1.
ProDom; PD000066; SH3; 1.
SMART; SM00454; SAM; 2.
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Pred. No.
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Name=rplJ; OrderedLocusNames=MYPE5740;
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InterPro; IPR001790; Ribosomal_L10.
InterPro; IPR002363; Ribosomal_L10eub.
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Matches 7; Conservative
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                                                      preliminary data
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Best Local Similarity
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Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
"The complete genomic sequence of Mycoplasma penetrans, an
"The complete genomic sequence of Mycoplasma penetrans, an
"Intracellular bacterial pathogen in humans.";

Nucleic Acids Res. 30:5293-5300(2002).

BMBL; BA000026; BAC44663.1; -; Genomic_DNA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016020; F:ATP binding; IEA.

GO; GO:0016020; F:ATP ase activity, acting on acid anhydrid. ..; IEA.

GO; GO:0016020; F:Hydrolase activity, acting on acid anhydrid. ..; IEA.

GO; GO:0016020; F:Hydrolase activity, acting on acid anhydrid. ..; IEA.

GO; GO:0016020; F:Hydrolase activity, acting on acid anhydrid. ..; IEA.

RO; GO:0016015; P:Hydrolase activity, acting on acid anhydrid. ..; IEA.

RO; GO:0016015; P:Hydrolase activity, acting on acid anhydrid. ..; IEA.

RO; GO:001015; P:Mareallike hydro.

InterPro; IPR005034; Dehal like hydro.

Rem; PR00122; Hydrolase: 1.

Pfam; PR00122; Hydrolase: 1.

RIGRPAMS; TIGR01494; ATPASE_E1_E2; UNRNOWN_I.

ROMPLETE PR00154.
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Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Micaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,
Micaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,
Anthouard V., Jubin C., Castelli V., Ratinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Arthouard V., Duprat S., Brottier P., Coutanceau J. P., Gouzy J.,
Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Anincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
T. the early vortebrate proto-karyotype.";
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Butaryota, Neopterygii, Teleostei, Buteleostei, Neoteleostei,

Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,

Tetradontoidea, Tetraodontidae, Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.6%; Score 33; DB 2; Length 671; 77.8%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                671 AA; 75854 MW; 8EEE005CA3E60671 CRC64;
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Last annotation update)
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ORFNames=GSTENG00023047001;
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Q4S703;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Conservative
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NUCLEOTIDE SEQUENCE.
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE=22354719; PubMed=12466555; DOI=10.1093/nar/gkf667; Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K., Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.; "The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans."; Nucleic Acids Res. 30:5293-5300(2002).
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                                                                                                                                                                                                                                                                                                                        Mycoplasma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=28227;
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PROSTIE: PS01109; RIBOSOMAL L10; FALSE NEG.
Complete proteome; Ribonucleoprotein; Ribosomal protein.
SEQUENCE 161 AA; 17949 MW; 1D95D1C29B5B87D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BA000026; BAC44364.1; ALT_INIT; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RESULT 15
RL10 MYCPE STANDARD; PRT; 161 AA.
AC QBEVÜ0,
DT 10-OCT--2003 (Rel. 42, Created)
DT 0-OCT--2003 (Rel. 42, Last sequence update)
DT 10-MY-2005 (Rel. 47, Last annotation update)
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Job time : 99.3333 secs



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Sequence 130, Application US/09502600A

Patent No. 6294344
GENERAL INFORMATION:
APPLICANT O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Barly Diagnosis of TITLE OF INVENTION: O'arian Cancer
FILE REPRENENCE: D622301P-C
CURRENT FILING DATE: 2000-02-11
CURRENT PAPLICATION NUMBER: US/09/502,600A
PRIOR PELING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 130
LENGTH: 9
INVERSE PRIOR SEQ ID NOS: 136
SEQ ID NO 130
LENGTH: 9
INVERSE PRIOR SEQ ID NOS: 136
SEQ ID NO 130
FERNISM: Homo sapiens
FEATURE:
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130, Appl
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14, Appl
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Sequence 130, App
                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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44 28 66.7 189 2 US-09-134-000C-4565 Sequence 27949, ALIGNMENTS  SULT 1 -09-520-600-99 Sequence 99, Application US/09502600A Betent No. 6294344 GENERAL INFORMATION: -1 TILLE OF INVENTION: -1 TILLE OF INVENTION: -1 COMPOSITION: -1 TILLE OF INVENTION: -1 COMPOSITION: -1 TILLE OF INVENTION: -1 TILLE	43	28	91		0	-248	796A-179	72	Seg	nence	2.	۷,
SULT 1  SULT 1  SULT 1  O95-502-600-99  Patent No. 6294344  GENERAL INFORMATION:  APPLICANT:  COMPOSITIONS and Methods for the Early Diagnosis of TITLE OF INVENTION:  CUTRENT FILING DATE:  CUTRENT PILICA DATE:  CUTRENT APPLICATION NUMBER:  SEQ ID NOS:	4 4	78	٠.	188	N (1	-134	300C-456 796A-279	0.4	Sed	uence	^ ~	Ap A
SULT 1  -09-502-600-99  Sequence 99, Application US/09502600A  Barent No. 6294344  GENERAL INFORMATION:  APPLICANT: O'Brien, Timothy J.  TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer  TITLE OF INVENTION: Ovarian Cancer  TITLE OF INVENTION: Ovarian Cancer  CURRENT APPLICATION NUMBER: US/09/502,600A  PRIOR PILING DATE: 001-02-11  CURRENT APPLICATION NUMBER: US/09/502,600A  PRIOR PILING DATE: 09/039,211  NUMBER OF SEQ ID NOS: 136  ENGTH: 9  LENGTH: 9  LENGTH: 9  LENGTH: 9  LENGTH: 9  LOGANISM: 100.0%; Score 42; DB 2; Length 9;  MATCH SEQ ID NOS: 100.0%; Score 42; DB 2; Length 9;  MATCH SEG ID NOS: 0; Mismatches 0; Indels 0; Gaps  SULT 2  SULT 2  SULT 2  SULT 2  SULT 2  SOCIE 22  SOCIE 22  SULT 2									•			
SULT 1  -09-502-600-99  Sequence 99, Application US/09502600A  Befacts No. 629344  GENERAL INFORMATION:  APPLICANT:  O'Brien, Vimothy J.  TITLE OF INVENTION:  COMPOSITIONS and Methods for the Early Diagnosis of TITLE OF INVENTION:  CURRENT PILING DATE:  CURRENT APPLICATION NUMBER:  19/039,211  PRIOR PILING DATE:  DENGRIP:  DENGRIP:  SEQ ID NO 99  LENGRIP:  DENGRIP:  SEQ ID NOS:  136  SEQ ID NO 99  LENGRIP:  ORGANISM: Homo sapiens  PEATURE:  OTHER INFORMATION: Residues 91-99 of the SCCE protein  OUTHER INFORMATION: Residues 91-99 of the SCCE protein  OUTHER INFORMATION: Residues 91-99 of the SCCE protein  OUTHER INFORMATION: Residues 0; Mismatches 0; Indels 0; Gaps  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps  SULT 2  SULT 2  SULT 2  SULT 2  SULT 2						ALIGNME	NTS					
Sequence 99, Application US/09502600A Patent No. 2244344  APPLICANT: O'Brien, Timothy J. TITLE OF INVENTION: Compositions and Methods for the Barly Diagnosis of TITLE OF INVENTION: Compositions and Methods for the Barly Diagnosis of FILE REFERENCE: D6223CIP-C. CURRENT PILIOR DATE: 2000-02-11 CURRENT APPLICATION NUMBER: U9/039,211 PRIOR FILING DATE: 03-14-1998  SEQ ID NO 99 LENGTH: 9	RESULT US-09-5	1 02-600-9	o									
GENERAL INFORMATION: APPLICANT: O'BTIEND: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: COMPOSITION: Ovarian Cancer FILE REFERENCE: D6223CHD-C CURRENT FILING DATE: 2000-02-11 CURRENT APPLICATION NUMBER: US/09/502,600A RRIOR APPLICATION NUMBER: US/09/502,600A RRIOR APPLICATION NUMBER: US/09/39,211 RRIOR PRIOR APPLICATION NUMBER: US/09/39,211 RRIOR FILING DATE: 03-14-1998 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: US/09/39,211 COMMANIAN: HOMO Sapiens FEATURE: PRT ORGANISM: HOMO Sapiens FEATURE: O'HER INFORMATION: Residues 91-99 of the SCCE protein -09-502-600-99. OUBLY MATCH BEST LOCAL SIMILATITY 100.0%; Pred. No. 4.6e+05; MATCHES 9; CONSERVATIVE 0; Mismatches 0; Indels 0; Gaps  SULT 2 SULT 2 -09-502-600-130	; Seque	nce 99, t No. 62	Applica	ation US	60/	02600A						
AFFLICANT: O'BITEN, INCORNY O' TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer FILE REFERENCE: D6223C10-C CURRENT FILING DATE: 2010-0-11 CURRENT APPLICATION NUMBER: 09/039,211 RRIOR APPLICATION NUMBER: 03-14-1998 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 106  , GENER	AL INFOR	MATION		į	,							
TITLE OF INVENTION: Ovarian Cancer FILE REPRENDE: 10523CIP-C CURRENT FILING DATE: 2000-02-11 CURRENT APPLICATION NUMBER: 09/039,211 RRIOR APPLICATION NUMBER: 09/039,211 RRIOR APPLICATION NUMBER: 03-14-1998 RIOR FILING DATE: 03-14-1998 SEQ ID NO 99 LENGTH: 9 TYPE: PRT ORGANISM: Homo sapiens FRATURE: PRT ORGANISM: Homo sapiens FRATURE: OTHER INFORMATION: Residues 91-99 of the SCCE protein -09-502-600-99. OTHER INFORMATION: Residues 91-99 of the SCE protein -09-502-600-99.  I QRIKASKSF 9  SULT 2 SULT 2 -09-502-600-130	TITI	E OF INV	ENTION	Ċ	ocny osit							ų
FILE KEKEKENES: 10223CL0. CURRENT PILING DATE: 2000-02-11 CURRENT PILING DATE: 2000-02-11 CURRENT APPLICATION NUMBER: 09/039,211 PRIOR APPLICATION NUMBER: 03-14-1998 BRIOR PILING DATE: 03-14-1998 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS: 136 SEQ ID NOS	, TITL		õ	- (	an (	ancer			ı			
CURRENT APPLICATION NUMBER: U9/039,211 PRIOR APPLICATION NUMBER: U9/039,211 PRIOR APPLICATION NUMBER: U9/039,211 PRIOR APPLICATION NUMBER: U3-14-1998 SEQ ID NO 99 LENGTH: 9 TYPE: PRT ORGANISM: Homo sapiens FRATURE: -09-502-600-99.  Query Match Best Local Similarity 100.0%; Score 42; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps  1 QRIKASKSF 9 1 QRIKASKSF 9 2017 2 -09-502-600-130	FILE	KEFEKEN		7	ر د د							
PRIOR APPLICATION NUMBER: 09/039,211 PRIOR APPLICATION NUMBER: 03-14-1998 NUMBER OF SEQ ID NOS: 136 SEQ ID NO 99 LENGTH: 9 LENGTH: 9 TYPE: PRT ORGANISM: Homo sapiens FEATURE: 07-502-600-99. OTHER INFORMATION: Residues 91-99 of the SCCE protein -09-502-600-99. OURLY MATCH Best Local Similarity 100.0%; Score 42; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 4.6e+05; MATCHES 9; Conservative 0; Mismatches 0; Indels 0; Gaps 1 ORIKASKSF 9 SULT 2 -09-502-600-130	CURR	ENT APPL	ICATION	N NUMBER		9/502.	A.					
PRIOR FILING DATE: 03-14-1998  NUMBER OF SEQ ID NOS: 136  SEQ ID NO 99  LENGTH: 9  LENGTH: 9  LENGTH: 9  TYPE: PRT  ORGANISM: Homo sapiens FRATURE:  O7HER INFORMATION: Residues 91-99 of the SCCE protein  O7HER INFORMATION: Residues 91-99 of the SCCE protein  O7HER INFORMATION: Residues 91-99 of the SCCE protein  O9-502-600-99  QUERY MATCH  Beet Local Similarity 100.0%; Pred. No. 4.6e+05;  MATCHES 9; Conservative 0; Mismatches 0; Indels 0; Gaps  I QRIKASKSF 9  SULT 2  -09-502-600-130	; PRIO	R APPLIC	ATION 1	NUMBER:								
SEQ ID NO 99  LENGTH: 9  LENGTH: 9  LENGTH: 9  CRGANISM: Homo sapiens FEATURE:  COTHER INFORMATION: Residues 91-99 of the SCCE protein  COTHER	, PRIO	R FILING	DATE	٠.	-19	8						
LENGTH: 9 TYPE: PRT ORGANISM: Homo sapiens FEATURE: OTHER INFORMATION: Residues 91-99 of the SCCE protein -09-502-600-99.  Query Match Best Local Similarity 100.0%; Score 42; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 1                     1	SEO I	D NO 99			2							
ORGANIENT Homo sapiens FEATURE: OTHER INFORMATION: Residues 91-99 of the SCCE protein -09-502-600-99.  Query Match Best Local Similarity 100.0%; Score 42; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps	LEN	GTH: 9										
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OTHER INFORMATION: Residues 91-99 of the SCCE protein -09-502-600-99.  Query Match Best Local Similarity 100.0%; Score 42; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps	; FEA	TURE:	'			;		•				
<pre>Query Match</pre>	S-0	02-600-9	MATION: 9.	: Residu		-99 Ot		rotein	_			
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps    QRIKASKSF 9	Query	Match	ָּבְּיִי בְּיִבְּיִי בְּיִרְיִּבְּיִי בְּיִבְּיִי בְּיִבְּיִבְּיִי בְּיִבְּיִי בְּיִבְּיִי בְּיִבְּיִבְּיִי בְּי		80.0	Score			o,			
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	US-09-5	02-600-13	30									

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Sequence 7, Application US/09261416A

Sequence 7, Application US/09261416A

Patent No. 6291663

GENERAL INFORMATION:
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease
TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
FILE REFERENCE: D6192
CURRENT APPLICATION NUMBER: US/09/261,416A
CURRENT FILING DATE: 1999-03-03
SEQ ID NO?: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic OTHER INFORMATION: enzyme (scce) catalytic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                APPLICANT: O'STILL INOCHY J.
APPLICANT: O'STILL LOWELL J.
TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
FILE REFERENCE: D602021P2
CURRENT APPLICATION NUMBER: US/09/618,259
CURRENT FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: US 09/127,444
PRIOR APPLICATION NUMBER: US 09/127,444
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 4
LENGTH: 144
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Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels
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100.0%; Score 42; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels
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US-08-944-483-33
; Sequence 33, Application US/08944483
                                                                                                                                                        Sequence 4, Application US/09618259
Patent No. 6642013
GENERAL INFORMATION:
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28 QRIKASKSF 36
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TYPE: PRT
ORGANISM: Unknown
PEBATURE:
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ORGANISM: unknown
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NAME/KEY: DOMAIN
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Sequence 130, Application US/09918243

Sequence 130, Application US/09918243

Sequence 130, Editor Caroline (62740)

APPLICANT: Caroline, Marchy J.

APPLICANT: Caroline, Marchin J.

APPLICANT: Santin, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

FILE REPERENCE: D6223CIP/C/D/CIP

CURRENT APPLICATION NUMBER: US/09/918,243

CURRENT PILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 130
                                                                                                                                                                                                                                                                                                              Sequence 99, Application US/09918243
; Sequence 99, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer; TILE REFERENCE: D623CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 2001-07-30
; RICH REVIEW OF SEQ ID NOS: 136
; SEQ ID NO 99
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; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-09-918-243-99
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; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-09-918-243-130
; OTHER INFORMATION: Residues 91-99 of the SCCE protein US-09-502-600-130
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Best Local Similarity 100.
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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1 ORIKASKSF 9
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US-09-918-243-99
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Patent No. 5972616

Sequence 4. Application US/09027337B

Patent No. 5972616

GENERAL INFORMATION:

APPLICANT: O'Brite in, Timothy J.

APPLICANT: Tanimoto, Hirotoshi

TITLE OF INVENTION: Breast and Ovarian Carcinomas

FILE REFERENCE: D6064

CURRENT APPLICATION NUMBER: US/09/027,337B

CURRENT FILING DATE: 1998-02-20

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 4

LENGTH: 225

LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to OTHER INFORMATION: similar domain in TADG-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 42; DB 1; Length 225; ilarity 100.0%; Pred. No. 0.38; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 42; DB 1; Length 225; 100.0%; Pred. No. 0.38; tive 0; Mismatches 0; Indel8
                                                                                                                                                  CURRENT APPLICATION DATA:
SOFTWARE: PERCENTIN Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILLING DATE: 14-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION FOR SEG ID NO: 12:
SEQUENCE GRARACTERISTICS:
TENNETH: 225 amino acids
COUNTRY: U.S.A.
ZIF: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 QRIKASKSF 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-09-154-344-12
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                                                                                             APPLICANT: FALEDAM, FANDAR N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: STEWART, CENT D.
APPLICANT: STEWART, KENT D.
APPLICANT: STEWOUPE, STEVEN D.
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
TITLE OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 42; DB 2; Length 224; Best Local Similarity 100.0%; Pred. No. 0.38; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/08557146
Fatent No. 5834290
GENERAL INFORMATION:
APPLICANT: Hanson, Lennart
ITILE OF INVENTION: Recombinant Stratum Corneum
TITLE OF INVENTION: Brayme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
CORRESSES: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FREALSEQ FOR Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6183.US.01
                         COLPITTS, TRACEY L. FRIEDMAN, PAULA N. GRANADOS, EDWARD N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFRENCE/DOCKET NUMBER: 6183
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 33: SEQUENCE CHARACTERISTICS: LENGTH: 224 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: No. 6232456e
US-08-944-483-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 ORIKASKSF 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-08-557-146-12
                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: 1
STATE:
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
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Best Local Similarity 100.
Matches 9; Conservative
                                                             Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: SCCE US-09-654-600A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                          63 QRIKASKSF 71
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                                                                                                                                      1 ORIKASKSF 9
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US-09-644-600-4
                                           Query Match
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; Batent No. 6451500
; GENERAL INFORMATION:
; APPLICANT: O'BIGHEN, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; TITLE OF INVENTION: O'VEREXPESSED in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/644,600
; CURRENT APPLICATION NUMBER: 09/421,213
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1998-10-20
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                 APPLICANT: Hansen, Lenart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Brayme (SCCE)
CORRESPONDERCE: 17
CORRESPONDERCE: 77
ADDRESSE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 42; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT AFFLICATION DATA

APPLICATION UNMBER: US/09/154,344

FILING DATE: 16-SEP-1998
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/557,146

FILING DATE: 14-DEC-1995
CLASSIFCATION NUMBER: US 08/557,146

FILING PATE: 14-DEC-1995
CLASSIFCATION NUMBER: 15,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELECHNONE: (212) 819-8783
                                                                                                                                                                                                          STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
COMPUTER: IBM PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS.DOS
Egelrud, Torbjorn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acid8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acida
STRANDEDNESS: single
TOPOLOGY: linear
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OTHER INFORMATION: SCCE
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 QRIKASKSF 71
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US-09-654-600A-4

US-09-654-600A-4

Sequence 4, Application US/09654600A

Parent No. 6649741

GENERAL INFORMATION:

APPLICANT: O'BITEN TIMOTO, HINOCOBHI

TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease

TITLE OF INVENTION: Overexpressed in Carcinomas

TITLE OF INVENTION OVEREXPERSES D6064CTP/D

CURRENT APPLICATION NUMBER: US/09/654,600A

CURRENT APPLICATION NUMBER: 09/421,213

09/027,337

PRIOR FILING DATE: 1999-10-20

1998-02-20

1998-02-20

NUMBER OF SEQ ID NOS: 98

SEQ ID NO 4

LENGTH: 225
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100.0%; Score 42; DB 2; Length 225; 100.0%; Pred. No. 0.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 42; DB 2; Length 225; 100.0%; Pred. No. 0.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIKERII NEW YORK
STATE: New YORK
STATE: New YORK
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                               Indels
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US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5814290
; GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hanson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                 0; Mismatches
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TOPOLOGY:
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US-09-154-344-2
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                                                                                                                                                                                                                                                    100.0%; Score 42; DB 1; Length 253; 100.0%; Pred. No. 0.43;
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                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYBE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08824874
; Sequence 3, Application US/08824874
; Patert No. 5962300
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L. APPLICANT: Hillman, Jennifer L. APPLICANT: Hall Preeti ; TITLE OF INVENTION: NOVEL KALLIKREIN NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSE: ; STREET: 3174 Porter Drive CITY: Palo Alto
CITY: Palo Alto
                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: B1111ngs, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEPHONE: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                    LENGTH: 253 amino acida
TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                          MOLECULE TYPE: protein US-08-557-146-2
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CLONE: 532504
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                                                                                                                                                                      : 253 amino acids
amino acid
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Best Local Similarity 100.
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                              March 11, 2006, 01:24:47; Search time 69.4444 Seconds (without alignments) 54.151 Million cell updates/sec
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                                GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-905-083-199

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US-10-310-75-99

US-10-831-075-130

US-10-831-075-130

US-10-262-511-98

US-10-262-511-96

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US-10-264-283-90

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Patent No. US20020146708A1

Patent No. US20020146708A1

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Owarian Cancer
FILE REFERENCE: D6223CIF/C/Dix CURRENT APPLICATION NUMBER: US/09/905,083

CURRENT APPLICATION NUMBER: US 09/502,600

PRIOR FILING DATE: 2000-02-11

PRIOR FILING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 130, Application US/09905083

Sequence 130, Application US/09905083

Batent No. US20020146708A1

GENERAL INFORMATION:
FAPPLICANT: O'Baten, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis. Of TITLE OF INVENTION: O'varian Cancer
FILE REPREBNCE: D6223CIP/C/Div
CURRENT APPLICATION NUMBER: US/09/905,083

CURRENT FILING DATE: 2001-07-13

PRIOR FILING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 130

LENGTH: 9
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100.0%; Score 42; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels
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Pred. No. 1.7e+06;
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                                                          , NAME/KEY: CHAIN
, OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-09-918-243-130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CHAIN
OTHER INFORMATION: Residues 91-99 of the SCCE protein US-09-905-083-99
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; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-09-905-083-130
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100.0%; Pred. No. 1.7e+06;
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Les 9; Conservative
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
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; Sequence 130, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION: Martin J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Cannon, Methods of TITLE OF INVENTION: Methods CITLE CITLE OF INVENTION: Methods CITLE CITLE OF INVENTION: Methods CITLE CITLE OF INVENTION: MARKER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; FRIOR APPLICATION NUMBER: US 09/918,243
; FRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 130
; LENGTH: 9
                                                                                                                                                                                                     APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santih, Abessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
FILE REFERENCE: D6223CIP/C/D/CIP2
CURRENT APPLICATION NUMBER: US/10/372,521
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/918,243
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-10-372-521-99
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; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-10-372-521-130
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100.0%; Score 42; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0;
  0; Mismatches
  9; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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                                             1 QRIKASKSF 9
                                                                                       1 ORIKASKSF 9
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US-10-372-521-130
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US-10-372-521-99
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; Sequence 4, Application US/09796294; Patent No. US20020037581A1
                                                                                                                                                                                                                                                      Zerhusen, Bryan D.
Anderson, David W.
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Catterton, Elina
Peyman, John A.
Kekuda, Ramesh
                                                                                                                                                                                                                                    Gorman, Linda
                                 Ju, Jingfang
Li, Li
                                                                                                                                                                                                                Ort, Tatiana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 ORIKASKSF 80
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US-09-796-294-4
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                      Sequence 99, Application US/10831075

Publication No. US20040224891A1

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: Cannon, Martin J.

APPLICANT: Cannon, Martin J.

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

FILE REFERENCE: D6223CFP/C/D/CIP3

CURRENT APPLICATION NUMBER: US/10/831,075

CURRENT APPLICATION NUMBER: US 10/372,521

PRIOR APPLICATION NUMBER: US 10/372,521

PRIOR APPLICATION OF 3003-02-21

NUMBER OF SEQ ID NOS: 140

LENGTH. 0

LENGTH. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 130, Application US/10831075

Publication No. US20040224891A1

GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
FILE REFERENCE: D6223CIP/C/D/CIP3
CURRENT APPLICATION NUMBER: US/10/831,075
CURRENT FILING DATE: 2004-04-23
PRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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100.0%; Score 42; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KRY: CHAIN
OTHER INFORMATION: Residues 91-99 of the SCCE protein US-10-831-075-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , NAME/KEY: CHAIN
, OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-10-831-075-130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 100, Application US/10262511; Publication No. US20040038223A1; GENERAL INFORMATION: APPLICANT: Smithson, Glennda; APPLICANT: Millet, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ORIKASKSF 9
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               -10-831-075-99
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APPLICANT: Shinkets, Richard.
APPLICANT: Shinkets, Nichard.
APPLICANT: Shinkets, Nichard.
APPLICANT: Leach, Martin D.
APPLICANT: Age, Michael L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462.
CURRENT APPLICATION NUMBER: 00/30-6483
PRIOR APPLICATION NUMBER: 00/313,815
PRIOR APPLICATION NUMBER: 60/313,815
PRIOR APPLICATION NUMBER: 60/313,612
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2002-10-09
PRIOR PILING DATE: 2002-10-09
PRIOR PILING DATE: 2002-10-09
PRIOR PILING DATE: 2002-10-09
PRIOR PILING DATE: 2002-04-17
PRIOR PRILING DATE: 2002-04-17
PRIOR PILING PAPLICATION NUMBER: 60/327,435
PRIOR PILING PAPLICATION NUMBER: 60/327,435
PRIOR PILING PAPLICATION NUMBER: 60/327,435
PRIOR PILING PAPLICATION NUMBER: 60/327,435
PRIOR PILING PAPLICATION NUMBER: 60/327,435
PRIOR PILING PAPLICATION NUMBER: 60/327,435
PRIOR PILING PAPLICATION NUMBER: 60/
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100.0%; Score 42; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 9; Conservative 0; Mismatches 0; Indels
Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ji, Weizhen
Miller, Charles B.
Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
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APPLICANT: SININGES, MACKER
APPLICANT: Rothenberg, Mark B.
APPLICANT: Rechenberg, Mark B.
APPLICANT: Apellolum Berghs, Constance
ITILE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
FILE REPERENCE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/336,483
PRIOR PILING DATE: 2001-10-02
PRIOR PILING DATE: 2001-10-03
PRIOR PILING DATE: 2001-10-09
PRIOR PLING DATE: 2002-04-17
PRIOR PLING DATE: 2002-05-17
PRIOR PLING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR PLING DATE: 2002-05-16
PRIOR PLING DATE: 2002-05-16
PRIOR PLING DATE: 2002-05-16
PRIOR PLING DATE: 2002-06-17
PRIOR PLING DATE: 2002-06-17
PRIOR PLING DATE: 2002-06-17
PRIOR PLING DATE: 2002-04-17
PRIOR PLING DATE: 2000-04-17
PRIOR PLING DATE: 2000-0
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                                                      Xiaojia (Sasha)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shimkets, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                          Miler, Charles E. Rastelli, Luca Stone, David J. Pena, Carol E. A. Shenoy, Suresh G.
                                                                                      Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
                                                                                                                                                                                   Ellerman, Karen
Malyankar, Uriel M.
                                                                                                                                                                                                                                                                                                Zerhusen, Bryan D.
Anderson, David W.
Zhong, Mei
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                                                                                                                                                                                                                                                                             Gorman, Linda
Jingfang
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Best Local Similarity
Matches 9; Conserv
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US-10-262-511-96
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; Sequence 4, Application US/10461787
; Publication No. US20030199010A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; FILE REFREEMENCE: D6020CIP2
; FILE REFREEMENCE: D6020CIP2
; CURRENT APPLICATION NUMBER: US/10/461,787
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US/09/618,259
; PRIOR PILING DATE: 2000-07-18
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 4
; LENGTH: 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: DOMAIN
OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
OTHER INFORMATION: enzyme (scce) catalytic domain
US-09-796-294-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: DOMAIN
OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
OTHER INFORMATION: enzyme (scce) catalytic domain
US-10-461-787-4
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100.0%; Score 42; DB 4; Length 144;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 42; DB 3; Length 144; Best Local Similarity 100.0%; Pred. No. 1.1; Matches 9; Conservative 0; Mismatches 0; Indels
                                      APPLICANT: Underwood Lowell J.
TITLE OF INVENTION: Extracellular Serine Protease
FILE REFERENCE: D6020CIP3
CURRENT APPLICATION NUMBER: US/09/796,294
CURRENT FILING DATE: 2001-02-28
PRIOR PILING DATE: 2000-07-18
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 4
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US-10-262-511-98
Sequence 98, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Reyman, John A.
APPLICANT: Rekuda, Ramesh
                            APPLICANT: O'Brien, Timothy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||||||||||
28 QRIKASKSF 36
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          LENGTH: 144
TYPE: PRT
ORGANISM: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: unknown
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Gaps

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Indels

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Publication No. US20040241646A1
GENERAL INFORMATION:
GENERAL INFORMATION:
COLDITTS, TRACEY L.
FRIEDMAN, PAULA N.
GRANADOS, EDWARD N.
KLASS, MICHAEL R.
KUSSELL, JOHN C.
STEWART, KENT D.
STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERIE PROTEASE REAGENTS
OF THE PROSTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: A...
STATE: 1...
STATE: 1...
STATE: 1...
COMPUTE: 1...
COMPUTE: 1...
COMPUTE: E0064-3500
COMPUTE: EACHSELE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1...
COMPUTE: 1...

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 104, Application US/10262511
Fublication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Rewman, John A.
APPLICANT: Rekuda, Ramesh
APPLICANT: Ju, Jingfang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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APPLICANT: AGE, MICHELE L.
APPLICANT: AGE, MICHELE L.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
THE REPREBRENCE: 21402-462C
CURRENT APPLICATION NUMBER: 60/326,483
FRICA FILING DATE: 2001-10-03
FRICA FILING DATE: 2001-10-09
FRICA FILING DATE: 2001-10-09
FRICA FILING DATE: 2002-04-19
FRICA FILING DATE: 2002-05-07
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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Malyankar, Uriel M.
Ort, Tatiana
Gorman, Linda
Zerhusen, Bryan D.
Anderson, David W.
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Rothenberg, Mark E.
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Miller, Charles E.
Rastelli, Luca
Stone, David J.
       Millet, Isabelle
Peyman, John A.
Kekuda, Ramesh
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Agee, Michele L.
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Best Local Similarity 100.
Matches 9; Conservative
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Li, Li
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Ju, Jingfang Li, Li Guo, Xiaojia (Sasha) Patturajan, Meera

APPLICANT:

; Sequence 33, Application US/09789210

RESULT 14 US-09-789-210-33

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APPLICANT: Bildrag: Shilamit A.
APPLICANT: Bildrag: Shilamit R.
APPLICANT: Bildrag: Shilamit R.
APPLICANT: Bildrag: Shilamit R.
APPLICANT: Ocenani, Linda
APPLICANT: Ocenani, Linda
APPLICANT: Cachusen, Baryan D.
APPLICANT: Andaraon, David W.
APPLICANT: Andaraon, David W.
APPLICANT: Shong, Weiler
APPLICANT: Shong, Weiler
APPLICANT: Shong, Weiler
APPLICANT: Shinketo, Richard A.
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Search completed: March 11, 2006, 01:37:26 Job time : 70.4444 8ecs

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US-10-412-748-19
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LENGTH: 253
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111, Appl
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117, Appl
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12604, Ap
1604, Ap
1605, Ap
6766, Ap
6766, Ap
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12111, Ap
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15474, A
15473, A
2242, Ap
8245, Ap
                                                                                                                     March 11, 2006, 01:27:17; Search time 8 Seconds (without alignments) 31.314 Million cell updates/sec
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8: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-412-748-11

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US-11-037-43-98

US-11-096-568A-5481

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US-11-097-099-11190

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US-11-096-568A-15475

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US-11-087-099-2242
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Match
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Perfect score:
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Sequence 78, Appl
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Sequence 462, Appl
Sequence 68, Appl
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Sequence 21357, A
Sequence 25357, A
Sequence 374, Appl
Sequence 1626, Appl
Sequence 1626, Appl
Sequence 11, Appl
Sequence 29804, Appl
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US-10-131-826A-374
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US-11-096-568A-29803
US-11-096-568A-29803
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100.0%; Score 42; DB 6; Length 181; 100.0%; Pred. No. 0.044; tive 0; Mismatches 0; Indels
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; Sequence 19, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOUTHWARE: Patentin version 3.2
; SEQ ID NO 18
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Sequence 11, Application US/10412748
Sequence 11, Application US/10412748
Sequence 11, Application US-10-412-748-11
GENERAL INFORMATION:
APPLICANT: Queensland University of Technology
APPLICANT: Clements, Judith A
TITLE OF INVENTION: Aberrant Kallikrein Expression
FILE REFERENCE: DAVI172.003AUS
CURRENT PAPLICATION NUMBER: US/10/412,748
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: AU PS1616/02
PRIOR FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
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Sequence 17, Application US/10412748
Sequence 17, Application US/10412748
Sequence 17, Application US/10412748
Sequence 17, Application US/10412748
Sequence 17, Application US/10412131
APPLICANT: Clements, Judith A
TITLE OF INVENTION: Aberrant Kallikrein Expression
FILE REFERENCE: DAVI12.003AUS
CURRENT APPLICATION NUMBER: US/10/412,748
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: AU PS1616/02
PRIOR FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
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Sequence 14, Application US/10412748

Publication No. US20060035219A1

GENERAL INFORMATION:

APPLICANT: Clementa, Undith A

TITLE OF INTERNICE: DAVI12. 003AUS

FILE REFERRICE: DAVI12. 003AUS

CURRENT FILING DATE: 2003-04-09

PRIOR APPLICATION NUMBER: US/10/412,748

CURRENT FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: AD PS1616/02

PRIOR FILING DATE: 2002-04-09

NUMBER OF SEC ID NOS: 41

SOFTWARE: PatentIn version 3.2
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Human
US-10-412-748-17
, ORGANISM: Human
US-10-412-748-11
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LENGTH: 253
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91 ORIKASKSF 99

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RESULT 5

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Sequence 5482, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
TITLE OF INVENTION:
THE REPERBORE: 2050-1892PHO.
CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 5482

LENGTH: 352

LENGTH: 352
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| LOCATION: (1) ... (352)
| OTHER INDEMATION: Ceres Seq. ID no. 14310397
| US-11-096-568A-5482
                                                                                          APPLICANT: ELCUMPLAY. CALCALL
APPLICANT: WHYTE, DAVID
APPLICANT: CHARYDEEL, SEAN
APPLICANT: CHARYDEZK, GLEN
APPLICANT: CHARYDEZK, GLEN
APPLICANT: BANNING, GERARD
APPLICANT: BUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/10/09/888,615
PRIOR APPLICATION NUMBER: 05/09/888,615
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-26
SOFTWARE: PARENTIN VORT: 2.1
SEQ ID NO 98
LENGTHING SACTORY
LENGTHING DATE: 2000-06-26
INUMBER OF SEQ ID NOS: 150
SOFTWARE: PARENTIN Ver. 2.1
LENGTHING DATE: 2000-06-26
INUMBER OF SEQ ID NOS: 150
SOFTWARE: PARENTIN VEY. 2.1
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; Publication No. US20060048240A1
; GENERAL INFORMATION:
Sequence 98, Application US/11037243
Publication No. US20050287546A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
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Best Local Similarity 55.6
Matches 5; Conservative
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176 QRLKASRAY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-11-037-243-98
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ORGANISM: Glycine max
FEATURE:
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Best Local Similarity
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US-11-096-568A-5482
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Sequence 1604, Application US/11051720
Publication No. US20060046257A1
ABDERAL INFORMATION:
TITLE OF INVENTION: THERBOF FOR DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 1847-11002
CURRENT APPLICATION NUMBER: US/11/051,720
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 1780
SEQ ID NO 1664
LENGTH: 726
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GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL INFORMATION:
TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: UNMER: US/11/051,720
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 1780
SEQ ID NO 1605
LENGTH: 747
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Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KINMERLY,
ITILE OF INVENTION: STAPHYLOCCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPREBLICE:
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
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Pred. No. 93;
2; Mismatches 0; Indels
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           Pred. No. 34;
2; Mismatches
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75.0%;
           66.78;
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Best Local Similarity 75.0.
                          6; Conservative
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                                                                                     237 QRLKSSLSF 245
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US-11-051-720-1604
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148 QKIKASRS 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-11-051-720-1605
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148 QKIKASRS 155
                                                              1 QRIKASKSF 9
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       Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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US-10-793-626-2424
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Sequence 5480, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

TITLE PEFERENCE: 2750-1522PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT PILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 5480
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                                                                                                                                                                                                                                                                               Length 356;
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Publication No. US20060041961A1
GENERAL INPORMATION:
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FIRE REPERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT PILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 3123
LENGTH: 299
                                                                                                                                                                                                                                                                               Score 31; DB 7;
Pred. No. 25;
4; Mismatches
                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (1) (356)
OTHER INFORMATION: Ceres Seq. ID no. 14310396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature
; LOCATION: (1)..(386)
; OTHER INFORMATION: Ceres Seq. ID no. 14310395
US-11-096-5688-5480
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
LENGTH: 356
                                                                                                                                                                                                                                                                             73.8%;
55.6%;
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55.6%;
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Matches 5; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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180 QRLKASRAY 188
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210 QRLKASRAY 218
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                                                                                                                                  TYPE: PRT
ORGANISM: Glycine max
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ORGANISM: Glycine max
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Search completed: March 11, 2006, 01:38:44 Job time : 9 secs
                                    Query Match
Best Local Similarity 55.6%;
Matches 5; Conservative '
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Best Local Similarity 85.7%;
Matches 6; Conservative
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21 KRLRASESF 29
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ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                  1 ORIKASKSF 9
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US-11-096-568A-6766

i Sequence 6766, Application US/11096568A

j Publication No. US20060048240A1

j Publication No. US20060048240A1

j APPLICANT: Alexandrov, Nickolai et al.

i TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

i TITLE OF INVENTION: Therby

i TITLE OF INVENTION: Therby

i TITLE OF INVENTION: Therby

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| Sequence 20947, Application US/11096568A
| Publication No. US20060048240A1
| SEMINICANT: Alexandrov, Nickolai et al.
| APPLICANT: Alexandrov, Nickolai et al.
| TITLE OF INVENTION: Therby
| TITLE OF INVENTION: Therby
| FILE REFERENCE: 2750-1522PUS2
| CURRENT APPLICATION NUMBER: US/11/096,568A
| CURRENT PILING DATE: 2005-04-01
| NUMBER OF SEQ ID NOS: 34471
| SEQ ID NO 20947
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                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: amino acid sequence
US-10-793-626-2424
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; LOCATION: (1). (294)
; OTHER INFORMATION: Ceres Seq. ID no. 12391401
US-11-096-568A-20947
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i LOCATION: (1)..(277)
cother information: Ceres Seq. ID no. 14316538
US-11-096-568A-6766
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ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                    69.0%;
55.6%;
                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2424
LENGTH: 203
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 55.6'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QRIKASKSF 9
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69 IRASKSF 75
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US-11-096-568A-20947
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RESULT 15
US-11-096-568A-6765
US-11-096-568A-6765
Sequence 6765, Application US/11096568A
Sequence 6765, Application No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I:
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
SEQ ID NOS: 34471
LENGTH: 296
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  DB 7; Length 294; 56;
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Pred. No. 56;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
i LOCATION: (1)..(296)
i LOCATION: (1)..(296)
US-11-096-568A-6765
                                             4; Mismatches
Score 29;
Pred. No. 5
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